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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*



## NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

### 2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, 5 diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1786 and 3573-5358. The polypeptides sequences are designated SEQ ID NO: 2n (wherein n = 1 to 20). The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in 10 the Sequence Listing, \* corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1786 and 3573-5358 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a 15 specific domain or truncation of the peptides encoded by SEQ ID NO:1-1786 and 3573-5358. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1786 and 3573-5358 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information 20 from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1786 and 3573-5358.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on 25 a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid 30 sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1786 and 3573-5358; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-1786 and 3573-5358. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1786 and 3573-5358; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

5 The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the  
10 protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA  
15 or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as  
20 expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide  
25 of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition  
30 which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein  
35 expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides  
5 a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the  
10 invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal  
15 antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate  
20 (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a  
25 compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is  
30 identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that  
35 modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

#### 4. DETAILED DESCRIPTION OF THE INVENTION

##### 4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1786 and 3573-5358. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because  $4^{20}$  possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ( $1/4^{25}$ ) times the increased probability for mismatch at each nucleotide position ( $3 \times 25$ ). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.



The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur  
5 in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing  
10 the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon  
15 substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain  
20 affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, i.e., conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic  
25 nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or  
30 "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or  
35 non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited  
5 for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological  
10 macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or  
20 polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial"  
25 defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3)  
35 appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55).

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

5 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about  
10 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a  
15 listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid  
20 sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most  
25 preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun  
30 Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the  
35 DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The

term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

## 4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 ; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1787-3572 and 5359-7144; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1787-3572 and 5359-7144. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1786 and 3573-5358 ; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:1787-3572 and 5359-7144. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

5       The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can  
10   be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 may be used as the  
15   basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

      The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information,  
20   representative fragment or segment information, or novel segment information for the full-length gene.

      The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about  
25   75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

      Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358, or complements thereof, which fragment is greater than  
30   about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1786 and 3573-5358, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1786 and 3573-5358 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1786 and 3573-5358, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*,



hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid  
5 insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and  
10 sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the  
15 site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids.  
20 When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this  
25 gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic  
30 code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

5 The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

10 In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1786 and 3573-5358, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

15 A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the  
20 invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular  
25 organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into  
30 which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially  
35 available for generating the recombinant constructs of the present invention. The following

vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

- 5       The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in*  
10 *Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

- Promoter regions can be selected from any desired gene using CAT (chloramphenicol  
15 transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.
- 20       Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid  
25 phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired  
30 characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the  
35 vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for

transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### 4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:1787-3572 and 5359-7144 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1786 and 3573-5358 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a

5 "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO:1-1786 and 3573-5358), antisense nucleic acids of the invention can be designed according

10 to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10,

15 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the

20 physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-

25 2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil,

30 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a

35 nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the

inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO:1-1786 and 3573-5358). For example, a derivative of a Tetrahymena L-19 IVS RNA can be

constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA

portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express



the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

10 The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the  
15 polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell,  
20 COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using  
25 RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant  
30 protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived  
35 from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, 5 SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. 10 Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast 15 or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it 20 may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of 25 inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, 30 negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the

protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1787-3572 and 5359-7144 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358 or (b) polynucleotides encoding any one of the amino acid sequences

set forth as SEQ ID NO:1787-3572 and 5359-7144 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1787-3572 and 5359-7144 or the corresponding  
5 full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides  
10 comprising SEQ ID NO:1787-3572 and 5359-7144.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer.*  
15 *Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding  
20 sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also  
25 provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid  
30 fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

5 The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either  
10 cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1787-3572 and 5359-7144.

15 The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or  
20 deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the  
25 molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved  
30 systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to  
35 retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing  
5 an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present  
10 invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification  
15 of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will  
20 facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen,  
25 respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other  
30 aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

#### 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

#### 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to



another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein. In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked  
5 in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal  
10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example,  
15 Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or  
20 artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease  
25 states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be  
30 inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the  
5 property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial  
10 xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436  
15 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or  
20 inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be  
25 prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT  
30 Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even  
35 replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

#### 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or

5 polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

10 indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation

15 or in one of the other physiological pathways described herein.

#### 4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

20 protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

25 disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

30 an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of

35 the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its  
5 receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

10 Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch  
15 and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional  
20 sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the  
25 polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

30 A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one  
35 or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

- 5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in  
 10 Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *I. Immunol.* 149:3778-3783, 1992; Bowman et al., *I. Immunol.* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,  
 15 Kruisbeek, A. M. and Shevach, E. M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- $\gamma$ , Schreiber, R. D. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells  
 20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse  
 25 and human interleukin 6--Nordan, R. In *Current Protocols in Immunology*. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In *Current Protocols in Immunology*. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin  
 30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In *Current Protocols in Immunology*. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in*  
 35 *Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober,



Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

*In vitro* cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

#### 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al.,  
5 Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21,  
10 Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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#### 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

20 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of  
25 artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of  
30 bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5 A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

10 Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

15 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### 20 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including  
25 severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be  
30 treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention  
35 include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.



Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

10 A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and  $\beta_2$  microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J.

Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production,

- 5 Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E.

- 10 M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al., J. Immunol. 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by  
15 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of  
20 Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry  
25 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development  
30 include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

#### 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 5        Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al. Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

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#### 4.10.10        HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including 20 hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

- 25        Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

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#### 4.10.11        CANCER DIAGNOSIS AND THERAPY

- Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For 35 example, the presence or increased expression of a polynucleotide/polypeptide of the invention

may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

5 Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic  
10 cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps  
15 associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central  
20 nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be  
25 administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

30 The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination  
35 with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, 5 Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, 10 Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically 15 effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

*In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), 20 tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., 25 Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

#### 4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, 30 receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, 35 integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

#### 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding



molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

5           **4.10.14           ASSAY FOR RECEPTOR ACTIVITY**

          The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used  
10   to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention.  
15   Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligand(s) are then compared. Alternatively, an expression library can be co-expressed with the  
20   polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.  
25   The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating  
30   the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

**4.10.15           ANTI-INFLAMMATORY ACTIVITY**

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

#### 4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

#### 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or

disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral

5 nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system  
10 results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease,  
15 tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous  
35 system disorder may be selected by testing for biological activity in promoting the survival or

differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- 5 (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by  
15 assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as  
20 well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy  
25 (Charcot-Marie-Tooth Disease).

#### 4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents,  
30 including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female  
35 subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain  
5 reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen  
10 in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such  
15 polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a  
20 polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally  
25 involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a  
30 single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the  
35 present invention can be used to detect polymorphisms. The array can comprise modified

nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could  
5 also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

#### 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid  
10 arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The  
15 route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the  
20 test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

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#### 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications  
30 include, but are not limited to, those exemplified herein.

##### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or  
35 disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

#### 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic



factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

5

#### 4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

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#### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

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manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding  
5 suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents  
10 may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be  
15 added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as  
20 lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of  
25 tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*,  
dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon-dioxide or  
30 other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for  
35 injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with

an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well

known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent.

5 Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

10 The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically  
15 acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

20 The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following  
25 presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as  
30 well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as  
35 micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated  
5 herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active  
10 ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the  
15 various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1  $\mu$ g to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition  
20 topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other  
25 active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or  
30 cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the  
35 compositions will define the appropriate formulation. Potential matrices for the compositions

may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential  
5 matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and  
10 biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

15 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,  
20 poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the  
25 protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and  
30 insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue  
35 regeneration will be determined by the attending physician considering various factors which

modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

#### 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the  $IC_{50}$  as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the  $LD_{50}$  (the dose lethal to 50% of the



population) and the  $ED_{50}$  (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between  $LD_{50}$  and  $ED_{50}$ . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the  $ED_{50}$  with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01  $\mu\text{g/kg}$  to 100  $\text{mg/kg}$  of body weight daily, with the preferred dose being about 0.1  $\mu\text{g/kg}$  to 25  $\text{mg/kg}$  of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

#### 4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

#### 4.13 ANTIBODIES

5 Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F<sub>ab</sub>, F<sub>ab</sub>' and F<sub>(ab)2</sub> fragments, and an F<sub>ab</sub> expression library. In general, an antibody molecule obtained from 10 humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG<sub>1</sub>, IgG<sub>2</sub>, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, 15 subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the 20 invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 1787, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. 25 Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the 30 antigenic peptide is a region of related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity 35 may be generated by any method well known in the art, including, for example, the Kyte

Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety.

Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

### 5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5

### 5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MABs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

### 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

### 5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

5 In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon  
10 challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature  
15 Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The  
20 endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate  
25 transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a  
30 polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker, and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

#### 5.13.4 $F_{ab}$ Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotype to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_v$  fragments.

#### 5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the



binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular

defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest  
5 binds the protein antigen described herein and further binds tissue factor (TF).

#### 5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention.

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies  
10 have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond.  
15 Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as  
20 to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992)  
25 and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).  
30

#### 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a  
35 radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

#### 4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

5 A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer  
10 readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded  
15 thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer  
20 software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may  
25 be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the  
30 present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored  
35 therein a nucleotide sequence of the present invention and the necessary hardware means and

software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

5       As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially  
10       available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present  
15       computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide  
20       residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a  
25       three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

30

#### 4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.  
35       Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are

designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

10

#### 4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

15

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

20

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

25

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

30

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid

35

probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

#### 4.17 MEDICAL IMAGING



The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of  
5 a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

#### 4.18 SCREENING ASSAYS

10 Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- 15 (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and  
(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of  
20 the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the  
25 invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time  
30 sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the  
35 activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

5 Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

#### 10 4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358. Because the corresponding gene is only  
15 expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides  
20 additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the  
25 cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The  
30 nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) *Human Chromosomes: A Manual of Basic Techniques*, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

#### 10 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) *J. Clin. Microbiol.* 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) *Mol. Cell Probes* 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. Covalink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. Covalink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to Covalink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) *Nucleic Acids Res.* 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) *Anal. Biochem.* 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the  
5 light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile  
10 combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

#### 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA,  
15 including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples  
20 may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 µl of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

25 Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA  
30 fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*II, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI*\*\*), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

#### 4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm<sup>2</sup>, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid  
5 being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations  
10 may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and  
15 variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

## 20 5.0 EXAMPLES

### 5.1.1 EXAMPLE 1

#### Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome  
25 using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

30 In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.



### 5.1.2 EXAMPLE 2

#### Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 3573-5358 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend  
5 the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage  
10 with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:3573-5358 as set forth below. The polypeptides was predicted using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98  
15 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

### 5.2.2 EXAMPLE 3

#### Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame  
20 shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank. Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1- 327.

25 Table 1 shows the various tissue sources of SEQ ID NO: 1-327.

The nearest neighbor results for SEQ ID NO: 1-327 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-327 from Genpept. The translated amino acid  
30 sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1-327 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the

signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were  
5 examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from  
10 Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by  
15 reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

#### 5.3.2 EXAMPLE 4

##### 20 Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117,  
25 UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 328-1413.

Table 1 shows the various tissue sources of SEQ ID NO: 328-1413.

30 The nearest neighbor results for SEQ ID NO: 328-1413 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 328-1413 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in

the Sequence Listing. The nearest neighbor results for SEQ ID NO: 328-1413 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were  
5 examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were  
10 examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from  
15 Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by  
20 reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

### 25 5.3.2 EXAMPLE 5

#### Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was  
30 checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1414-1652.

Table 1 shows the various tissue sources of SEQ ID NO: 1414-1652.

The nearest neighbor results for SEQ ID NO: 1414-1652 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1414-1652 from  
5 Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1414-1652 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were  
10 examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were  
15 examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from  
20 Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by  
25 reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

#### 5.4.2 EXAMPLE 6

##### 30 Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118,

UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1653-1745.

5 Table 1 shows the various tissue sources of SEQ ID NO: 1653-1745.

The homology for SEQ ID NO: 1653-1745 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 118, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1653-1745 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues  
10 with identifiable functions for SEQ ID NO: 1653-1745 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature,  
15 the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain  
20 within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also  
25 disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in  
30 each of the polypeptides and the maximum score and mean score associated with that signal peptide.

## 5.5.2 EXAMPLE 7

### Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 119, gb pri 119, UniGene version 119, Genpept release 119). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1746-1768.

Table 1 shows the various tissue sources of SEQ ID NO: 1746-1768.

The homology for SEQ ID NO: 1746-1768 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 119, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1746-1768 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1746-1768 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the PFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

## 5.6.2 EXAMPLE 8

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genpept release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1769-1786.

Table 1 shows the various tissue sources of SEQ ID NO: 1769-1786.

The homology for SEQ ID NO: 1769-1786 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1769-1786 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1769-1786 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by

reference. A maximum S score and a mean S score, as described in the Nielson et al reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5           Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.



TABLE 1

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS:  |
|---------------|------------|--------------------|--|
| adult brain   | GIBCO      | AB3001             | 9 19-21 50-51 65-66 72 78 80 82<br>85 87 107-108 113 116 123 138<br>140 150-152 159 169 177 192-193<br>202-203 212-214 225-226 235-236<br>251 258 268-269 272 280-281 295<br>298 301 321 326 331-332 334 356-<br>357 362 369 379 382-383 416 423<br>443 459-460 473 475 477 488 496<br>500 503 519 526 547 574 582 587<br>608-609 613 618 633-634 645-646<br>652 657-658 660 669-671 678 687<br>695 697 710 715 724 731 775-777<br>796 804 811 857-859 862 869 899-<br>900 912 919 922 924-929 933 936<br>962 979 988-989 996 1001 1004-<br>1008 1018 1039 1047 1059 1064<br>1067 1070 1078 1082 1107 1113<br>1116-1117 1131 1134-1137 1140<br>1149 1151 1157 1180 1206 1229<br>1234 1241 1243 1258 1272-1273<br>1279 1288-1290 1294 1307-1308<br>1312 1320 1323 1330 1356 1360-<br>1361 1368 1373-1375 1379 1391<br>1400 1417 1446 1468 1482 1493-<br>1494 1501-1503 1506-1507 1512<br>1517 1522-1524 1530-1533 1537<br>1549 1565 1578 1598 1606 1608<br>1623 1625 1627 1639 1643 1648-<br>1649 1653 1664 1667 1671 1696<br>1734 1741 1743-1744 1760-1761<br>1771   |
| adult brain   | GIBCO      | ABD003             | 3 12-14 18-19 25 30-31 34-36 43-<br>45 50-51 56 58 60 65-66 68-69 80<br>82 85 87 92 104 107-108 112-113<br>115-116 123-124 131-132 135-137<br>139 142 146 148-149 152 154 157<br>159 163 165 167 169 172 180 192-<br>193 196-197 199 203 208 210 212-<br>214 223 233 235-237 247 257 259<br>261 268-269 272 276 280-281 284-<br>288 291-292 295 297 300-301 304<br>307 317 320-321 323 327 329-331<br>333-334 345-349 356-357 379-381<br>393 401 408 414 419 424 426-428<br>430 433-436 438-439 443 445 449<br>453-454 459-461 468 471-473 476-<br>478 483 491 494 496 500 503 507-<br>508 516 519-520 525-527 534 536-<br>540 542-543 545 553 555 560 569-<br>570 574-576 586-588 593 595 597<br>601 606-609 615-620 622-623 625<br>628-633 635-636 643 645-649 653<br>655-656 660-665 668-670 676 681<br>687 701 710 715 717 724-728 735<br>743 745-746 750 753 759 765-766<br>773 775-778 786 789 796 799-800<br>802-803 810-811 815 817 820-821<br>832 834-836 840 845-847 851 858-<br>861 864 869 874 878 883 897 901-<br>902 904-905 908 911-914 916 921-<br>922 924-927 929 932-934 936-939<br>941-942 945 955-958 963 966-969<br>977 979-980 985-986 990 992-993<br>997-1001 1005-1007 1012 1017-<br>1020 1023-1024 1029-1031 1034<br>1036 1039 1050 1059 1063-1066<br>1078 1081-1082 1085-1086 1089 |

| Tissue Origin | RNA Source | Hyseq<br>Library Name | SEQ ID NOS:  |
|---------------|------------|-----------------------|--|
|               |            |                       | 1097 1103 1107 1109 1112 1116-<br>1117 1119 1121 1124 1127 1130<br>1134 1144-1145 1149 1151 1157-<br>1158 1167 1170 1178 1184 1188<br>1190 1193-1194 1200 1202 1215-<br>1217 1220 1226-1227 1229 1231<br>1241 1243 1247 1252 1258 1263<br>1267 1269 1279 1281 1284 1286-<br>1289 1293-1294 1306-1307 1312<br>1316-1320 1326 1333 1338 1341<br>1344 1348 1351 1355-1357 1368<br>1374 1377 1380 1386 1389-1390<br>1394 1400 1409 1414 1422-1423<br>1425-1427 1437 1443 1446 1454<br>1456 1458-1459 1468 1470-1472<br>1478 1482-1483 1487-1488 1493<br>1497 1499 1506 1508-1511 1517<br>1522-1524 1530-1533 1545-1546<br>1548-1550 1552 1557-1559-1563<br>1565 1567 1569 1571 1586 1588<br>1591 1593 1595 1598-1601 1608<br>1611 1620-1621 1624-1626 1628<br>1630-1632 1636 1640-1641 1644-<br>1645 1647 1649 1653-1655 1657<br>1664 1667 1669 1673 1678-1681<br>1686 1690 1694-1696 1701 1709<br>1711 1719 1722-1723 1726-1727<br>1731-1733 1738 1740 1743-1744<br>1747 1749 1753 1757-1758 1760-<br>1761 1765 1771 1785 |
| adult brain   | Clontech   | ABR001                | 9 29 68-69 113 115 146 152 206<br>223 245 277 307 320 324 330-331<br>344 348 352 362 379 384 393 404<br>408 414 441-442 454 469 481 490<br>506 517 586 597 631 641 659 691<br>715 799 803 833 865 871 875 880<br>882 908 920 937 1000 1005-1006<br>1027 1036 1041 1043 1075 1107<br>1112 1121 1127 1136-1137 1144-<br>1147 1231 1238-1239 1280 1293<br>1320 1345 1355 1361 1383-1384<br>1400 1417 1448 1456 1476 1507<br>1570 1572 1609-1610 1614 1620<br>1626 1645 1653 1754 1759 1770<br>1786  |
| adult brain   | Clontech   | ABR006                | 5-8 15-16 168 212-213 271 278<br>280-281 291-292 300-301 310 314<br>321 326 336-338 341 352 357 359-<br>360 362 369 374 379 384 393 396-<br>397 414 419-420 426-428 430 441-<br>442 453 506 616-617 661 689 785<br>798 845 1018 1109 1113 1124 1148<br>1167 1187 1207 1227 1252 1265<br>1285 1312 1317-1319 1324-1327<br>1344 1369 1381 1400 1416 1421<br>1427 1430-1431 1436 1471 1501<br>1557-1559 1586 1588 1651 1653<br>1664-1665 1671 1673 1690 1697-<br>1698 1700 1711 1717 1719-1720<br>1728 1736 1740 1743-1744 1757<br>1760-1761  |
| adult brain   | Clontech   | ABR008                | 5-10 13-19 22-23 25 29 33 37-39<br>43-45 50-51 54-55 57-58 60-66<br>68-70 72 75 77-80 83 85 89-92 94<br>99-105 108-110 112-113 116-117<br>123 128 133 135-137 139 143 145-<br>146 148 152 154-155 157 166 168-<br>172 174-175 181-184 188-190 193-<br>194 196 198-200 202 204-205 207-   |

| Tissue Origin | RNA Source | Hyseq<br>Library Name | SEQ ID NOS:  |
|---------------|------------|-----------------------|--|
|               |            |                       | 208 210 214-215 218 221-226 229<br>231-232 234-241 245-247 251-253<br>255 257-259 268-269 271 276-281<br>285-286 288 290-292 300-302 304<br>307 309-311 313 315 317-318 320-<br>322 325-326 328 330-331 333-338<br>341 344-347 349 352 354 356-357<br>362 369-373 376 379-380 382 384<br>387 390-391 393-394 397 399-403<br>405-411 414-415 417-420 426-428<br>437-438 440-444 453-455 462 464<br>467 469-471 476 478 482-484 488-<br>491 497 503 506-513 516-517 520<br>524-526 528-530 532-534 537-540<br>542 544 547-551 553 561 565-567<br>572-574 577 581 585 587-588 590-<br>591 597 599 601-602 606-610 612<br>615-617 619-620 622-623 628-629<br>631 633-634 636-641 643 645-647<br>651-653 655-664 669-671 673 679<br>682 687 689 691-700 702 706 710<br>715-717 720-721 725-734 736-739<br>742-743 746 750-752 756 758-759<br>762-764 766 768 773-778 780-782<br>784-785 787-789 794 796 799 802-<br>803 805 811 814-815 818 825-826<br>834-837 839-840 842-843 856-859<br>861-862 865 867-872 874-875 881<br>883-884 887 889-892 894-895 897-<br>898 901 904 908 910 912 914 917<br>919 921-924 926-927 930-932 935-<br>941 943 945 949 953-954 958 961-<br>963 967 969 971 975 977 981-983<br>986 988-990 992 997 999-1002<br>1004-1006 1008 1012 1018-1023<br>1027 1029-1031 1035-1037 1047-<br>1048 1053 1057 1059 1063 1068<br>1070 1072-1075 1077 1081-1083<br>1085-1093 1095-1096 1108-1112<br>1114-1125 1127 1131-1133 1135-<br>1138 1142-1145 1148-1158 1160-<br>1163 1167 1169 1172 1175 1177<br>1180 1183-1188 1191-1195 1199-<br>1200 1204 1206 1211 1213-1216<br>1222-1223 1226-1227 1229-1231<br>1234-1235 1241-1242 1244-1263<br>1266 1269-1271 1276-1277 1279-<br>1281 1284-1286 1292 1294-1295<br>1299 1305-1309 1312 1314 1316-<br>1319 1322 1324-1327 1330 1332<br>1334-1335 1339 1344-1346 1351<br>1354-1355 1357-1358 1365-1367<br>1369-1370 1373-1374 1376-1379<br>1381-1384 1386-1388 1392 1394<br>1396-1397 1400 1403-1407 1410<br>1414 1419-1420 1423 1432-1433<br>1435 1437-1438 1440-1442 1446<br>1448 1453-1455 1457 1461 1463-<br>1464 1466 1468 1471 1477 1480<br>1482-1483 1496 1502-1504 1507-<br>1509 1513 1519-1520 1524-1526<br>1536 1547 1549-1552 1567 1573-<br>1574 1578 1586-1589 1597-1598<br>1601-1602 1605 1607-1609 1611-<br>1617 1619-1621 1623 1625-1626<br>1635-1641 1643-1645 1649 1651<br>1653 1656-1658 1664 1669 1671-<br>1674 1676-1684 1686 1689-1690<br>1694-1696 1704-1705 1708-1709 |

| Tissue Origin             | RNA Source | Hyseq Library Name | SEQ ID NOS:   |
|---------------------------|------------|--------------------|---|
|                           |            |                    | 1720-1724 1726-1728 1730-1733<br>1737-1740 1742-1745 1753 1756-<br>1757 1759-1761 1765 1767 1771-<br>1772 1776-1777 1779-1780 1786  |
| adult brain               | Clontech   | ABR011             | 24 75 103 186 210 310-311 364-<br>365 508 623 710 937 1002-1003<br>1059 1204 1609 1731-1732   |
| adult brain               | BioChain   | ABR012             | 46 182-184 204-205 300 739 767<br>1371 1549 1620 1684   |
| adult brain               | Invitrogen | ABR013             | 185 204-205 364-365 393 497 595<br>687 692-694 830 845 1068 1320<br>1413 1640   |
| adult brain               | Invitrogen | ABR014             | 187 301 357 364-365 375 454 463<br>731 859 939 983 1073 1262 1270<br>1320 1403 1640 1651 1657 1696<br>1722 1738   |
| adult brain               | Invitrogen | ABR015             | 419 434-435 441-442 763 789 983<br>1320   |
| adult brain               | Invitrogen | ABR016             | 312 364-365 379 1320 1334-1335<br>1674 1722 1785  |
| adult brain               | Invitrogen | ABT004             | 14-16 22-23 25 37-39 43 58 60<br>70-72 78 86 94 107 113 116 136-<br>137 143-146 152 161 173 182-184<br>194 196 198 210 218 229 259 267<br>295 298 309-310 320-321 324 336-<br>338 346-347 349-350 356-357 362<br>371 379-380 382-383 391 393 396<br>399 401 408 428 438 459 461 476<br>482 490 502 507-509 516 526 531<br>557 562 597 602 607-609 624 652<br>655 667 669 671-672 687-689 695-<br>696 710 712 715 721 732 739 743<br>750 753 766 778 780-781 789 803<br>814 826 830 837 841 857 869 874<br>894-895 925 937 949 954-956 960-<br>961 963 968-969 988-989 1000<br>1005-1006 1016-1019 1021 1036-<br>1037 1052 1086 1090 1109 1113<br>1115 1120-1121 1123-1124 1136-<br>1137 1140 1144-1147 1151 1167<br>1170 1174 1188 1193-1194 1205<br>1225 1229 1231 1254 1258 1262<br>1280 1285 1309 1312 1334-1335<br>1341 1343-1344 1356-1357 1370<br>1378-1379 1383-1384 1403-1404<br>1423 1429 1434 1442 1448 1451-<br>1452 1454 1470-1472 1482 1499<br>1525 1528-1529 1532 1536 1547<br>1554 1557-1559 1561-1562 1567<br>1585 1588 1590 1595 1601-1604<br>1608 1610-1613 1615 1619 1624<br>1627 1640 1644 1647 1660 1664<br>1666 1670 1675 1696 1704 1715<br>1723 1727 1738 1760-1761 1768<br>1779 1785-1786 |
| cultured<br>preadipocytes | Stratagene | ADP001             | 5-8 11 17 25 68-69 80 82 87 103<br>105 110 116 136-138 168 171 188-<br>189 196-198 261 267 276 288 293<br>301 318 331 336-338 379-380 391<br>400 428 430-431 510-512 520 524<br>527 549 557 561 602 618 620 622<br>631 637 647 670 681-682 710 731<br>748 782 793-794 817 834-836 843<br>845 858-859 879 882 893-895 934<br>960 982 986 995-996 1000 1002<br>1005-1007 1025 1027-1028 1032<br>1039 1045 1071 1078 1097 1099-<br>1102 1136-1137 1140 1219-1220   |

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|               |            |                       | 1260 1271 1297-1298 1314 1320<br>1322 1329 1339 1345 1365-1366<br>1370-1371 1398 1408 1423 1431<br>1437 1466 1468 1533 1539 1594<br>1602 1608 1614 1631 1649-1650<br>1660 1662 1673 1687-1688 1696<br>1711 1719-1720 1742 1746 1749<br>1760-1761 1765 1767 1771 1785   |
| adrenal gland | Clontech   | ADR002                | 4-10 15-16 25 29-31 43-45 47 50-<br>51 55 60 62-63 65-66 75 80 102<br>116 118 122 126 130 137 150 169-<br>170 181 192 198 201-203 215 227-<br>228 247 251 255 267-269 271 280-<br>281 285 295 298 311 336-338 342<br>349 351-352 354 372-373 383-385<br>391 400 410 415-416 424 426-427<br>431 434-437 439 445 454 461 473<br>477 483 491 493 497-498 503 516<br>519 527 535 546 549 552 572-573<br>581 588 595 600 602 608-610 620<br>628-630 637 645-646 670 679 703<br>713 715 719 732 734 744-746 758<br>773-778 789 816 829 837 845 848<br>869 875 883 898 904 912 922-923<br>930-931 942 948 952 965 967 969<br>976-977 981 990 992-993 1001<br>1004 1049 1055 1059 1071-1072<br>1076 1112-1113 1115 1121 1127<br>1134-1135 1151 1158 1163 1175<br>1181 1188 1209 1218 1224-1225<br>1227 1231 1243 1270-1271 1274<br>1280 1285 1290 1293 1307 1324-<br>1325 1327 1330 1342-1343 1345<br>1348 1365-1366 1369 1378-1379<br>1387 1398 1400 1405 1417 1425-<br>1426 1436 1440-1441 1444 1454<br>1463-1464 1488 1491 1507 1512<br>1538 1546 1567 1573-1575 1588<br>1598 1609 1614 1618 1622 1624<br>1627 1634 1636 1649 1651 1658<br>1671 1674 1678-1679 1691-1692<br>1703 1717 1727 1731-1732 1737<br>1765 |
| adult heart   | GIBCO      | AHR001                | 4-8 10-11 15-16 18-21 34-39 44-<br>46 50-52 57-58 60 62-63 71 75 82<br>85 87 89 94 97 100 103-104 108-<br>110 112 114 116 118-119 122-123<br>127 130-132 134 136-138 141-144<br>147-151 153 163-164 168-171 179<br>186 192 195 197 199 204-205 212-<br>215 220 225-226 229-230 232 234-<br>236 251 257-260 262 265 272 274<br>277 280-282 285-286 289-292 296<br>298-301 304 307 309 314 321 324-<br>325 330 333 336-338 345 349 351-<br>352 354 358 361 368 370 380 383-<br>384 387-398 391 393 397 401 406<br>408-409 411-412 414-416 430-431<br>433-439 445-446 449 452 454-455<br>457 459 462 469 472-473 476-480<br>483-484 487-490 492-493 496-498<br>503 506 508 510-513 516 519-522<br>526 534 536-540 542 546 549 553<br>560-562 574-577 581-582 584 586-<br>587 589 593 595 597 604-609 611-<br>612 615-620 622-623 626 632 637<br>645-652 656-660 665-666 670-672<br>674-675 683-684 687 692-694 697<br>701 709 712 715-716 719-720 725-  |

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| adult kidney  | GIBCO      | AKD001                | 4-8 10-11 17-21 29-31 35-39 42-<br>45 50-51 56-58 60-61 64 68-69 75<br>77 80 82 85 87 92-94 97 100 102-<br>104 107-108 112 116-117 119 123<br>127-133 136-137 139-141 143-144<br>147-154 157 161-163 165-166 169<br>172 176 178-179 192 194-197 199<br>201 203-206 209-210 212-213 215-<br>216 223-228 234-236 238 247 251-<br>253 257-259 261-262 265-269 271-<br>272 274 276-277 279-281 284-286<br>290 293 295 298-299 301-302 304<br>307 311-313 321 325-326 329-331<br>333 341 344 348-350 352 356 358-<br>359 362 364-365 368 370-372 374<br>376-377 380-382 392 395 398 400-<br>401 404 407-409 414-415 423-424<br>430-437 443-444 446 449 451 453-<br>455 459 461-462 464 467 469 471-<br>474 476-477 480-481 483 487-488  |

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| adult kidney  | Invitrogen | AKT002                | 20-21 37-39 47 52 57 60 65-66<br>68-69 80 104 107-108 122 130 133<br>136-137 140 142-143 149 169 174  |

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| adult lung    | GIBCO      | ALG001                | 4-8 14 37-39 44-46 50-51 56 62-<br>63 75 82 88 93 103-104 113 125<br>133 140 143 150 152 154 157 162<br>171-172 174-175 190-191 196 200<br>211 214 219 223-224 227-228 251-<br>252 256 265 272 274 280-281 285<br>310 332 345 351 362 371 381-382<br>394 408-409 431 436 445 454 459<br>461 467 469 471 476-477 488 504<br>513 527 537-540 544 547-548 554<br>564 583 607 616-617 621 623-624<br>634 645-646 662-664 670 695 716<br>719 743-744 763 766 774 789 803<br>811 814 817 831-832 837-838 845<br>852-853 858-859 861 866 880 887<br>901 905 941 954-957 966 971 977<br>979 981 987 990 992 996 1001<br>1005-1006 1014 1017 1045 1047<br>1054 1059 1062 1064 1072 1080<br>1086-1089 1094 1107 1126 1134<br>1136-1137 1142 1150 1157 1173<br>1190 1200 1208 1220 1241 1272-<br>1273 1280 1282 1295 1306 1320<br>1331-1332 1353 1374 1379 1383-<br>1384 1404 1409 1423 1434 1436<br>1442 1474 1478 1494 1509 1522<br>1525 1531-1532 1547 1549 1553-<br>1554 1571 1598 1606 1613 1624<br>1627-1629 1632 1642 1644 1662<br>1669 1676-1677 1684 1696 1727<br>1731-1732 1737-1738 1748-1749<br>1786      |
| lymph node    | Clontech   | ALN001                | 4 24 50-51 82 105 137 153 198<br>201 223-224 234 268-269 272 280-<br>281 287 301 312 329 343 382 421<br>430 433 445 451 461-462 475 481-<br>482 503 526 529 537-540 546-547  |



| Tissue Origin | RNA Source | Hyseq<br>Library Name | SEQ ID NOS:   |
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|               |            |                       | 621 626 649 679 719 725-726 738<br>793 803 831 834-836 838 844 857-<br>858 866 879 905 913 928 963 976<br>1005-1006 1012 1038 1050 1116-<br>1117 1151 1199 1204 1226 1243<br>1265 1274 1324-1325 1339 1353<br>1374 1377 1440-1441 1447 1504<br>1549 1600 1618-1619 1631 1641<br>1644 1653 1687-1688 1691-1692<br>1741 1771  |
| young liver   | GIBCO      | ALV001                | 5-8 11 20-21 46 50-51 58 65-66<br>75 79 82 93 97 102-103 108 110<br>116 139 143-144 148-149 171-172<br>174 187-189 194-195 198 209 214-<br>215 230 250 258 267-269 280-281<br>306 309 342 351 356 359 362 372<br>374 392 394 398 401 407-408 410<br>414 431 444 455 459 476 478 483<br>493 510-512 516 520 522 526 536<br>549 571 574-577 585 592 601-602<br>607 621-624 628-630 632-633 637<br>648 660 666-667 678 697-698 700<br>717 719 728 730 734 738 744-745<br>766 770 773 779 788 800 808 812<br>814 841 849-851 871 874 879 887<br>893 898-900 902-904 906-907 911<br>919 922 924 934 953 957 963 965<br>970 984 986 997 1001 1004 1007<br>1012 1029-1030 1033-1034 1052<br>1061 1066 1070 1076 1086 1089<br>1093 1099-1102 1110-1112 1116-<br>1117 1119 1121 1125 1136-1137<br>1144-1145 1156-1157 1159 1196<br>1199-1200 1209 1211 1219-1220<br>1241 1244 1262 1270 1275 1279<br>1283 1295 1317-1320 1332 1339<br>1344 1359 1362-1363 1379 1383-<br>1384 1403 1415 1430-1431 1437<br>1450 1467 1475-1476 1483-1484<br>1494-1495 1498 1505 1512 1516<br>1518-1519 1526 1529 1547 1550-<br>1552 1557-1559 1565 1583 1587<br>1597 1609 1614 1620 1631 1637<br>1641 1644 1654-1655 1662 1667<br>1669 1684 1691-1692 1702 1711<br>1725 1738 1741 1743-1744 1758<br>1760-1761 1763-1765 1769 |
| adult liver   | Invitrogen | ALV002                | 5-8 17 20-21 32-33 41 55 58 64<br>75 77 86 89 102 108 117 119 175-<br>176 198 200 209 231 235-236 250<br>272 275-276 284 306 316 321 325<br>333 356 359 374 376 398 401 408<br>414 428 430 433-435 454 476 494<br>503-505 517-518 528 534 544 552<br>561-563 567 578 581 608-609 630<br>632 637 644 650 661 665 672 702<br>707 710 721-722 750 753 778 782<br>794 814 820 826 834-837 847 849-<br>850 858 861 874 879 893 898 904<br>911 918 921-922 925 946 948 972<br>978 986 996 1020 1027 1031 1034<br>1053 1063 1068 1070 1073 1086<br>1089 1093 1097 1113 1119 1156<br>1159 1195 1198-1199 1208 1220<br>1227 1241 1261 1272-1273 1277<br>1285 1308 1315 1320 1324-1325<br>1330 1362-1363 1375 1403 1408-<br>1409 1415 1431-1432 1435 1467<br>1469 1482 1504 1524 1542 1547  |

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| adult liver   | Clontech   | ALV003             | 29 676 997 1063 1119 1536 1766  |
| adult ovary   | Invitrogen | AOV001             | 1 4-18 20-23 29 35-40 42-48 50-<br>51 53-58 61-63 65-66 68-69 73-75<br>77-78 80 82 85 87 89 97 100-101<br>103-104 106-108 110 113 115 118<br>122-124 126 128 133-134 136-140<br>142 145-147 149-157 161 166 168-<br>170 174 177-178 180 182-186 188-<br>189 192-203 207 209 211-215 219<br>221-224 229-230 234 242-243 246-<br>247 255 258 260-262 265-269 271-<br>272 274 277-281 284-286 288 290<br>295 299 301-302 304 307 309-311<br>313-314 316 321 323-326 330 332-<br>333 335-338 341 344 349 352-353<br>356 358 360 362 370-372 376-377<br>379-384 387 390-392 394 397-398<br>400 403 408-410 412 414-416 423-<br>424 426-427 430-435 439 443-446<br>448-449 451 453-455 462-463 468-<br>471 473 476-479 481-484 487 489-<br>494 496-497 499-501 503-505 509-<br>514 516-517 519-520 522 524 526<br>528-534 541-544 546-547 549 552<br>554-555 561-564 566-567 569-570<br>572-573 575-576 579 581 583 585-<br>588 590-591 593 595 597 599 601-<br>605 607-613 615 618-622 624-627<br>630 632-633 636-640 642 644-647<br>649-652 654-655 657-665 667-675<br>677-678 681 683-684 692-695 697-<br>710 714-721 723 725-727 729 732<br>734-735 743-746 750-751 753 758<br>763 765 767 772-773 775-778 780<br>783-784 786 788 790-791 794-796<br>800 803 805 809-811 813-815 818-<br>819 821-824 826 828-829 831-832<br>837-838 843-850 852-857 859-864<br>867 869 871-872 874-875 878-883<br>887-888 890-895 898-910 912-914<br>916 919-922 924 926-927 929-939<br>941 943-946 948-951 953 955-958<br>961-964 966-967 970-979 981-982<br>985-986 988-990 992 995-997 999-<br>1001 1004-1009 1011-1013 1016<br>1019-1020 1024-1025 1029-1031<br>1033-1035 1037 1039 1041-1047<br>1050-1051 1054-1060 1062-1064<br>1067-1070 1072-1073 1075-1076<br>1078-1079 1085-1086 1089-1090<br>1094-1096 1098-1103 1106-1108<br>1112-1117 1119-1120 1123-1127<br>1131-1135 1142-1143 1146-1149<br>1153 1156 1158 1163 1165-1166<br>1169-1171 1173-1175 1177-1178<br>1180 1183-1185 1190-1191 1195<br>1197-1200 1202 1205-1214 1217-<br>1219 1221-1226 1232-1235 1238-<br>1241 1243-1244 1247 1249 1252-<br>1254 1256-1258 1262 1265 1267-<br>1268 1270 1275 1278 1280-1283<br>1286-1289 1291 1293-1294 1298- |

| Tissue Origin  | RNA Source | Hyseq<br>Library Name | SEQ ID NOS:  |
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|                |            |                       | 1299 1306 1308 1312 1317-1321<br>1323 1327 1329-1330 1332-1333<br>1338-1339 1341 1343-1351 1356<br>1359 1361 1365-1366 1371-1375<br>1377-1379 1383-1384 1386 1389<br>1394 1400 1404 1416-1417 1422-<br>1427 1429-1431 1435-1436 1439-<br>1443 1445-1450 1453-1454 1459<br>1463-1464 1466 1468 1470 1474-<br>1481 1484-1485 1488 1491 1493-<br>1494 1496-1498 1501-1504 1506-<br>1507 1511-1517 1519 1521-1524<br>1526-1527 1530-1531 1534-1536<br>1538-1539 1541 1545 1548-1550<br>1553 1555-1559 1561-1563 1566-<br>1567 1569-1570 1572 1574-1575<br>1578 1580-1581 1587-1588 1590-<br>1591 1595 1597-1598 1600-1606<br>1609 1611-1621 1623-1630 1634<br>1636 1638 1641 1643 1645 1647-<br>1657 1659-1662 1664 1667 1669-<br>1671 1673-1674 1676-1681 1683-<br>1690 1699 1702-1707 1710-1711<br>1713-1714 1716-1719 1723-1724<br>1726-1728 1731-1733 1735 1737-<br>1738 1740-1741 1743-1744 1748-<br>1751 1753 1755-1756 1760-1762<br>1765 1767-1768 1770-1771 1776<br>1778-1779 1783-1784 1786 |
| adult placenta | Clontech   | APL001                | 5-8 44-45 90-91 107-108 159 178<br>311 351 414 476 503 545 574 624<br>636 719 755 773 860 890-891 924<br>947 955-956 962 990 992 1002<br>1045 1202 1320 1369 1628 1686<br>1713-1714 1743-1744  |
| placenta       | Invitrogen | APL002                | 14-16 26 29 43 60-61 79-80 103<br>106 116 135 171 177 180 194 196<br>198 210 216 235-236 272 290 299<br>309 329 334 339 359 379-380 417<br>423 430 434-435 448 454 483 490-<br>491 517 522 631 723 725-726 728<br>738 746 769 818 843 854-855 857-<br>858 916 948 953-954 976 988-989<br>1005-1006 1013 1033 1036 1064<br>1068 1070 1086 1139 1144-1145<br>1160 1277 1285 1317-1320 1343<br>1345 1429 1435 1438 1454 1482<br>1486 1490 1512 1519 1532 1549<br>1592-1593 1602 1626 1647 1649<br>1664 1673 1675 1722 1727 1730<br>1746 1776  |
| adult spleen   | GIBCO      | ASP001                | 3 5-8 12 15-16 19-21 24 29 34-36<br>44-45 57 60 82-83 87 89 94 98-99<br>103 106 108 117 119-121 139 141<br>147 152-153 155 166 169 171 174<br>178-180 196 198 201-206 209-211<br>215 219 234 253-254 256 258 264<br>272 280-281 290 295 302 309 312<br>325 333 341 349 358 372 382 385-<br>387 394 406 414 431 434-436 446<br>448 451 473 481 490-493 500 503<br>505 517 519 530 534 536-540 547<br>554 557 574-576 582 592 595 604<br>611-612 620-621 623 631-632 642<br>652 659 661 667 671 673-675 684<br>700 721 728 730 732 738 742-744<br>746 762 765 774 780 788-789 794<br>810-811 817 822 830 832 845 848<br>852-853 858 862 866 874 879 882  |

| Tissue Origin              | RNA Source                           | Hyseq Library Name | SEQ ID NOS:  |
|----------------------------|--------------------------------------|--------------------|--|
|                            |                                      |                    | 884 906-908 912 919 921-923 926-927 934 942 949 957-958 963 977-978 983 990 992-994 996-997 999 1005-1007 1010 1012 1031 1036 1042-1044 1046 1049 1059 1068 1070 1076 1089-1090 1094 1103 1109 1113 1115 1124 1140 1163 1170 1174 1177 1190 1196 1219-1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1353 1359-1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1474 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782   |
| testis                     | GIBCO                                | ATS001             | 5-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 522 526 547 552-553 563-564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 |
| Genomic DNA from BAC 63118 | Research Genetics (CITB BAC Library) | BAC001             | 686 1352 1412  |
| Genomic DNA from BAC 39316 | Research Genetics (CITB BAC Library) | BAC002             | 1411-1412  |

| Tissue Origin              | RNA Source                           | Hyseq Library Name | SEQ ID NOS:  |
|----------------------------|--------------------------------------|--------------------|--|
| Genomic DNA from BAC 39316 | Research Genetics (CITE BAC Library) | BAC003             | 1352   |
| adult bladder              | Invitrogen                           | BLD001             | 5-8 17-18 22-23 33 37-39 56-57<br>80 93 100 120-121 169 201 237<br>251-252 272 278 311 348 353 382<br>413 415 424 430 443 483 502 542-<br>543 562 564 607 616-617 626 635<br>652 667 671 710 727 755-756 762<br>773 786 788 837 840 866 893 898<br>909 918 929 966 977 983 1016<br>1025 1055 1073 1082 1140 1167<br>1185 1189 1199 1270 1369 1481<br>1536 1560 1573 1596 1614 1636-<br>1637 1649-1650 1654-1655 1658<br>1669 1671 1690 1719 1727 1731-<br>1732 1739 1741 1760-1761 1779  |
| bone marrow                | Clontech                             | BMD001             | 3-8 11 13 18 29-31 33 35-36 40<br>43-45 47-48 50-51 57 60 65-66 75<br>80 82 85 88-89 94 100 103 107<br>110 115 118-119 124-125 133-134<br>136-137 139-141 146 150 152-153<br>155 161 163 168-170 172 178-180<br>187 192-193 197-198 203-205 210-<br>213 215 217 219 222 224-226 233<br>235-237 242-244 255 258 260 263-<br>264 266 273 276 278 283 286 290<br>295 301-302 307 312-313 321 330<br>333 339 343 352 357-358 370-371<br>382 384-385 387 389 394 408 410<br>412 416 421 424-427 429-431 436-<br>437 439 441-442 445 447 454-456<br>461-462 471-472 475 477-479 481-<br>482 485 488 493 498 500 503-506<br>513 516 519 523-524 526 530 535-<br>540 542 544-545 549 555 565 567<br>569-577 581 583-586 588 593 601<br>603-604 608-609 613-619 621-622<br>632-633 636-637 642 649-650 656-<br>660 666 670 672 674-675 679 683<br>701 708 716 718-720 731 735-736<br>740-742 744-745 752 761 765 772-<br>773 775-778 780 785-786 789-791<br>796 798 802 810-812 823-824 826<br>830 832-833 837-838 843-844 848-<br>855 858-859 866-867 869 878-880<br>883 890-892 896 903 905 908 912-<br>914 922-924 927 930-931 937 939-<br>941 952-953 955-958 963 969 973<br>976 981 985 987 990 992 995 1000<br>1002 1005-1007 1013 1016 1025<br>1028-1031 1033 1035 1037 1039<br>1042 1044 1047 1050 1053-1054<br>1059 1061 1063 1066 1070-1071<br>1079 1106 1110-1113 1115-1117<br>1124 1126 1134-1135 1142 1144-<br>1145 1163 1172 1178 1197 1199-<br>1200 1202 1216-1217 1224 1227-<br>1228 1240 1246 1254 1261 1266<br>1270 1278 1281 1295 1287 1290-<br>1291 1293 1299-1301 1308 1314<br>1317-1320 1327 1331 1339 1343<br>1346 1349 1353 1356 1361 1367<br>1369 1372-1374 1379-1380 1394<br>1400 1403 1406 1408 1413 1417<br>1419 1423 1425-1427 1430-1431<br>1433 1439 1443 1446-1449 1459<br>1463-1464 1482 1486 1493-1494 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS:   |
|---------------|------------|--------------------|---|
|               |            |                    | 1506 1509 1513 1521-1522 1524<br>1526 1528 1531 1536-1537 1543<br>1546 1548-1549 1552 1554-1555<br>1557-1559 1571-1572 1581 1589-<br>1592 1597-1600 1609 1614 1621<br>1626-1628 1630-1632 1634 1636<br>1638-1639 1641 1646-1647 1651<br>1653-1655 1661-1662 1676-1681<br>1684 1686 1690 1702 1707 1711<br>1713-1714 1717 1720 1722-1723<br>1727 1737-1738 1740 1758 1767<br>1772 1781-1782 1785-1786  |
| bone marrow   | Clontech   | BMD002             | 11 15-16 19 30-31 35-36 68-69 75<br>83-84 93 99 103 108-109 118 137<br>139 169-170 174 177 180 190 193<br>212-213 219 222 225-226 232 237<br>255 259 264 273-274 284 286 290-<br>292 295 301 303-304 307 312-313<br>316 324 326 330 334-335 348 352-<br>353 357 360 370-373 384 386-387<br>397 403-404 414-416 421 425-427<br>429-430 433-436 440 444 451 454<br>465-466 472 475 478 491 493 516<br>520 523 525 531 545 548 552 566<br>569-570 581 583 590-591 597-598<br>601 616-617 621 641 650 652 656<br>659 671 674-675 679 684 710 718-<br>719 728 734 737-738 742 761 765<br>774-778 790 811 814 818 830 834-<br>836 854-855 859 866 869 871 878-<br>879 884 889 892 904 922-923 932<br>990 992 998 1001 1004 1016 1036<br>1042 1048 1051 1054-1055 1058<br>1088-1089 1106 1112-1114 1155<br>1157 1192 1200 1223 1227-1228<br>1236-1237 1260-1261 1282-1283<br>1285 1287 1295 1314 1317-1321<br>1324-1327 1330 1333 1341 1343<br>1347 1350 1353 1355-1357 1367<br>1369-1370 1373 1377 1379 1381<br>1383-1384 1394 1397 1400 1406<br>1413 1417 1425-1427 1438 1442<br>1446 1459-1460 1470 1493 1505<br>1521 1536 1546-1549 1560 1573-<br>1574 1578 1598-1600 1621 1626<br>1631 1634 1646 1649 1653 1656<br>1658 1669-1670 1683-1684 1687-<br>1688 1690-1693 1696 1699 1702<br>1704 1707-1709 1711 1720 1722-<br>1723 1725 1727 1729 1731-1733<br>1738-1740 1743-1746 1752 1755<br>1760-1761 1767 1777 1781-1782<br>1786 |
| bone marrow   | Clontech   | BMD004             | 73-74 503 922 1036 1711   |
| bone marrow   | Clontech   | BMD007             | 95-96 866 1320 1475   |
| adult colon   | Invitrogen | CLN001             | 17 56-58 103 110 117 144 150 171<br>179 185 188-189 201 204-206 210<br>218-221 225-226 231 237 251 277<br>288 310 312 320 333 359 386 388<br>394 408 420 455 481 485 503 510-<br>512 590-591 615 635 647-648 665<br>672 684 697 710 725-726 743 780<br>786 788 826-827 848-850 854-855<br>858 866 872 898 918 921-923 953<br>976 983 993 1005-1006 1017 1020<br>1025 1027 1054-1055 1063 1068-<br>1069 1140 1153 1170 1185 1196<br>1199 1220 1280 1314-1315 1320<br>1345 1351 1355 1369 1428 1439   |

| Tissue Origin                  | RNA Source      | Hyseq Library Name | SEQ ID NOS:  |
|--------------------------------|-----------------|--------------------|--|
|                                |                 |                    | 1462-1464 1512 1556 1583 1587<br>1594 1596 1614 1625-1626 1631<br>1639 1645 1650 1675-1677 1687-<br>1688 1701 1713-1714 1724 1740<br>1765  |
| Mixture of 16 tissues - mRNAs  | Various Vendors | CTL016             | 401 1490 1686  |
| Mixture of 16 tissues - mRNAs* | Various Vendors | CTL021             | 312 782 1132-1133 1403 1712 1715   |
| adult cervix                   | BioChain        | CVX001             | 1 4-8 11 13 18-21 25-26 30-31 33<br>37-39 43 46-47 58 61 64-66 71<br>73-74 82 85 94 100 103-104 113<br>118 122 126 130 134 140 147 153-<br>156 163 170 179 181 186 192 195-<br>196 198 201-202 218-219 222 229-<br>231 257 266 276-277 285-286 288<br>298 301-302 304 307 312-314 324<br>326 329-330 332 335 342 352 358<br>362 371-372 376 379 381-382 384<br>388 398 400 410 414 416 419-420<br>426-427 430-431 433-436 439 446<br>448 461-462 464 471-477 479 482-<br>483 491 493 496 503 506 510-513<br>516-517 526 530 535 542-544 546-<br>547 557 561 572-573 575-577 581-<br>582 585-586 588-589 593-594 600<br>602 604-605 607-609 612 615-619<br>623 644 650 654 657-658 662-665<br>670 672 680 683 691-694 698 706<br>708-709 711 713 720-721 727 729<br>731-732 737 745-747 753-754 760<br>765 771 774-777 780 790 793 796<br>798 800 803 805 818 826 828 831-<br>832 834-836 843 847-848 851-855<br>857-860 864-866 869 871 876 878-<br>880 882 887 890-891 897 899-902<br>905-908 912-913 916 918-919 922<br>927 932 934-938 944 948 955-956<br>958 963-964 967 969-970 972 976<br>978-979 983 985 990 992 1000<br>1005-1007 1016-1017 1024 1027<br>1033 1036 1038 1045 1047 1053-<br>1056 1066-1067 1071 1073 1075<br>1079 1082 1098 1113 1124 1129<br>1134 1139 1146-1149 1163 1167<br>1170 1173 1175 1177 1181 1197<br>1200 1202 1211 1214 1216 1221-<br>1222 1225 1227 1232-1234 1240-<br>1241 1243 1258 1264-1265 1268<br>1270 1279 1287-1290 1308 1310-<br>1311 1316 1320 1323 1327 1345<br>1349 1353-1354 1360 1372-1374<br>1383-1384 1386 1394 1397 1405- |

\* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

| Tissue Origin     | RNA Source | Hyseq Library Name | SEQ ID NOS:  |
|-------------------|------------|--------------------|--|
|                   |            |                    | 1406 1416 1425-1427 1431 1436-1437 1442 1446 1448 1453 1459 1466 1472 1478 1482 1496 1501-1503 1506 1512 1522 1527-1528 1531 1533 1541 1547 1569 1571 1585 1589 1597-1598 1600 1608-1609 1614-1616 1620 1623-1624 1626-1628 1630 1638 1641 1643 1649 1653 1656 1662 1667 1669 1674-1675 1683 1685-1688 1699 1702 1709-1710 1715 1717 1722 1724 1729 1731-1732 1735-1739 1741 1743-1744 1748-1749 1755 1760-1762 1767 1773 1778 1785-1786   |
| diaphragm         | BioChain   | DIA002             | 137 282 289 730 780 986 1409 1478 1599 1614  |
| endothelial cells | Strategene | EDT001             | 3 5-10 13 15-21 24-26 29 34 37-39 42 44-45 50-51 53-55 57-58 60-61 65-66 68-69 73-74 77-78 80 82-83 85 87 89 93-96 101-105 108 110 112-114 116 118-122 124 128 133-134 137-142 147-150 152-153 161-163 166-172 176-179 187 190 192 194 196-201 204-207 210 212-214 220 224 229-230 233 235-236 240-241 251-252 258 261-262 265 267-269 272 276-277 279-281 284-285 288 290 295-296 301-302 310-311 313 316 321 325 329 331-333 335 340-342 351-355 360 371 375 380-382 384 387 390 392 397 400 407-408 410 412 414 416 425-427 431 434-436 439 444-445 449 454 463-464 472-475 477-479 486 488-490 497-498 500-504 510-513 516-519 522 524 526-528 532-534 536-540 542-546 548 561-563 566-567 572-576 579 581 585-586 589 593 595 597 599 603 607-612 615-617 620 622 626 630 632-634 638-641 644 647 656-660 662-664 670 673 678 680-682 692-697 707 709-710 712-713 719 730 732 734 736 738 743-746 751 759 768 771 773 775-778 783 786-789 793 800 803 805-807 810-811 814 816-818 821-822 824 826 828-829 832 834-838 842-845 848-850 854-860 862 864 869 871 874 876-879 883 885 887 890-891 894-895 898-900 903 908 910-913 916 919-922 924 926-928 930-935 939 943 948-949 951-954 957 959-961 964 969-970 973 975-978 983-984 988-990 992-993 996-997 1000 1002 1004-1013 1016-1020 1022-1025 1028 1031 1033-1034 1038-1046 1050 1055-1056 1059-1060 1062-1064 1067-1070 1072-1074 1076 1078 1082 1086-1087 1089-1090 1093-1097 1099-1103 1107 1109-1113 1116-1117 1124-1126 1128-1131 1134-1135 1138 1140 1144-1145 1148-1149 1153 1157 1160 1163 1171 1183-1184 1198-1199 1202 1205-1207 1211 1216-1217 1219 1221 1225 1229 1232-1235 1238-1241 1243-1244 1246 1250 1253 1257-1258 1261 |



| Tissue Origin   | RNA Source                                 | Hyseq Library Name | SEQ ID NOS:   |
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|   |  |                    | 1265-1266 1268 1270-1271 1274-1277 1280-1283 1285-1286 1288-1290 1293 1295 1298 1308 1312 1317-1320 1324-1325 1327 1329-1330 1334-1335 1338 1342-1343 1345-1347 1350 1355-1356 1359 1367 1369 1374 1376 1379 1398 1400 1406 1408 1414 1417 1419 1424-1426 1428-1431 1434-1438 1440-1442 1448 1450 1462-1466 1468 1472 1474 1478 1487-1488 1491-1493 1501-1504 1506 1509 1511 1516 1520-1521 1526 1529 1531 1536-1537 1539-1540 1546-1547 1549 1552 1555 1557-1559 1561-1565 1568 1571 1575 1578-1579 1581-1583 1587-1588 1590 1592 1597 1605-1606 1611 1613 1615 1618-1621 1624-1628 1630-1631 1634 1636 1638 1641 1643-1650 1652-1659 1664 1666-1667 1669 1671 1675-1681 1683-1688 1696-1698 1703 1711 1715-1716 1719 1722-1723 1726 1731-1733 1736 1739-1741 1743-1744 1749 1755 1760-1761 1765 1767-1768 1771-1773 1776 1779 1783-1786 |
| Genomic clones from the short arm of chromosome 8 esophagus | Genomic DNA from Genetic Research BioChain | EPM001 ESO002      | 286 686 1297 1303-1304 1352 1411-1412 1754 131-132 261 289 380 503 860 892 1000 1007 1397   |
| fetal brain   | Clontech                                   | FBR001             | 62-63 89 112 126 194 322 336-338 379 391 411 481 546 563 607 679 710 867 1012 1031 1055 1251 1262 1320 1407 1643 1652 1686 1731-1732 1746 1765  |
| fetal brain   | Clontech                                   | FBR004             | 68-69 90-91 139 212-213 301 331 362 374 403 436 611 645-646 659 668 670 691 785 805 845 1163 1209 1216 1232-1233 1238-1239 1387 1410 1416 1430 1496 1536 1547 1593  |
| fetal brain   | Clontech                                   | FBR006             | 5-9 25 43 60 62-63 65-66 70 72 80 87 92 101 103 108 114 136 139 149 152-153 157 168 171-172 175 207-208 210 212-213 221-226 237-238 251-253 266 272 279-281 295 301-302 307 310 317-318 321-324 330 333-334 336-338 346-347 352 357 370 373 377 379-380 382 384 391-392 397 399 402 406-408 410-411 417 421 424 426-427 430 436-437 440-443 454 460 464 467 473 476 483 488-489 495 497 508 510-513 516 519-520 524 530 537-540 544 547 550 561 567 572-574 582 590-591 595 597 604 607-609 615 623 628-629 631 634 638-640 655 657-658 660 665 669 674-675 679 689 691-694 696-697 699 701 706 710 716 720 728 732 734 736 742-744 757-760 763 775-778 780 799 806-807 810 817-818 826 839 843 858 861 864 871-872 884 890-891 894-895 898 904 915 921-923 935-936 938 945 950 952 955-956 958-959 961 963 967 969-971 990 992           |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS:   |
|---------------|------------|--------------------|---|
|               |            |                    | 999 1001 1005-1006 1008 1013<br>1016 1022 1024 1029-1030 1032<br>1035 1042 1047-1048 1052 1056<br>1065 1067 1070 1082 1089 1109<br>1114-1115 1119 1131 1143-1149<br>1151 1153-1156 1160 1163 1167<br>1172-1173 1178 1184 1186 1188<br>1190-1200 1211 1216 1222-1223<br>1226-1227 1229 1231 1236 1245<br>1253-1255 1258 1260 1262 1266<br>1270-1273 1281 1287 1308-1309<br>1314 1317-1320 1326 1334-1335<br>1339 1341 1344 1350 1356 1369-<br>1371 1373 1376 1379 1381-1382<br>1386 1392 1396-1398 1419 1423<br>1425-1426 1428-1429 1432 1437<br>1440-1441 1448 1466 1470 1482<br>1502-1503 1507 1511 1513 1516<br>1519 1536 1544 1549-1550 1557-<br>1559 1573 1589-1590 1598 1608<br>1611-1614 1619 1621 1625-1626<br>1640 1651 1657-1658 1676-1679<br>1693 1696 1703-1704 1713-1714<br>1718 1720 1722 1724 1726 1728<br>1730-1733 1735-1736 1738-1739<br>1742 1745 1755 1759-1761 1765<br>1767 1771-1772 1777 1779-1780<br>1786  |
| fetal brain   | Clontech   | FBRs03             | 235-236 520 864 1068 1188 1587  |
| fetal brain   | Invitrogen | FBT002             | 15-18 20-21 24-25 29 34 43 61-63<br>77-78 98 101 103 107-108 128 130<br>136 146 148 165-166 171 174 181<br>185 196-198 204-205 208 223 230<br>235-236 251 253 261 268-269 280-<br>281 284-285 288 309-311 321 329<br>334 339 346-347 350 357-359 381-<br>383 390 407 418-419 430 434-435<br>438 443-444 461 464-466 483 490<br>494 509 516 519 522 527 557 561-<br>562 572-573 590-591 595 597 623<br>632 647-648 650 655 669-670 672<br>682 690-691 700-701 710 717 736<br>746 782 784 788-789 814-815 825<br>829 840-841 847 854-855 857-858<br>897-900 904 919 925 935-937 946<br>948-949 954 960-962 966 969-970<br>986 996 1000-1001 1005-1007 1012<br>1014 1022-1028 1045 1052 1055<br>1068 1070 1072 1078 1082 1085<br>1090 1109 1115 1118 1120 1128<br>1136-1137 1144-1145 1149 1156-<br>1157 1193-1195 1198 1204-1205<br>1220 1222 1234 1257 1262 1271<br>1274-1275 1280 1285-1286 1294<br>1312 1314 1317-1320 1330 1342<br>1344-1345 1349-1350 1355-1356<br>1358 1364 1369 1379 1383-1384<br>1431 1435 1476 1507 1519 1532<br>1536 1547 1554 1564 1567 1578<br>1582 1587 1593 1595 1601 1608<br>1615 1619-1621 1638 1644 1661<br>1665-1666 1673 1687-1688 1690<br>1715 1723 1728 1749 1753 1757<br>1759-1761 1765 1771 1774 1776<br>1778 1781-1782 1786 |
| fetal heart   | Invitrogen | PHR001             | 105 124 180 289 864 1036 1148<br>1229 1614 1616 1762 1785   |
| fetal kidney  | Clontech   | PKD001             | 5-8 11 40 47 57 65-66 82 85 102<br>124 163 171 216 222 224 235-236  |

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| fetal kidney       | Clontech            | FKD002             | 352 384 426-427 440 583 602 1060<br>1131 1324-1325 1636   |
| fetal kidney       | Invitrogen          | FKD007             | 20-21 82 163 335 679 988-989<br>1000 1227 1230 1320 1554  |
| fetal lung         | Clontech            | FLG001             | 35-36 94 323 371 398 426-427 445<br>473 549 560 604 616-617 626 631<br>649 651 719 746 786-787 832 842<br>849-850 864 894-895 1075 1178<br>1182 1200 1206 1309 1311 1345<br>1429 1493 1567 1576 1620 1686   |
| fetal lung         | Invitrogen          | FLG003             | 9 15-16 29 41 47 68-69 83 88-89<br>102 124 137 152-153 165 196 224<br>229 231 249 254 256 267 291-292<br>300 325 333 344-345 352 373 376<br>379 384 408 426-427 430 432 467-<br>468 475 483 488 493 516 531 535<br>545 547 549 564 582 602 623 644<br>660 662-664 670 673 725-726 728<br>761 766-767 774 805 830 852-853<br>864 875 921 932 937 946 949 963<br>988-989 1014 1016-1017 1024 1027<br>1090 1097 1170 1185 1200 1215-<br>1216 1224 1258 1290 1309 1320<br>1342 1347 1355 1369 1381 1413-<br>1414 1431 1438 1449 1491 1512<br>1536 1547 1557-1560 1567 1590<br>1601 1636 1644 1653-1655 1662<br>1667 1671 1675 1680-1681 1706<br>1739 1760-1761 1769   |
| fetal lung         | Clontech            | FLG004             | 103 276 334 465-466 737 843 1131<br>1614 1658   |
| fetal liver-spleen | Columbia University | FLS001             | 3-11 13 15-21 25 30-39 41-48 50-<br>51 54 56-58 60-66 68-69 72 75<br>77-80 82-83 85 87 89 92-103 105-<br>110 112 116-124 126-127 130 133<br>135-139 141 144 147-149 152-153<br>157 163-165 167-172 174 176-178<br>180 186 188-190 193-194 196 198-<br>200 202-206 210-214 219 221-231<br>233-236 240-244 246-247 250-251<br>255-256 258 261-265 268-269 272<br>274 276-278 280-281 284-286 288<br>293 295 299-301 304 306-307 309<br>311 314 316 318 320-321 326 329-<br>332 342 344-345 350 352-353 356-<br>358 360 362 370-374 376 378-384<br>386-387 390 392-393 400-401 403<br>406 408 410-412 415 417 419 422-<br>437 439-442 444-445 448 452-454<br>456 459 461-470 472-479 481-483<br>487-488 490-491 493 500-501 503-<br>506 509-513 515-520 522-524 526-<br>529 531 534 536-540 542 547-549<br>553-554 561-562 564 567-568 571-<br>576 579 581 583 585-597 599-605 |

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| fetal liver-spleen | Columbia University | PLS002             | 3-11 13 15-21 26 29 32 35-39 42<br>44-45 48 50-51 54-55 57-58 61 54<br>68-69 73-75 78 80 82 84 87 95-98<br>100 103 105 107-108 110 112-113<br>116-119 122-125 128 130 137-138<br>145 147-153 155 157 159 161-163<br>166 168 171-172 174-175 177 181<br>188-189 193-194 196-198 200-203  |

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| fetal liver-<br>spleen | Columbia<br>University | FLS003                | 103 300 318 321 352 372 379 381<br>384 392-393 403 422 424 429 434-<br>435 440 444 453 503 515 544 592<br>978 1064 1324-1325 1327 1333<br>1357 1369 1378 1418 1424 1622<br>1646 1649 1680-1681 1689-1690<br>1717 1743-1744 1769   |
| fetal liver            | Invitrogen             | FLV001                | 15-16 26 34 58 61 64 70 75 78 89<br>98 105 112 116 120-121 123 133<br>151 166 176 180 194-196 198 200<br>204-206 210-211 220 225-226 230<br>235-236 239 247 259 261 267 272<br>277 280-281 303 310 313 317 320-<br>321 329 344 356 371 374 376 379-<br>382 395 408 412 414 419 429 434-<br>435 441-442 465-466 490 494 504-<br>506 509 522 527 534 552-553 562<br>567 569-570 572-574 607 631 657-<br>658 667 669 672 685-686 702 717<br>725-726 732 748 759 761 778 784<br>786 809 817 829 837 857 861 872-<br>873 875 881 889 894-895 909 911<br>916 954 963 967 974 977 986 988-<br>989 993 995 997 1000 1005-1006<br>1008 1014-1015 1020 1042-1043<br>1070 1086-1087 1089-1090 1118-<br>1119 1122 1144-1145 1148 1153<br>1157 1159 1183 1195-1196 1227<br>1250 1257-1258 1262 1267 1280<br>1285 1307 1312 1314 1317-1320<br>1344-1345 1349-1350 1355 1362-<br>1363 1403 1405 1415 1419 1425-<br>1426 1429 1431 1442 1448 1463-<br>1464 1469-1470 1489 1528 1536<br>1539 1549-1550 1557-1562 1577<br>1583 1598 1601 1611 1615 1622<br>1644 1649 1666 1674 1706 1721<br>1738 1746 1763-1765 1774 1776<br>1779 |
| fetal liver            | Clontech               | FLV002                | 676 998 1719  |
| fetal liver            | Clontech               | FLV004                | 93 133 214 301 355 374 379 555<br>581 601 679 837 847 859 1123<br>1236 1270 1313 1324-1325 1327<br>1355 1367 1425-1426 1536 1690<br>1733 1760-1761  |
| fetal muscle           | Invitrogen             | FMS001                | 26 37-39 50-51 58 84 86 89 98<br>113 128 131-132 139 155 172 186<br>194 198 201 206 211 230-231 256<br>261 276 282 286 302 325 359 361<br>375 379 383 398 412-413 419 430<br>436 448 452 462-463 473 477 503<br>519 529 561 569-570 590-591 597<br>607 623 626 635 647 660 672 715<br>725-726 730 733 761 775-777 788<br>826 837 860 874 913 915 921 935<br>970 980 986 988-990 992 1000-<br>1001 1007 1014 1027 1035-1036<br>1045 1060 1064 1070 1083 1097   |

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| fetal muscle  | Invitrogen | FMS002             | 119 221 273 402 426-427 463 547<br>599 736 869 1000 1033 1083 1266<br>1431 1440-1441 1468 1545 1599<br>1673 1678-1679 1687-1688 1710<br>1712-1714 1723 1725 1731-1733<br>1743-1744 1760-1761 1767  |
| fetal skin    | Invitrogen | PSK001             | 1 4-11 15-16 20-23 25 29 33 40<br>43 46 56-57 60-61 64-66 75 82 87<br>97-98 105 107-108 113 118-119<br>123 133 135-137 139 144 146 148<br>151-153 156 163 170 176 180 188-<br>189 197-198 200 202-203 210 218<br>222 231 246-247 261 263 265-270<br>277 285-286 290 293 299 301 307<br>311 321 325 328 330 333-335 339<br>341 345 351-352 355-356 358-359<br>362 368 370 372 376 379-382 384<br>388 394 404-405 408-409 411-412<br>419-420 424 426-427 436 441-442<br>445 448-449 454 462 465-466 472<br>476 490 493 504 506 509 515-517<br>519 526 531 537-540 547 549 560-<br>561 567 572-573 581 584 589 611-<br>612 615 623 630-631 635 647 649<br>651 657-658 660 662-665 667 669<br>672 676 678 681 688 701 704-705<br>709-710 713 717 720-721 725-726<br>728-729 732 748 750 753 759 764<br>766 770 775-777 780-781 786 788-<br>789 798 809 811 814 816-817 822<br>824-826 831 842 857 859 861 863-<br>864 881 894-895 908 910-911 916<br>918 922-923 928 932-933 935 937<br>946 948-949 953 960-961 966-967<br>970 975 977 986 990 992-993 999-<br>1000 1004 1007 1013 1018 1025<br>1027 1032 1035 1041-1043 1054<br>1057-1058 1060 1062-1064 1069<br>1072 1077 1090-1091 1097 1099-<br>1103 1108 1113 1119 1123 1128<br>1131 1134 1140 1148-1149 1152-<br>1153 1156 1163 1167 1178 1182<br>1189 1192 1195-1196 1198 1201-<br>1205 1208 1211-1212 1216 1219-<br>1220 1222 1225 1240 1243 1258<br>1266-1267 1274 1277 1280 1282-<br>1285 1299 1310 1317-1322 1324-<br>1325 1329-1330 1342 1344 1346<br>1349-1351 1354-1357 1365-1366<br>1369 1371 1373 1376 1378 1380<br>1383-1384 1387 1399-1400 1405<br>1410 1427 1429 1431 1433-1435<br>1439-1441 1448-1449 1454 1457<br>1468 1470 1472 1475 1480-1481<br>1487 1490-1491 1493 1498 1509<br>1512 1521 1525-1526 1529 1535-<br>1536 1547 1549 1557-1559 1588<br>1592 1595 1597-1598 1601 1603-<br>1604 1608 1611 1614 1618 1624- |

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| fetal skin     | Invitrogen | FSK002                | 13 286 302 307 313 321 330 335<br>339 341 354 370 372 385 400 402<br>408 414 426-427 433 436 450 454<br>515 544 585 598 767 810 845 939<br>1076 1109 1155 1317-1320 1326<br>1333-1335 1343 1347 1350 1369-<br>1371 1377-1378 1391 1397 1422<br>1466 1647 1656 1678-1679 1687-<br>1688 1693 1718 1721 1725 1731-<br>1732 1739 1755  |
| fetal spleen   | BioChain   | FSP001                | 110 137 211 353 589 927 1108<br>1639 1771  |
| umbilical cord | BioChain   | FUC001                | 4-8 10 12 14 17 33-36 44-46 57<br>64 68-69 75 82 85 101 104 113-<br>114 116 119 122-124 133 137 153-<br>154 157 161 163 166-167 175 181-<br>184 186 192 197-198 200-202 212-<br>215 230 234 246-247 251 256 263<br>267 271-272 280-281 284 295 301<br>314 317 321 326 333-335 345 351<br>356 368 371-373 379-380 386 390<br>392 394 406 408-410 412 414 416<br>420 424 427 430-436 438 444-446<br>454 459 461 463 467 473 482-483<br>486 488 490 495 504 509 524 526<br>537-540 547 555 561 574-577 588-<br>591 593 606 615 620-621 632 637<br>645-647 650 659-660 662-664 667-<br>668 674-675 684 687 696 698 701<br>703-705 709 711 714 719-720 725-<br>727 732 749-750 762 765 771 775-<br>777 780 789-791 793 796 802-803<br>814-817 822 833 843 845 848 858<br>861 864 875 879 888 894-895 897-<br>900 903 906-907 911-912 925 930-<br>933 936 940 948 953 960 966 977<br>984 990 992 998 1000-1001 1005-<br>1007 1016 1023 1025 1037 1046-<br>1047 1059 1061-1063 1073 1076-<br>1077 1089 1094-1097 1112-1113<br>1115 1134 1144-1148 1151 1154<br>1156 1163 1171 1197 1204-1205<br>1208 1216 1218-1224 1234-1235<br>1243-1244 1246 1279 1283 1286-<br>1287 1298 1316 1320 1344 1346<br>1350 1357 1359 1371 1373 1375<br>1381 1398 1400 1403 1408 1414<br>1424 1427-1428 1431 1433 1440-<br>1442 1446 1454-1455 1479 1482<br>1484-1485 1489 1492-1493 1504-<br>1505 1513 1525 1527 1536 1538<br>1546 1565 1567 1571 1573 1575-<br>1576 1578-1579 1591 1595 1600-<br>1601 1608 1612 1615 1621 1624<br>1626 1636-1637 1647-1648 1651<br>1653 1656 1658 1661-1662 1672<br>1675 1682 1684 1686-1688 1690<br>1709-1710 1722 1727 1729 1735-<br>1738 1740-1741 1760-1761 1768 |
| fetal brain    | GIBCO      | HFB001                | 4 9 11-13 17-18 22-23 25 37-39<br>42-47 50-51 54-55 58 60-61 65-66   |



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| macrophage    | Invitrogen          | HMP001             | 5-8 110 204-205 503 634 678 859<br>878 933 988-989 1379 1448 1504  |
| infant brain  | Columbia University | IB2002             | 10 12-13 15-18 22-23 25 29 34<br>37-39 43 47 50-51 54-56 58 60-63<br>65-66 68-69 72-74 80 82-83 86<br>88-92 97 100 102-104 106-108 110<br>112-113 115-116 118 123 128 130<br>134-136 138-139 143 147-149 151-<br>152 154-155 163 165-167 169 172-<br>175 181-184 186 193-196 198 201<br>203-205 209-210 214-215 222 224-<br>226 231-232 235-236 239 246-247<br>252 257 260 263-269 272 276-277<br>279-281 286 288 291-292 295 298<br>300-301 304 307 310 313 321-323<br>330-331 333-334 339 345-347 349<br>352 356-357 362 371-372 377 379-<br>380 383-384 392 397 401 406 408<br>411 413-414 416 418-419 422 428<br>430-431 434-435 438 443 449 453-<br>454 461 464-466 469-470 472-473<br>475-476 478 482-483 487 490 492<br>494 497 503 507-508 510-513 516<br>519-520 524-526 530-534 536-540<br>547 550-551 561 563-564 566-567<br>572-576 579 581-582 584-587 590-<br>591 593 595-597 607-609 611-613<br>616-617 620 622-624 627 631 637<br>641 645-647 650-655 657-658 660-<br>665 667-675 689 691 695 697 699<br>703 707 713-715 717 721 728-731<br>733-736 739 743 745 751 755 759<br>763 769-770 772 778 780-781 785<br>788-789 793-794 799 803 808 811<br>814 825-826 830 834-836 840-843<br>845 848-850 854-855 860 862 864-<br>865 870 872 875-876 878 886 888<br>890-891 894-896 898 903-904 916-<br>917 919 922-925 927-928 930-932<br>934-936 938 941 945-946 948-950<br>953-954 959-962 966-969 977 979<br>981 986-990 992 997 999-1000<br>1004-1006 1014 1016 1018-1019<br>1024-1025 1033 1036 1047 1051-<br>1052 1054-1055 1057-1059 1063-<br>1064 1068-1070 1073 1081-1082<br>1085 1089 1108-1113 1118-1120<br>1123-1124 1130 1132-1138 1140<br>1149 1151 1153-1154 1163-1170<br>1172 1174-1175 1183-1184 1188<br>1190 1193-1194 1196-1197 1199<br>1204 1208-1209 1211 1218-1222<br>1226-1227 1229 1231 1234 1241<br>1247 1249 1251 1256 1258 1261-<br>1262 1269 1274 1279 1281 1283<br>1285 1287-1289 1294-1295 1305<br>1307 1313-1314 1316-1320 1329<br>1332 1341-1342 1345 1349 1356<br>1362-1363 1365-1366 1368-1370<br>1374 1381 1383-1384 1388 1400<br>1403 1406-1407 1413 1417 1420 |

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| infant brain  | Columbia<br>University | IB2003                | 17-18 20-23 29 34 43 60 68-69<br>78-80 88 100-101 107 110 112 118<br>123 128 133 135-137 146 148 152<br>159 166 169 174 194 198 203 215<br>223 225-226 229 235-236 247 260<br>276-281 286 290-292 295 300-301<br>310 322 324 331 334 339 346-347<br>349-350 352 357 371 376-377 382<br>384 403 408-409 414-415 453-455<br>472 476 478-479 490 503 507 516<br>520 530 534 536-540 551 563 572-<br>576 585 587 590-591 593 595-596<br>601 606 612 616-617 620 622-624<br>650 652-653 661 665 670-671 674-<br>675 678 689 715 717 727-728 730<br>734 759 775-777 780-781 785 796<br>806-807 811 824 845-846 864 869<br>875 882 889 894-895 898 904 917<br>919 921-923 932 935-936 946 950<br>954 962 977 979 997 999-1000<br>1005-1006 1009 1011 1017 1024<br>1033 1037 1043 1055 1057 1109<br>1114-1115 1120 1123 1127 1144-<br>1145 1149 1151-1153 1160 1167<br>1170 1174 1193-1194 1196 1199<br>1202 1206 1209 1220-1221 1226<br>1229 1240-1241 1251 1258 1284<br>1288-1289 1305 1314 1327 1333<br>1344 1347 1350 1356-1357 1365-<br>1366 1378-1379 1388 1400 1403<br>1421 1423 1431 1436 1440-1441<br>1446-1447 1457 1459 1471 1499<br>1503 1507 1509 1536 1546 1557-<br>1559 1567 1572 1587 1595 1598<br>1610-1612 1615 1631 1639 1644<br>1647 1657-1658 1673 1678-1681<br>1683-1684 1701-1702 1708-1709<br>1713-1714 1719 1757 1760-1761<br>1765 1771 1778 |
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| lung,<br>fibroblast | Stratagene | LFB001                | 5-9 17 20-21 25 63-69 82 94 105<br>153 157 197-198 203 207-208 212-<br>213 223 262 266 283 302 321 326<br>333 356 370 427 430 436 446 462<br>472 493 498 503 516 519 527 535<br>537-540 542-544 562-565 567 586<br>599-600 607 615 630 647 662-664<br>692-694 712 719 745 748 775-777<br>794-796 810 837 843-847 849 854-<br>856 869 876 903 934 953 955-956<br>964 975-976 984 1000 1005-1007<br>1024-1025 1033 1039 1053 1064<br>1070 1072 1082 1112-1113 1134<br>1136-1138 1140 1195 1223 1232-<br>1233 1246 1279 1285 1295 1311<br>1320 1334-1335 1343 1427-1428<br>1446 1478 1482 1493 1504 1537<br>1552 1555 1567 1575 1582 1598<br>1620 1625 1632 1638 1645 1654-<br>1655 1662 1680-1681 1684 1686<br>1690 1696 1702 1711 1733 1741<br>1760-1761 1778 1785  |
| lung tumor          | Invitrogen | LGT002                | 5-10 18 20-21 29 33-36 40 43 52<br>54-55 61 65-66 68-70 73-75 80 85<br>88-89 93-94 100 103 106-108 112-<br>113 115-116 118-119 123-124 126<br>130-132 135-137 139-141 143-144<br>147-148 151-153 155-156 159 161<br>164 169 171 179-180 185 190 193<br>194 196-199 203-208 210 212-214<br>216-217 219 222 233 240-241 244<br>246 251-252 255-256 261-262 266<br>272 276-277 279-281 284 286 288<br>290 295 298 301-302 309-312 317<br>321 329 332 341-342 344-345 348<br>352 358-360 363 368 370-371 376<br>380-381 384 389-390 398 400 409<br>414 423 426-427 430 432-436 443-<br>444 450-451 454 462 468 472-477<br>480-483 487-488 490-491 493 496-<br>498 500 503-506 509-512 515-516<br>519 521-523 526 530 534 541 544<br>547 554 557 564 566-567 572-576<br>585-586 588-589 595-596 601 607<br>611-612 615 619 621 623 626 630<br>632-633 644 647 649 651 655-656<br>660 662-665 667 669 672 683-684<br>696 700 706 710 713 716 718-719<br>722-723 728 734-739 743 750 752<br>763 765-766 773-778 784-785 787-<br>789 791 800 802-803 809-812 814<br>824 826 828-829 832 838-839 841-<br>845 849-850 852-855 857-861 864<br>866 874 878-880 882 887 890-891<br>897-898 902 904 906-907 910 916<br>918-920 922 924-925 927 930-932<br>934-935 937 947 950 953 955-956<br>961 963 966-967 969 971 977-979<br>981 984 986-987 990 992-993 995<br>997 999-1001 1005-1007 1009<br>1012-1013 1018 1020 1022-1024<br>1026 1029-1030 1033 1038 1041 |

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| lymphocytes   | ATCC       | LPC001                | 4 11-12 18 24-25 30-31 48 50-51<br>56-57 68-69 80 92 98 103 105 110<br>126 137 152-153 157 165 172 188-<br>189 197 203 210 217-218 222-223<br>225-226 229 231 247 251 256 264<br>272 280-281 284 300-301 321 325-<br>326 339 348 352 357 371 382 384<br>390 400 404 412 414 421 423 426-<br>427 430-431 445 447-448 451 454-<br>455 475 503 516 526-527 530 537-<br>540 549 556-560 563 574 577 589<br>602 613 615-617 621 623 628-630<br>636-637 647 649 657-659 690 697<br>717 723 755 764 775-777 780 786<br>789-790 793 800 802 822 838 849<br>866 869 876 881-883 892 898 906-<br>907 911 921-923 928 975 990 992<br>996 1001 1004-1007 1033 1050<br>1054 1078 1107 1135 1140-1141<br>1143 1148 1158 1163 1177 1199<br>1205 1216 1226 1231 1236 1241<br>1244 1250 1258 1260 1265 1269-<br>1271 1290-1293 1308 1312 1317<br>1319-1320 1339 1345-1346 1348<br>1350-1351 1357 1367 1369 1379<br>1381 1383-1384 1386-1387 1389<br>1394 1397 1405 1423 1425-1428<br>1431 1437 1446 1448 1461 1466<br>1470 1472 1474 1482 1492 1506<br>1528 1537 1546 1549 1591 1598<br>1600 1603-1604 1606 1627 1636  |

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| leukocyte     | GIBCO      | LUC001                | 3-4 10-11 13 15-18 20-21 24-25<br>30-31 35-36 40 43-45 48 50-51<br>54-58 60-63 68-69 75 79-80 82-83<br>85 88-91 93-96 98 100 103-104<br>107-108 112 116 119 123 125-128<br>134-140 142 147-149 151 153 155<br>157 162-163 167 169-172 174 177-<br>179 186 190 192-199 203-207 210<br>212-215 217-219 222-223 229 235-<br>236 247 251 255-258 260 262 272<br>274-277 280-281 285-286 297-301<br>307-310 313-314 316-317 321 325-<br>330 333-334 340-342 348-349 352<br>354-358 370-371 380-385 387-388<br>400 405 408-410 412 414-416 421-<br>425 430-431 434-435 437 439 441-<br>442 445-451 453-454 456 459 461-<br>464 468-472 474-479 481 483-485<br>487-491 496 499-501 503-504 509-<br>513 516-519 522 526-527 529-531<br>534 536-540 542 547-549 553-559<br>566-567 571 574-577 579 582 584-<br>586 589 593 595-597 601-602 604<br>606-607 611-613 615-621 623 627-<br>629 633 636-637 642 644-650 655<br>659-660 662-665 667 669 674-675<br>678 682-684 692-696 698 700 706<br>708 710 716-720 725-726 729-736<br>738-739 743-746 749 751 753 756<br>759 765-766 768 770-773 780 784-<br>786 788-790 793 796 798 800 802-<br>803 810-811 814 817 819 826 828-<br>830 832 834-836 838 843 845-860<br>863-864 866-871 877-879 881-892<br>894-896 898 902 904-914 916 919-<br>925 927 930-932 935-936 941-942<br>945 948-949 953 955-956 958 960-<br>962 964 967 970-971 973 975 977<br>985-990 992-993 995-996 999-1002<br>1004-1009 1011 1014 1017-1019<br>1022-1023 1025 1027 1029-1031<br>1033-1036 1038 1041 1043 1047<br>1050 1053-1054 1058-1059 1061-<br>1062 1064 1068 1070 1072 1078<br>1085-1086 1089-1091 1093 1097<br>1106-1107 1110-1113 1115-1117<br>1122-1123 1125 1129 1132-1133<br>1135-1137 1140-1145 1152 1158<br>1163 1168 1170-1174 1176-1178<br>1180 1182-1183 1186 1195 1198-<br>1200 1202 1205-1206 1211 1216<br>1219-1221 1223-1227 1230-1236<br>1238-1242 1247 1252 1254 1256<br>1258 1261-1262 1264-1265 1269-<br>1270 1272-1275 1277 1280-1284<br>1287-1293 1299-1300 1306 1308<br>1312-1313 1317-1320 1322 1324-<br>1330 1333-1335 1339 1341 1343-<br>1347 1349 1353-1357 1359-1361<br>1365-1367 1369-1370 1373-1374<br>1377 1379-1381 1386-1387 1394<br>1400 1403 1409 1419 1423 1425-<br>1428 1430-1431 1433-1434 1437-<br>1438 1440-1442 1446-1448 1450 |

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|  |            |                       | 1453 1458-1459 1463-1464 1468<br>1470-1471 1474 1477-1478 1482-<br>1488 1490-1493 1496-1501 1504<br>1506 1509 1512-1513 1516 1519<br>1521-1522 1524-1525 1527-1528<br>1531 1534 1538 1541 1545-1547<br>1549-1550 1553 1555-1556 1560<br>1565 1567 1575 1580 1589 1591<br>1594 1596 1598 1600-1602 1606-<br>1608 1611 1614 1620-1621 1624<br>1626-1629 1631-1632 1636 1638-<br>1639 1641 1644-1645 1648-1650<br>1653-1655 1658-1660 1662 1669-<br>1670 1675-1679 1684-1688 1690-<br>1692 1696 1700 1702 1707-1709<br>1711 1716-1717 1720 1723 1725-<br>1727 1733 1737-1738 1741 1743-<br>1744 1748-1749 1752 1755 1760-<br>1762 1765 1769 1771-1772 1781-<br>1784 1786  |
| leukocyte                                    | Clontech   | LUC003                | 4 35-36 44-45 61 68-69 75 82 102<br>119 139 154 179 197 244 280-281<br>324 372 404 430-431 455 461 476-<br>477 481 503 537-540 554 575-576<br>581 589 608-609 621-622 624 630<br>632 647 662-664 669 679 698 764<br>773 775-777 802 848 851 856-857<br>879 905-907 915 949 952 990 992<br>1002 1113 1119 1170 1183 1216<br>1236-1237 1241 1275 1346 1353<br>1357 1359 1377 1506 1515 1534<br>1553 1591 1600 1613-1614 1621<br>1628 1670 1676-1677 1691-1692<br>1699 1733 1738 1772   |
| melanoma from<br>cell line ATCC<br>#CRL 1424 | Clontech   | MEL004                | 25 35-36 43 80 104 126 128 150<br>163 166 188-189 197 210 215 220<br>271 277 280-281 310 317 336-338<br>345 351 372 380-381 383 387 412<br>415-416 430 445 448 454 456 467<br>481 490 499 503 526 528 546 548<br>567 575-576 588 601 613 615 647<br>660 665 734-735 737 759 778 787<br>790 800 832 845 856 859 869 878<br>883 887 905 914 932 934 958 976<br>985 990 992 999-1000 1025 1031<br>1038 1050 1055 1068 1074 1088<br>1099-1102 1107 1136-1138 1149<br>1156 1163 1172 1190 1195 1200<br>1214-1215 1217 1226-1227 1235<br>1238-1239 1244 1253 1278 1290<br>1293 1311 1320 1330 1334-1335<br>1345 1355 1367 1386-1387 1394<br>1403 1406 1414 1423 1437 1442<br>1465 1521 1529 1536 1539 1541<br>1547-1548 1582 1620 1626 1631<br>1638 1647 1653 1660 1667 1669-<br>1670 1680-1681 1696 1704 1715<br>1724-1725 1731-1732 1750 1760-<br>1761 |
| mammary gland                                | Invitrogen | MMG001                | 5-8 10 12 14-18 20-21 24-25 29<br>33-39 42-43 52 55-58 60-64 68-69<br>71 73-74 79-80 82 89 98 100 103<br>106 108 112 123 128 133-137 144-<br>146 148 150-152 154 158-159 165-<br>166 170-172 174 176 178 181-185<br>188-190 194-198 201-206 210 217-<br>222 224 227-228 231 233-237 247<br>251 253-254 256 261-263 266-267<br>271 276-277 279-281 284-286 288  |

| Tissue Origin           | RNA Source | Hyseq<br>Library Name | SEQ ID NOS:  |
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| induced neuron<br>cells | Stratagene | NTD001                | 29 35-36 80 116 123 156 163 181<br>214 230 280-281 284-285 307 321<br>330 340 358 371 375 377 380 382<br>422 424 492 497 532-533 542 546   |



| Tissue Origin                              | RNA Source | Hyseq Library Name | SEQ ID NOS:  |
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|  |            |                    | 549 566 586 595 612 645-647 654<br>734 775-778 780 792 799 821 826<br>856 858 875 936 953 985 990 992<br>1041-1043 1055 1072 1104 1193-<br>1194 1206 1223 1246 1253 1274<br>1288-1289 1291 1294 1311 1320<br>1349 1359 1412 1423 1485 1620<br>1623 1645 1684 1705 1715 1751  |
| retinoid acid<br>induced<br>neuronal cells | Stratogene | NTR001             | 5-8 78 268-269 277 383 431 506<br>623 677 731 999-1000 1199 1425-<br>1426 1547   |
| neuronal cells                             | Stratogene | NTU001             | 29 65-66 80 82 110 119 146 152<br>166 174 181-185 198 227-228 253<br>284 309 325 332 334 336-338 375<br>391 393 406 414-416 454 465-466<br>470 488 503 506 510-512 519 537-<br>540 572-574 597 602 607 623 647<br>661 700 702 716 743 771 792 858<br>904 948 954 977 1000 1005-1006<br>1025 1064 1068 1122 1148 1185<br>1219 1226 1234 1246 1271 1283<br>1295-1296 1311 1317-1320 1329-<br>1330 1350 1355 1365-1366 1378<br>1383-1384 1400 1412 1445 1505<br>1539 1547 1578 1647 1656 1683<br>1690 1738 1749 1783-1784   |
| pituitary<br>gland                         | Clontech   | PIT004             | 311 314 379 408 419 430 454 1055<br>1095-1096 1272-1273 1312 1320<br>1378 1652 1671 1720 1725 1736<br>1741 1755  |
| placenta                                   | Clontech   | PLA003             | 5-8 124 208 277 370 843 906-907<br>1280 1317-1319 1369 1609 1621<br>1737   |
| prostate                                   | Clontech   | PRT001             | 9 46 57 71 107 147 171 177 197<br>201 229 231 242-243 274 280-281<br>307 310 317 330 358 373 382-383<br>400 430 434-436 461-462 469 477<br>489 497 500 505-506 513 521 526<br>531-533 547 618 649 657-658 662-<br>664 710 729 767 771 789 820 861<br>871 874 890-891 905 938 945 963-<br>964 988-989 1002 1025 1033 1045<br>1061 1095-1096 1112 1125 1142<br>1196 1198 1202 1232-1233 1241<br>1258 1272-1273 1287 1295 1313<br>1333 1341 1344 1349 1360 1362-<br>1363 1367 1437 1442 1447 1475<br>1478-1479 1482 1489 1513 1517<br>1527 1531 1536 1598-1599 1628<br>1636 1657 1680-1681 1687-1688<br>1717 1738 1743-1744 |
| rectum                                     | Invitrogen | REC001             | 17-18 29 33 62-63 71 73-74 83 86<br>113 126 146 153 158 167-169 195<br>200 206 261 309 312 341 344 368<br>373 388 395 408 414 420 430 441-<br>442 446 448 464 468 483 517 537-<br>540 547 567 585 589 602 623 628-<br>629 632 645-647 651 657-658 669<br>717-719 721 725-726 738 748 750<br>756 762-763 766 770 774 790 819<br>825 843 849 851 881 903 909 948-<br>949 960 986 996 1020 1023 1033-<br>1034 1064 1067 1070 1075 1086<br>1108-1109 1113 1130 1139 1153<br>1159 1172 1178 1185 1187-1189<br>1205 1220 1225 1240 1244 1271<br>1317-1320 1323 1334-1335 1350-<br>1351 1355 1369 1373 1375 1425-               |

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| salivary gland  | Clontech   | SAL001             | 10 55 97 103 110 140 149 152 158<br>198 217-218 242-243 256 301 308<br>312 321 333 351 354 360 410 437<br>448 473 487 494 496 501 535 555<br>569-570 572-573 590-551 624 636<br>651 759 762 764 768 771 788 800<br>809 826 848 865 879 906-907 925<br>933 963 1016 1020 1025 1040 1046<br>1055 1066 1103 1150 1172 1181<br>1234 1281-1282 1288-1289 1298<br>1315 1320 1333 1336-1337 1346<br>1359 1373 1379 1424 1447 1449<br>1474 1482 1492 1494 1498 1511<br>1523-1524 1537 1554 1596 1626-<br>1627 1636 1652-1655 1658 1665<br>1671-1672 1691-1692  |
| salivary gland  | Clontech   | SALs03             | 158 326 1423 1463-1464   |
| skin fibroblast | ATCC       | SFB001             | 1320 1400  |
| skin fibroblast | ATCC       | SFB002             | 262 736 1025 1253  |
| skin fibroblast | ATCC       | SFB003             | 709 1119 1350 1631 1653  |
| small intestine | Clontech   | SIN001             | 25 142 146-147 151 155 198 203<br>244 260 271 280-281 286 288 298<br>301-302 308 312 334 340 371 398<br>408 412 414 416 423 425-427 430<br>434-435 445 452 454 478 503 516<br>519 521 523 543 547 549 555 559<br>563 569-570 585 592 604 611 626<br>628-629 632 650 659 681 710 714<br>718 750 764 780 798 829 842 857<br>859 866 887 892 894-895 901 904<br>906-907 912 919 935 997-998 1000<br>1007-1008 1026-1028 1044 1055<br>1089 1097 1116-1117 1131 1148<br>1169 1199 1219 1234 1247 1264<br>1279 1316 1320 1326 1341 1343<br>1349 1351 1374 1387 1398 1400<br>1403 1407 1423 1428 1468 1498<br>1501 1521 1550 1556 1585 1597<br>1636 1638-1639 1645 1653 1656<br>1662 1671 1675 1684 1691-1692<br>1704 1711 1717 1719 1722 1725-<br>1726 1729 1733-1734 1743-1744<br>1762 1767 1780 1785 |
| skeletal muscle | Clontech   | SKM001             | 18 20-21 82 84 101 118 134 148<br>151 153 166 225-226 258 274 277<br>289 329 361 412 414 424 440 452<br>459 470 488 503-504 537-540 647<br>660 673-675 715 773 780 786 830<br>905 922 950 963 982 990 992 1020<br>1047 1063 1115-1117 1121 1134<br>1228 1268 1284 1298 1321 1329<br>1336-1337 1343 1409 1413-1414<br>1509 1599 1624 1644 1653 1712   |
| skeletal muscle | Clontech   | SKM002             | 168 1683 1712  |
| skeletal muscle | Clontech   | SKMs03             | 235-236 1409   |
| skeletal muscle | Clontech   | SKMs04             | 235-236  |
| spinal cord     | Clontech   | SPC001             | 4 9 11 17 30-31 35-36 43 46 60   |

| Tissue Origin | RNA Source | Hyseq<br>Library Name | SEQ ID NOS:  |
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|               |            |                       | 82 85 92 94 108 110 116 139 157<br>167 198 204-205 210 215 229 256<br>259 277 280-281 300-302 304 315<br>317 372 379 387 392 419 426-427<br>430 433 448 467 473 487 489 506<br>509 513 519 524 526 537-540 543<br>547 549 551 559 567 569-570 593<br>607 616-617 623 625 637 649-650<br>652 657-658 670-671 673 679 681-<br>682 709 711 715 719 728-729 734<br>749-750 753 775-777 781 789 791<br>809 820 832 834-836 847-849 854-<br>855 858 861 864 871-872 875 884<br>898 906-908 917 919 924 934 942<br>944 970 985 990 992-993 998 1013<br>1039 1053 1059 1065 1072 1075<br>1077 1082 1085 1097 1103 1109<br>1116-1117 1128 1134 1151 1170<br>1174 1192-1194 1215 1225 1241<br>1243 1283 1294 1307 1312 1320<br>1323 1327 1330 1350 1353-1354<br>1356 1359 1368 1375 1400 1406-<br>1407 1423 1429 1437 1443 1448<br>1454 1470 1482 1492 1501 1508<br>1511 1529 1538 1548-1549 1565<br>1571 1578 1598 1600 1614 1625<br>1627 1630 1639 1646 1651-1652<br>1670 1686 1696 1740 1751 1755<br>1771 |
| adult spleen  | Clontech   | SPLc01                | 117 312 326 348 424 426-427 431<br>845 866 1320 1330 1333 1344<br>1355-1357 1371 1387 1397 1446<br>1538 1579 1669 1686 1739 1767   |
| stomach       | Clontech   | STO001                | 10 15-16 61 68-69 100 117 149<br>197 201 227-228 231 249 273 280-<br>281 287 291-292 302 312 358 362<br>426-427 430 446 462 475 479 535<br>597 620 630 651 662-664 722 739<br>780 782 785 846 919 960 964 966-<br>967 976 1008 1012 1032 1042 1063<br>1071 1135 1170 1208 1234-1235<br>1259 1277 1280-1281 1322 1349<br>1359 1369 1449 1468 1474 1478<br>1487 1493 1498 1557-1559 1622<br>1634 1651 1653 1729  |
| thalamus      | Clontech   | THA002                | 9 11 25 85 87 112 137 146 180<br>190 198 206 210 212-213 235-236<br>239 261 268-269 279 290 301 325<br>333-334 341 351 356 364-365 379<br>388 393 396 419-420 441-442 458<br>477 483 508 525 531 549 567 606<br>608-609 647 681 715 725-727 736<br>774 782 784 794 827 883 890-891<br>899-900 961 997 999-1001 1004<br>1034 1055 1097 1129 1144-1145<br>1150-1151 1157 1172-1173 1177<br>1193-1194 1208 1220 1249 1280<br>1305 1345 1355 1369 1434-1435<br>1440-1441 1454 1496 1546 1549<br>1562 1572 1578 1590 1594 1613-<br>1614 1640 1651-1652 1671 1687-<br>1688 1703 1743-1744 1746-1747<br>1753  |
| thymus        | Clontech   | THM001                | 44-45 54 57-58 62-64 79 104 123<br>126 134 153 193 212-213 218 242-<br>243 258 274 277 279 297 301 307<br>327 330 333 342 351 358 371 410<br>430 445 465-466 468 471 483 487<br>493 503 506 509 517 526 535 537-   |

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| thymus        | Clontech   | THMc02                | 5-9 15-21 25 33 35-36 43-45 48<br>50-51 54-55 60 75 83 87 89 93<br>98-100 102 105 112 117 135-137<br>141 143 146 157 167 169 192 196<br>211 217-219 222 224 229 233 235-<br>236 240-241 244 251-252 256 261-<br>262 268-269 286 288 290 295 297<br>301-302 309-310 315-317 321 324<br>327 334 342 350 352-353 360 370-<br>373 382 384 400 403 410 414-416<br>424 430-431 436 445 454-456 461<br>464-467 470 472 474-476 483 488<br>497 500 504 506 513 516 519-520<br>524 526 530-531 534 537-540 549<br>554-555 565-566 569-570 572-573<br>575-577 586-587 595 603-604 606<br>612 630-632 634 636 647 650 657-<br>660 666-667 669 673-675 678 698<br>700 703 708 720 725-726 731 738-<br>739 743-744 750-753 757 759 763-<br>765 767 772-779 787 789-790 798<br>800 810 823 829 834-836 841 848<br>854-856 859 861 864 870-871 881<br>890-891 898 908-909 913 928 933<br>941 949 958 961 963 967 969 975<br>981 986 988-990 992 999 1007-<br>1008 1014 1016 1039 1041 1073-<br>1074 1079 1089 1097 1109 1114-<br>1117 1122 1131 1140-1141 1144-<br>1145 1163 1172 1175-1177 1186<br>1196 1198 1206 1211 1216 1220<br>1223 1227 1234-1243 1261-1262<br>1267 1271 1280-1281 1284 1290<br>1308 1317-1320 1322 1324-1325<br>1327 1330 1334-1335 1339 1346<br>1350-1351 1355 1357 1360 1370<br>1374 1377-1379 1386 1389-1390<br>1392 1397 1400 1402 1406-1407<br>1417 1423 1425-1427 1440-1441<br>1466 1474 1477 1483 1493 1498<br>1504 1506 1525 1536 1545 1549<br>1566 1594 1598-1600 1608 1611<br>1614 1621 1623 1625 1632 1639<br>1641 1644 1647 1649 1653-1656<br>1658 1662-1663 1671 1673 1678-<br>1681 1686-1688 1693 1705 1707<br>1711 1717-1718 1726-1727 1731-<br>1733 1737-1738 1743-1745 1758-<br>1761 1771-1772 1779 1786 |

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| thyroid gland | Clontech   | THR001             | 4 9-10 20-21 37-39 48 50-51 54-<br>57 60-61 65-66 71 83 94-96 98-<br>100 102 104 110 112 115-117 119<br>123 127 133 136-137 140 149 152-<br>153 155-158 163-164 168-169 171<br>186 190-192 197 201-203 219-220<br>229 233-237 246-247 253 256 258<br>262 265-266 268-269 277 280-281<br>284-286 288-289 298-299 302 309-<br>311 317 321 326 332 335 341-342<br>344 348 350 354 358-359 363 368<br>371-373 382-383 385 394 398 400-<br>401 411 414-415 421 424 430-431<br>433-436 443-446 450-452 454-455<br>458 472-474 476-478 482 484-485<br>487-488 490-494 496-497 500-501<br>503-504 506 509-513 516-517 519<br>524 526-527 529 535-540 547 549<br>562 564 569-570 575-576 588 594-<br>595 601-602 604 606 610 612 615-<br>617 619-623 628-630 634-635 642<br>647 649-651 660 662-665 668 670<br>681 690-694 696 698 700 709 721<br>727-729 732 734 738 740-741 743<br>745 750 759 761 763 765 770 773<br>780 785 795-796 798 802 804 823-<br>824 826 828 833 838 841-845 847<br>849 857-860 867 874-875 878 880-<br>881 887-888 890-892 894-895 898<br>908 910-911 913-914 922-923 926-<br>927 929 932-934 937 939 941-942<br>948 953 957 961 963-964 966 978-<br>979 981-982 987 990 992 1001<br>1004-1006 1010 1014 1020 1024<br>1033 1038-1039 1044 1047 1050<br>1052-1054 1056 1058 1068 1070-<br>1071 1077-1079 1088 1094-1097<br>1105-1106 1112-1113 1116-1117<br>1124 1126 1128-1129 1131 1134<br>1136-1137 1142-1143 1146-1147<br>1149-1150 1156 1161-1164 1167<br>1170-1173 1177-1181 1190 1192<br>1197 1200 1204 1208-1209 1214<br>1217 1219 1222 1230 1232-1233<br>1235 1241 1245 1247 1254 1257-<br>1258 1260 1262 1271-1273 1283<br>1286-1289 1299 1306 1314 1320<br>1330-1332 1334-1335 1342 1345<br>1349 1365-1367 1370-1372 1374<br>1381 1394 1407 1419 1428 1436-<br>1437 1440-1441 1443 1446-1449<br>1454 1459 1461-1462 1468 1470-<br>1471 1475 1477 1479 1482 1491<br>1497-1498 1504-1505 1507 1513<br>1522 1524-1526 1528 1531 1534<br>1536-1537 1548 1550 1553 1555-<br>1559 1562 1567 1578 1590-1591<br>1597 1599-1601 1612 1614 1616<br>1619-1620 1622 1624-1626 1628<br>1631-1632 1634 1636 1639 1644-<br>1645 1648 1651 1653-1656 1658<br>1660 1662-1663 1667 1669 1671<br>1675 1678-1681 1683-1686 1689<br>1691-1692 1703 1709-1711 1717<br>1724-1726 1729 1734 1737-1738<br>1740 1743-1744 1749 1753 1759-<br>1761 1770 1777 1786 |
| trachea       | Clontech   | TRC001             | 9 29-31 46 48 87 104 107 110 135<br>158 222 262 266 286 301 318 331   |

| Tissue Origin | RNA Source | Hyseq<br>Library Name | SEQ ID NOS:  |
|---------------|------------|-----------------------|--|
|               |            |                       | 352 372 377 384 414 424 445-446<br>454 472 474 491 496 560 579 588<br>593 597 607 612 626 681 702 719<br>810 859 866 878 894-895 912 916<br>922 932 935 1046 1075 1080 1099-<br>1102 1113 1208 1215 1232-1233<br>1237 1281 1312 1385 1387 1405<br>1414 1424 1430 1437 1447 1505<br>1569 1579 1586 1600 1641 1653<br>1667 1671 1676-1677 1683 1691-<br>1692 1711 1717 1726 1772   |
| uterus        | Clontech   | UTR001                | 17 19 25 41 46 57-58 61 89 104<br>108 139 152 174 198 200-201 206<br>263-265 274 290 387 408 420 438<br>446 448 452 473 491 493 499 503<br>506 513 519 522 526 530 542-543<br>560 601 610 632 659 665 720 751<br>773 780 833 845 857 872 877 912<br>929 934 937 996 1009-1011 1018<br>1050 1075 1107 1124 1170 1219<br>1258 1279 1287 1310 1320 1323<br>1343-1344 1375 1437 1451-1452<br>1478 1481 1498 1519 1521 1536<br>1552 1579 1597 1602 1606 1620<br>1626-1627 1649 1652 1661 1670<br>1719 1722-1723 |

TRADOCs:1416191.1(%CQN01!.DOC)

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                  | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------|--|----------------------|------------|
| 1          | Y41736           | Homo sapiens             | Human PRO1114 protein sequence.  | 1398                 | 100        |
| 2          | Y66656           | Homo sapiens             | Membrane-bound protein PRO943.   | 2389                 | 99         |
| 3          | AF113136         | Homo sapiens             | IL-1 receptor-associated-kinase-M; IRAK-M  | 3043                 | 100        |
| 4          | AF017806         | Mus musculus             | Zn-15 transcription factor   | 6351                 | 77         |
| 5          | X02761           | Homo sapiens             | fibronectin precursor  | 10535                | 98         |
| 6          | X02761           | Homo sapiens             | fibronectin precursor  | 8990                 | 89         |
| 8          | X02761           | Homo sapiens             | fibronectin precursor  | 12564                | 99         |
| 9          | A0011679         | Homo sapiens             | Rab6 GTPase activating protein, GAPCena  | 5251                 | 99         |
| 10         | W88501           | Homo sapiens             | Human stomach carcinoma clone HP10415-encoded protein.                             | 2381                 | 100        |
| 11         | AF117754         | Homo sapiens             | thyroid hormone receptor-associated protein complex component TRAP240              | 11336                | 98         |
| 12         | Z97630           | Homo sapiens             | dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G))) | 896                  | 100        |
| 13         | Y58620           | Homo sapiens             | Protein regulating gene expression PRGE-13.  | 1894                 | 98         |
| 14         | AF213457         | Homo sapiens             | triggering receptor expressed on myeloid cells 2                                   | 1238                 | 100        |
| 16         | AF233453         | Homo sapiens             | RACK-like protein PRKCBP1  | 3124                 | 99         |
| 17         | AF201303         | Homo sapiens             | dhfr oribeta-binding protein RIP60   | 3130                 | 98         |
| 18         | AF064205         | Homo sapiens             | dynactin 1 p150 isoform  | 6377                 | 100        |
| 19         | U00059           | Saccharomyces cerevisiae | Yhr121wp   | 174                  | 26         |
| 20         | AB032903         | Homo sapiens             | guanosine monophosphate reductase isolog   | 1801                 | 99         |
| 21         | AB032903         | Homo sapiens             | guanosine monophosphate reductase isolog   | 1485                 | 99         |
| 22         | AF140507         | Homo sapiens             | Ca2+/calmodulin-dependent protein kinase kinase beta                               | 3083                 | 99         |
| 23         | AF140507         | Homo sapiens             | Ca2+/calmodulin-dependent protein kinase kinase beta                               | 2300                 | 99         |
| 24         | AJ289131         | Homo sapiens             | chondroitin 4-O-sulfotransferase   | 2211                 | 99         |
| 25         | U33460           | Homo sapiens             | DNA-directed RNA polymerase I, largest subunit                                     | 8777                 | 98         |
| 26         | Y44488           | Homo sapiens             | ACRP30R2 variant protein.  | 1387                 | 100        |
| 27         | U43701           | Homo sapiens             | ribosomal protein L23a   | 791                  | 100        |
| 28         | U02032           | Homo sapiens             | ribosomal protein L23a   | 767                  | 97         |
| 29         | Y41324           | Homo sapiens             | Human secreted protein encoded by gene 17 clone HNF1Y77.                           | 1083                 | 99         |
| 30         | W71749           | Homo sapiens             | Human ubiquitin conjugation system protein 2.                                      | 715                  | 90         |
| 31         | W71749           | Homo sapiens             | Human ubiquitin conjugation system protein 2.                                      | 631                  | 82         |
| 32         | AF231917         | Homo sapiens             | long-chain 2-hydroxy acid oxidase HAOX2  | 1811                 | 100        |
| 33         | Z29481           | Homo sapiens             | 3-hydroxyanthranilic acid dioxygenase  | 1507                 | 99         |
| 34         | AB001451         | Homo sapiens             | Sck  | 2869                 | 100        |
| 35         | Y00644           | Homo sapiens             | precursor polypeptide (AA -34 to 287)  | 1667                 | 99         |
| 36         | Y00644           | Homo sapiens             | precursor polypeptide (AA -34 to 287)  | 1104                 | 98         |
| 37         | Y78795           | Homo sapiens             | Human antizua-2 (AZ-2) amino acid sequence.  | 3586                 | 78         |
| 38         | Y78795           | Homo sapiens             | Human antizua-2 (AZ-2) amino acid sequence.  | 4726                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 39         | Y78795           | Homo sapiens              | Human antizual-2 (A2-2) amino acid sequence.                     | 3556                 | 77         |
| 40         | U93121           | Homo sapiens              | M-phase phosphoprotein-1   | 3747                 | 100        |
| 41         | Y42750           | Homo sapiens              | Human calcium binding protein 1 (CaBP-1).                        | 795                  | 100        |
| 42         | AP282626         | Homo sapiens              | latexin  | 1189                 | 100        |
| 43         | G02150           | Homo sapiens              | Human secreted protein, SEQ ID NO: 6231.                         | 384                  | 94         |
| 44         | U19617           | Mus musculus              | Elf-1  | 2724                 | 88         |
| 45         | U19617           | Mus musculus              | Elf-1  | 2062                 | 86         |
| 46         | AF100758         | Homo sapiens              | osteoinductive factor OIF  | 1538                 | 100        |
| 47         | Y87591           | Homo sapiens              | Human SPROUTY-1 protein, SEQ ID NO:24.                           | 1737                 | 99         |
| 49         | X04145           | Homo sapiens              | T3 gamma precursor (aa -22 to 160)                               | 942                  | 99         |
| 51         | X63547           | Homo sapiens              | oncogene   | 5845                 | 99         |
| 52         | M94043           | Rattus norvegicus         | rab-related GTP-binding protein                                  | 1089                 | 96         |
| 53         | L31783           | Mus musculus              | uridine kinase   | 917                  | 71         |
| 54         | X83973           | Homo sapiens              | transcription factor   | 4486                 | 98         |
| 55         | AF224741         | Homo sapiens              | chloride channel protein 7                                       | 4128                 | 99         |
| 56         | W74805           | Homo sapiens              | Human secreted protein encoded by gene 77 clone HOEAS24.         | 1491                 | 100        |
| 57         | Z50907           | Homo sapiens              | Human TBC-1 cDNA from second transcript.                         | 4824                 | 100        |
| 58         | D79994           | Homo sapiens              | similar to ankyrin of Chromatium vinosum.                        | 6089                 | 99         |
| 59         | D79994           | Homo sapiens              | similar to ankyrin of Chromatium vinosum.                        | 4014                 | 91         |
| 60         | Y59738           | Homo sapiens              | Human normal ovarian tissue derived protein 15.                  | 601                  | 100        |
| 61         | AB031069         | Homo sapiens              | protein containing CXXC domain 1                                 | 1390                 | 100        |
| 62         | Y66660           | Homo sapiens              | Membrane-bound protein PRO783.                                   | 2492                 | 99         |
| 63         | Y66660           | Homo sapiens              | Membrane-bound protein PRO783.                                   | 1709                 | 99         |
| 64         | S70011           | Rattus sp.                | tricarboxylate carrier   | 895                  | 55         |
| 65         | AF139518         | Rattus norvegicus         | A-kinase anchor protein  | 178                  | 24         |
| 66         | W29666           | Homo sapiens              | Homo sapiens DH1308_1 clone secreted protein.                    | 157                  | 30         |
| 67         | AJ245738         | Homo sapiens              | claudin-15   | 1206                 | 100        |
| 68         | AF099138         | Rattus norvegicus         | GLUT4 vesicle protein  | 4183                 | 87         |
| 69         | AF099138         | Rattus norvegicus         | GLUT4 vesicle protein  | 4906                 | 86         |
| 70         | Z82059           | Caenorhabditis elegans    | Similarity to Drosophila ring canal protein comes from this gene | 1285                 | 44         |
| 71         | AF224278         | Homo sapiens              | PMEPA1 protein   | 1282                 | 100        |
| 72         | AF126426         | Homo sapiens              | neurotrimin  | 1809                 | 100        |
| 73         | Y41652           | Homo sapiens              | Human MEK2 protein sequence.                                     | 2065                 | 99         |
| 74         | Y41652           | Homo sapiens              | Human MEK2 protein sequence.                                     | 1207                 | 100        |
| 75         | AF188622         | Mus musculus              | selectively expressed in embryonic epithelia protein-1           | 1485                 | 74         |
| 76         | AB000406         | Escherichia coli          | putative DNA topoisomerase                                       | 950                  | 100        |
| 77         | X99302           | Homo sapiens              | Pop1   | 655                  | 100        |
| 78         | AL136538         | Schizosaccharomyces pombe | similarity to S. cerevisiae ktl12 protein                        | 210                  | 31         |
| 79         | AF129756         | Homo sapiens              | G4   | 1554                 | 99         |



TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES              | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|----------------------|--|----------------------|------------|
| 80         | AL096768         | Homo sapiens         | dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))                  | 2033                 | 100        |
| 81         | AL096768         | Homo sapiens         | dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))                  | 1220                 | 96         |
| 82         | X57351           | Homo sapiens         | 1-8D   | 677                  | 98         |
| 83         | AC005594         | Homo sapiens         | R26984_1   | 2700                 | 98         |
| 84         | X73113           | Homo sapiens         | fast MyBP-C  | 5959                 | 99         |
| 85         | AF097330         | Homo sapiens         | H1 chloride channel; p64H1; CLIC4  | 1305                 | 99         |
| 86         | AB018423         | Mus musculus         | SH2 domain-containing protein  | 1360                 | 78         |
| 87         | AF272151         | Homo sapiens         | adaptor protein CIKS   | 3084                 | 99         |
| 88         | AF196329         | Homo sapiens         | triggering receptor expressed on monocytes 1                                       | 1214                 | 100        |
| 89         | AB016879         | Arabidopsis thaliana | contains similarity to pre-mRNA splicing factor-gene id:MRB17.2                    | 634                  | 36         |
| 90         | AJ133721         | Mus musculus         | homeodomain protein  | 654                  | 57         |
| 91         | AJ242864         | Mus musculus         | phtf protein   | 619                  | 61         |
| 92         | A61971           | unidentified         | MCSP   | 11676                | 99         |
| 93         | Y99365           | Homo sapiens         | Human PRO1250 (UNQ633) amino acid sequence SEQ ID NO:86.                           | 3890                 | 100        |
| 94         | Y87231           | Homo sapiens         | Human signal peptide containing protein HSpp-8 SEQ ID NO:8.                        | 1031                 | 100        |
| 95         | AF227741         | Rattus norvegicus    | protein kinase WNK1  | 2428                 | 95         |
| 96         | AF227741         | Rattus norvegicus    | protein kinase WNK1  | 1961                 | 94         |
| 97         | Y92513           | Homo sapiens         | Human OXRE-10.   | 1626                 | 100        |
| 98         | AL021366         | Homo sapiens         | cICK0721Q.3 (Kinesin related protein)  | 3423                 | 100        |
| 99         | AC005783         | Homo sapiens         | R33083_1   | 1974                 | 99         |
| 100        | Y95293           | Homo sapiens         | Human GEF containing NEK-like kinase substrate sGNK.                               | 4092                 | 99         |
| 101        | AL118501         | Homo sapiens         | dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069)) | 1509                 | 100        |
| 102        | AJ006267         | Homo sapiens         | ClpX-like protein  | 3233                 | 100        |
| 103        | AF100753         | Homo sapiens         | ancient ubiquitous 46 kDa protein AUP1   | 2042                 | 96         |
| 104        | AB015982         | Homo sapiens         | serine/threonine kinase  | 4718                 | 100        |
| 105        | AF151074         | Homo sapiens         | HSPC240  | 831                  | 64         |
| 106        | M35522           | Canis familiaris     | GTP-binding protein (rab7)   | 354                  | 50         |
| 107        | R99800           | Homo sapiens         | NTII-1 nerve protein, facilitates regeneration of nerve cells.                     | 2337                 | 93         |
| 108        | AF125533         | Homo sapiens         | NADH-cytochrome b5 reductase isoform   | 1290                 | 93         |
| 109        | AC005614         | Homo sapiens         | F23269_2   | 3369                 | 99         |
| 110        | AF064729         | Homo sapiens         | RAN binding protein 16   | 3285                 | 100        |
| 111        | X52425           | Homo sapiens         | interleukin 4 receptor   | 4496                 | 100        |
| 112        | Y41686           | Homo sapiens         | Human PRO274 protein sequence.   | 2285                 | 100        |
| 113        | W15506           | Homo sapiens         | Mitogen activating protein kinase ERK1.  | 1991                 | 100        |
| 114        | Y71071           | Homo sapiens         | Human membrane transport protein, MTRP-16.   | 1190                 | 99         |
| 115        | AL049548         | Homo sapiens         | dJ398G3.1 (ortholog of rat CPG2)   | 3497                 | 99         |
| 116        | AF189817         | Mus musculus         | evectin-2  | 1124                 | 90         |
| 117        | W30891           | Homo                 | Human cytoskeleton III protein.  | 715                  | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                  | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------|---|----------------------|------------|
|            |                  | sapiens                  |   |                      |            |
| 118        | AF116618         | Homo sapiens             | PRO1038   | 1469                 | 100        |
| 119        | Y08915           | Homo sapiens             | alpha 4 protein   | 1748                 | 100        |
| 120        | AF098070         | Drosophila melanogaster  | Lis1 homolog  | 192                  | 39         |
| 121        | AF052432         | Homo sapiens             | katanin p80 subunit   | 181                  | 37         |
| 122        | Y70743           | Homo sapiens             | PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling. | 2637                 | 98         |
| 123        | AF083246         | Homo sapiens             | HSPC028   | 2132                 | 100        |
| 124        | Y27096           | Homo sapiens             | Human viral receptor protein (ACVRP).                                   | 833                  | 99         |
| 125        | M63109           | Leishmania major         | glycoprotein 96-92  | 172                  | 27         |
| 126        | U75467           | Drosophila melanogaster  | Atu   | 935                  | 36         |
| 127        | Z68220           | Caenorhabditis elegans   | Similarity to Human ADP/ATP carrier protein                             | 438                  | 43         |
| 128        | AF095927         | Rattus norvegicus        | protein phosphatase 2C  | 1927                 | 94         |
| 129        | W92958           | Homo sapiens             | Human zsig44 protein.   | 463                  | 100        |
| 130        | AF115391         | Lactobacillus sakei      | ribokinase RbsK   | 508                  | 37         |
| 131        | X93498           | Homo sapiens             | 21-Glutamic Acid-Rich Protein   | 1250                 | 100        |
| 132        | X93498           | Homo sapiens             | 21-Glutamic Acid-Rich Protein   | 916                  | 87         |
| 133        | W52811           | Homo sapiens             | Human DBI/ACBP -like protein (DBIH).                                    | 705                  | 97         |
| 134        | Y84444           | Homo sapiens             | Amino acid sequence of a human RNA-associated protein.                  | 3230                 | 100        |
| 135        | M69181           | Homo sapiens             | non-muscle myosin B   | 189                  | 20         |
| 136        | W74882           | Homo sapiens             | Human secreted protein encoded by gene 154 clone HE6FL83.               | 480                  | 100        |
| 137        | W78200           | Homo sapiens             | Human secreted protein encoded by gene 75 clone HHGAU81.                | 855                  | 99         |
| 138        | AL033520         | Homo sapiens             | dJ349A12.1 (similar to KIAA0701 protein)                                | 424                  | 39         |
| 139        | AF020261         | Santalum album           | proline rich protein  | 119                  | 30         |
| 140        | X70394           | Homo sapiens             | zinc finger protein   | 1634                 | 100        |
| 141        | Y06439           | Homo sapiens             | Human protease HUPM-8.  | 936                  | 100        |
| 142        | Z68493           | Caenorhabditis elegans   | predicted using Genefinder  | 365                  | 42         |
| 143        | AB018107         | Arabidopsis thaliana     | ADP-ribosylation factor-like protein                                    | 596                  | 65         |
| 144        | AF161483         | Homo sapiens             | HSPC134   | 580                  | 51         |
| 145        | Y84902           | Homo sapiens             | A human proliferation and apoptosis related protein.                    | 480                  | 100        |
| 146        | AB004906         | Ipomoea purpurea         | transposase   | 146                  | 20         |
| 147        | AC007357         | Arabidopsis thaliana     | F3F19.18  | 647                  | 31         |
| 148        | W75155           | Homo sapiens             | Human secreted protein encoded by gene 41 clone HNTME13.                | 1494                 | 98         |
| 149        | AF056490         | Homo sapiens             | cAMP-specific phosphodiesterase 8A                                      | 3710                 | 99         |
| 150        | Y58171           | Homo sapiens             | Human hydrolase homologue HHH-7.  | 785                  | 99         |
| 151        | U10397           | Saccharomyces cerevisiae | Yhr146wp  | 515                  | 53         |
| 152        | X73478           | Homo sapiens             | phosphotyrosyl phosphatase activator                                    | 1719                 | 99         |
| 153        | AL049697         | Homo sapiens             | dJ382I10.5.1 (novel protein   | 2034                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                              | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|--|----------------------|------------|
|            |                  |                                      | similar to arginyl-tRNA)   |                      |            |
| 154        | AF169802         | Homo sapiens                         | cytochrome b5 reductase b5R.2  | 1455                 | 99         |
| 155        | X94703           | Homo sapiens                         | rab28  | 1126                 | 99         |
| 156        | Y25716           | Homo sapiens                         | Human secreted protein encoded from gene 6.  | 1471                 | 100        |
| 158        | W77404           | Homo sapiens                         | Secreted salivary polypeptide zsig32.  | 937                  | 100        |
| 159        | Y17248           | Homo sapiens                         | Human protein kinase inhibitor-2 (PKI-2).  | 383                  | 100        |
| 160        | J04970           | Homo sapiens                         | carboxypeptidase M precursor   | 2395                 | 100        |
| 161        | W54040           | Homo sapiens                         | Human interferon-inducible protein, HIF1.  | 484                  | 98         |
| 162        | AL022724         | Homo sapiens                         | dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1) | 1357                 | 100        |
| 163        | AF125535         | Homo sapiens                         | pp21 homolog   | 193                  | 45         |
| 164        | G03632           | Homo sapiens                         | Human secreted protein, SEQ ID NO: 7713.   | 463                  | 97         |
| 165        | AJ250839         | Homo sapiens                         | serine/threonine protein kinase  | 1442                 | 71         |
| 166        | L09649           | Zymomonas mobilis                    | zm2  | 173                  | 37         |
| 167        | Y73337           | Homo sapiens                         | HTRM clone 1944530 protein sequence.   | 1204                 | 100        |
| 168        | W88645           | Homo sapiens                         | Secreted protein encoded by gene 112 clone HUKFC71.  | 1084                 | 100        |
| 169        | AF214731         | Homo sapiens                         | ATP-dependent RNA helicase   | 4402                 | 100        |
| 170        | AE000871         | Methanobacterium thermoautotrophicum | conserved protein  | 166                  | 27         |
| 171        | Y27684           | Homo sapiens                         | Human secreted protein encoded by gene No. 118.  | 821                  | 100        |
| 172        | AF226044         | Homo sapiens                         | HSNFRK   | 2904                 | 100        |
| 173        | AJ245946         | Homo sapiens                         | neuroglobin  | 779                  | 100        |
| 174        | D43949           | Homo sapiens                         | This gene is novel.  | 3202                 | 100        |
| 175        | Y07923           | Homo sapiens                         | GTP-binding protein  | 1205                 | 100        |
| 176        | W90338           | Homo sapiens                         | Human DP1 homologue protein.   | 966                  | 100        |
| 177        | Y41675           | Homo sapiens                         | Human channel-related molecule HCRM-1.   | 1122                 | 100        |
| 178        | Y41674           | Homo sapiens                         | Human channel-related molecule HCRM-2.   | 936                  | 99         |
| 179        | AF220492         | Homo sapiens                         | krueppel-like zinc finger protein HZF2   | 4100                 | 99         |
| 180        | X03084           | Homo sapiens                         | C1q B-chain precursor  | 1240                 | 100        |
| 181        | U57344           | Mus musculus                         | Meis3  | 1813                 | 89         |
| 183        | U57344           | Mus musculus                         | Meis3  | 1743                 | 86         |
| 184        | U57344           | Mus musculus                         | Meis3  | 1070                 | 86         |
| 185        | AF033120         | Homo sapiens                         | p53 regulated PA26-T2 nuclear protein  | 1389                 | 58         |
| 186        | AF200357         | Mus musculus                         | pantothenate kinase 1 beta   | 1605                 | 82         |
| 187        | W75058           | Homo sapiens                         | Human secreted protein encoded by gene 2 clone HLDBG33.                                      | 1188                 | 99         |
| 188        | AJ292529         | Homo sapiens                         | suppressor of sterile four 1   | 2424                 | 100        |
| 190        | X54134           | Homo sapiens                         | protein-tyrosine phosphatase   | 3705                 | 100        |
| 191        | Y22203           | Homo sapiens                         | Human calcium-binding phosphoprotein, CBPP-1, protein sequence.                              | 1083                 | 99         |
| 192        | W63692           | Homo sapiens                         | Human secreted protein 12.   | 1975                 | 100        |
| 193        | W87772           | Homo sapiens                         | Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.                            | 2605                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 194        | AF084259         | Mus musculus              | bromodomain-containing protein BP75                            | 693                  | 54         |
| 195        | Y00752           | Rattus norvegicus         | serine dehydratase (AA 1 - 327)                                | 994                  | 61         |
| 196        | W95349           | Homo sapiens              | Human foetal brain secreted protein fh170_7.                   | 2596                 | 100        |
| 197        | AB028859         | Homo sapiens              | hdj9   | 1890                 | 100        |
| 198        | W95633           | Homo sapiens              | Homo sapiens secreted protein gene clone hm236_1.              | 1614                 | 100        |
| 199        | Y44277           | Homo sapiens              | Human nucleic acid methylase-2.                                | 2096                 | 99         |
| 200        | AB030039         | Homo sapiens              | hPACPL1  | 2258                 | 100        |
| 201        | X54162           | Homo sapiens              | 64 Kd autoantigen  | 2918                 | 99         |
| 202        | G02061           | Homo sapiens              | Human secreted protein, SEQ ID NO: 6142.                       | 558                  | 99         |
| 203        | X13885           | Nicotiana tabacum         | extensin (AA 1-620)  | 185                  | 33         |
| 204        | J04204           | Bos taurus                | 32 kd accessory protein  | 1837                 | 100        |
| 205        | J04204           | Bos taurus                | 32 kd accessory protein  | 1101                 | 100        |
| 207        | Y87283           | Homo sapiens              | Human signal peptide containing protein HSP60-60 SEQ ID NO:60. | 1318                 | 100        |
| 208        | Y02860           | Homo sapiens              | Fragment of human secreted protein encoded by gene 65.         | 936                  | 98         |
| 209        | AL121889         | Homo sapiens              | dJ1076E17.1 (KIAA0823 protein (continues in AL023803))         | 694                  | 54         |
| 210        | AF226732         | Homo sapiens              | NPD007   | 1345                 | 76         |
| 211        | X66295           | Mus musculus              | Clq C chain  | 970                  | 73         |
| 212        | Z29328           | Homo sapiens              | Ubiquitin-conjugating enzyme Ubch2                             | 966                  | 100        |
| 213        | Z29328           | Homo sapiens              | Ubiquitin-conjugating enzyme Ubch2                             | 542                  | 98         |
| 214        | AJ002030         | Homo sapiens              | progesterone binding protein                                   | 1163                 | 100        |
| 215        | X70649           | Homo sapiens              | member of DEAD box protein family                              | 3933                 | 100        |
| 216        | AF250558         | Homo sapiens              | claudin-2  | 1169                 | 99         |
| 217        | AL021453         | Homo sapiens              | dJ821D11.1 (PUTATIVE protein)                                  | 259                  | 100        |
| 218        | Y08565           | Homo sapiens              | UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase       | 3331                 | 99         |
| 219        | Y94452           | Homo sapiens              | Human inflammation associated protein                          | 2067                 | 100        |
| 220        | AL035521         | Arabidopsis thaliana      | putative protein   | 315                  | 42         |
| 221        | AL031786         | Schizosaccharomyces pombe | putative proline-trna synthetase                               | 811                  | 41         |
| 222        | AL109736         | Schizosaccharomyces pombe | WD repeat protein  | 626                  | 40         |
| 223        | X52493           | Glycine max               | DNA-directed RNA polymerase                                    | 136                  | 23         |
| 224        | AL035659         | Homo sapiens              | dJ979N1.1 (dJ979N1.1)  | 5199                 | 98         |
| 225        | AB032401         | Mus musculus              | mmDj4  | 1761                 | 92         |
| 226        | AB032401         | Mus musculus              | mmDj4  | 1988                 | 92         |
| 227        | X83502           | Saccharomyces cerevisiae  | J1007  | 112                  | 26         |
| 228        | X83502           | Saccharomyces cerevisiae  | J1007  | 79                   | 25         |
| 229        | AF143723         | Homo sapiens              | heat shock protein HSP60                                       | 2557                 | 99         |
| 230        | Y66677           | Homo sapiens              | Membrane-bound protein PR0828.                                 | 982                  | 100        |
| 231        | AB027466         | Homo sapiens              | spondin 2  | 1756                 | 99         |
| 232        | W95634           | Homo sapiens              | Homo sapiens secreted protein.                                 | 1391                 | 100        |
| 233        | W00365           | Homo sapiens              | Human cyclin B1.   | 2218                 | 99         |
| 234        | Y53762           | Homo sapiens              | A GTP-binding polypeptide                                      | 1017                 | 100        |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                              | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|---|----------------------|------------|
|            |                  |                                      | designated RAQ.   |                      |            |
| 235        | Z50749           | Homo sapiens                         | yeast sds22 homolog   | 1800                 | 100        |
| 236        | Z50749           | Homo sapiens                         | yeast sds22 homolog   | 1754                 | 98         |
| 237        | AB026491         | Homo sapiens                         | PICK1   | 2137                 | 100        |
| 238        | AJ270205         | Entodinium caudatum                  | putative phosphatidylinositol-4-phosphate 5-kinase  | 114                  | 37         |
| 239        | AB030189         | Mus musculus                         | contains transmembrane (TM) region and ATP binding region                                   | 710                  | 93         |
| 240        | W56538           | Homo sapiens                         | Human hedgehog interacting protein (HIP).   | 3785                 | 99         |
| 241        | W56538           | Homo sapiens                         | Human hedgehog interacting protein (HIP).   | 3436                 | 99         |
| 242        | AF155107         | Homo sapiens                         | NY-REN-37 antigen   | 996                  | 99         |
| 243        | AF155107         | Homo sapiens                         | NY-REN-37 antigen   | 1005                 | 100        |
| 244        | AL031320         | Homo sapiens                         | dJ20N2.1 (novel protein similar to yeast and bacterial cytosine deaminase)                  | 763                  | 99         |
| 245        | U37026           | Rattus norvegicus                    | sodium channel beta 2 subunit   | 162                  | 30         |
| 246        | AL078599         | Homo sapiens                         | dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:P91086))                        | 2391                 | 98         |
| 247        | U32274           | Saccharomyces cerevisiae             | Ydr386wp; CAI: 0.12   | 191                  | 37         |
| 248        | Y41719           | Homo sapiens                         | Human PRO864 protein sequence.  | 1879                 | 100        |
| 249        | AB029434         | Homo sapiens                         | ghrelin precursor   | 611                  | 100        |
| 250        | X97831           | Rattus norvegicus                    | carnitine/acylcarnitine carrier protein   | 246                  | 38         |
| 251        | W80993           | Homo sapiens                         | Human RIP-interacting factor RIF.   | 1724                 | 100        |
| 252        | Y94873           | Homo sapiens                         | Human protein clone HP02632.  | 1876                 | 100        |
| 253        | W59878           | Homo sapiens                         | Amino acid sequence of the cDNA clone AIF-2 (HEBGM49).                                      | 765                  | 100        |
| 254        | AL354533         | Leishmania major                     | possible adenylate kinase   | 265                  | 34         |
| 255        | AF233322         | Mus musculus                         | zinc transporter like 2   | 1916                 | 95         |
| 256        | Y78113           | Homo sapiens                         | Human cytokine signal regulator CKSR-1 SEQ ID NO:1.   | 2247                 | 99         |
| 257        | AL035539         | Arabidopsis thaliana                 | putative amino acid transport protein   | 390                  | 27         |
| 258        | W74787           | Homo sapiens                         | Human secreted protein encoded by gene 58 clone HHFHN61.                                    | 1171                 | 100        |
| 259        | AL035689         | Homo sapiens                         | dJ187J11.1 (novel protein similar to protein kinase C inhibitors)                           | 974                  | 100        |
| 260        | AE000909         | Methanobacterium thermoautotrophicum | serine/threonine protein kinase related protein   | 363                  | 30         |
| 261        | AL050131         | Homo sapiens                         | hypothetical protein  | 626                  | 100        |
| 262        | AF019661         | Mus musculus                         | zeta proteasome chain; PSMA5  | 1214                 | 100        |
| 263        | AL035593         | Homo sapiens                         | dJ310J6.1 (novel protein)   | 821                  | 100        |
| 264        | AL022318         | Homo sapiens                         | dK150C2.3 (PUTATIVE novel protein similar to APOBEC1)                                       | 1072                 | 100        |
| 265        | AF205940         | Homo sapiens                         | endomucin   | 1289                 | 100        |
| 266        | AL023583         | Homo sapiens                         | dJ500L14.1 (novel protein)  | 789                  | 100        |
| 267        | AL034548         | Homo sapiens                         | dJ1103G7.3 (novel protein kinase domains containing protein similar to phosphoprotein C8FW) | 1888                 | 99         |

TABLE 2

| SEQ ID NO. | ACCESSION NUMBER | SPECIES              | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|----------------------|---|----------------------|------------|
| 268        | AF161470         | Homo sapiens         | HSPC121   | 1884                 | 98         |
| 269        | AF161470         | Homo sapiens         | HSPC121   | 1232                 | 96         |
| 270        | X90763           | Homo sapiens         | Hha5 hair keratin type I intermediate filament                        | 2190                 | 99         |
| 271        | AF207600         | Homo sapiens         | ethanolamine kinase   | 1952                 | 100        |
| 272        | M32334           | Homo sapiens         | intercellular adhesion molecule 2                                     | 1436                 | 100        |
| 273        | AF161483         | Homo sapiens         | HSPC134   | 663                  | 61         |
| 274        | Y53652           | Homo sapiens         | Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.  | 587                  | 100        |
| 276        | Y77576           | Homo sapiens         | Human cytoskeletal protein (HCTT) (clone 2195418).                    | 762                  | 100        |
| 277        | AF077042         | Homo sapiens         | 30S ribosomal protein S7 homolog                                      | 1269                 | 100        |
| 278        | Y94907           | Homo sapiens         | Human secreted protein clone cal06_19x protein sequence SEQ ID NO:20. | 1619                 | 98         |
| 279        | Y68788           | Homo sapiens         | Amino acid sequence of a human phosphorylation effector PHSP-20.      | 2801                 | 99         |
| 280        | Z75134           | Canis familiaris     | rod transducin  | 1816                 | 100        |
| 281        | Z75134           | Canis familiaris     | rod transducin  | 1718                 | 96         |
| 282        | AF249873         | Homo sapiens         | muscle-specific protein   | 1395                 | 100        |
| 283        | AL050007         | Homo sapiens         | hypothetical protein  | 405                  | 98         |
| 284        | AF201931         | Homo sapiens         | DC1   | 1859                 | 99         |
| 285        | AF156102         | Homo sapiens         | ELL complex EAP30 subunit   | 1318                 | 99         |
| 286        | Y35897           | Homo sapiens         | Extended human secreted protein sequence, SEQ ID NO. 146.             | 1250                 | 99         |
| 287        | U88964           | Homo sapiens         | HEM45   | 923                  | 100        |
| 288        | AL050143         | Homo sapiens         | hypothetical protein  | 598                  | 100        |
| 289        | AJ011098         | Homo sapiens         | telethonin  | 574                  | 100        |
| 290        | Y66724           | Homo sapiens         | Membrane-bound protein PRO836.  | 2321                 | 100        |
| 291        | AF034801         | Homo sapiens         | liprin-alpha4   | 2565                 | 98         |
| 292        | AF034801         | Homo sapiens         | liprin-alpha4   | 2590                 | 100        |
| 293        | AL049851         | Homo sapiens         | dJ889J228.1 (novel protein (isoform 1))                               | 1738                 | 100        |
| 294        | Y73348           | Homo sapiens         | HTRM clone 839651 protein sequence.                                   | 1245                 | 99         |
| 295        | L11672           | Homo sapiens         | zinc finger protein   | 1694                 | 44         |
| 296        | AL035423         | Homo sapiens         | dJ2013.1 (brain mitochondrial carrier protein-1 (BMCP1))              | 1024                 | 79         |
| 297        | AF198532         | Homo sapiens         | lymphoid enhancer binding factor-1                                    | 2173                 | 100        |
| 298        | AF161417         | Homo sapiens         | HSPC299   | 1147                 | 85         |
| 299        | AF159141         | Homo sapiens         | breast cancer metastasis-suppressor 1                                 | 1236                 | 99         |
| 300        | U26397           | Rattus norvegicus    | inositol polyphosphate 4-phosphatase                                  | 160                  | 30         |
| 301        | AF036145         | Homo sapiens         | meningioma-expressed antigen 5  | 3458                 | 100        |
| 302        | Z82022           | Homo sapiens         | GlcNAc-1-P transferase  | 2067                 | 99         |
| 303        | AF269232         | Mus musculus         | butyrophilin-like protein BUTR-1                                      | 271                  | 50         |
| 304        | AJ222644         | Arabidopsis thaliana | asparaginyl-tRNA synthetase   | 659                  | 50         |
| 305        | AF054180         | Homo sapiens         | hematopoietic cell derived zinc finger protein                        | 351                  | 79         |
| 306        | AJ272079         | Homo sapiens         | APOBEC-1 stimulating protein  | 3056                 | 100        |
| 308        | Y44486           | Homo sapiens         | Human GPRW receptor polypeptide.                                      | 1721                 | 100        |
| 309        | AJ131891         | Homo sapiens         | DNA polymerase mu   | 2598                 | 100        |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES  | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--|--|----------------------|------------|
| 310        | AF293335         | Homo sapiens   | p30 DBC  | 1248                 | 92         |
| 311        | AF176525         | Mus musculus   | F-box protein FBL12  | 1501                 | 93         |
| 312        | X57802           | Homo sapiens   | immunoglobulin lambda light chain                                    | 959                  | 81         |
| 313        | Z36715           | Homo sapiens   | Net  | 2048                 | 98         |
| 314        | AF161532         | Homo sapiens   | HSPC047  | 727                  | 100        |
| 315        | AF208068         | Homo sapiens   | kelch-like protein KLHL3a  | 3046                 | 100        |
| 316        | Y66666           | Homo sapiens   | Membrane-bound protein PRO1013.                                      | 1166                 | 100        |
| 317        | Y29666           | Homo sapiens   | Human Ras protein RAPR-1.  | 1253                 | 98         |
| 318        | AJ387747         | Homo sapiens   | sialin   | 2614                 | 99         |
| 319        | AF161362         | Homo sapiens   | HSPC099  | 224                  | 40         |
| 320        | Y68773           | Homo sapiens   | Amino acid sequence of a human phosphorylation effector PHSP-5.      | 2243                 | 99         |
| 321        | AJ238379         | Homo sapiens   | putative TH1 protein   | 3013                 | 100        |
| 322        | AB040812         | Homo sapiens   | protein kinase PAK5  | 3792                 | 99         |
| 323        | Y95013           | Homo sapiens   | Human secreted protein vc48_1, SEQ ID NO:66.                         | 913                  | 100        |
| 324        | Y13381           | Homo sapiens   | Amino acid sequence of protein PRO271.                               | 1976                 | 100        |
| 325        | Y94944           | Homo sapiens   | Human secreted protein clone bf157_16 protein sequence SEQ ID NO:94. | 2305                 | 98         |
| 326        | Y76884           | Homo sapiens   | Retinoblastoma binding protein-7sequence.                            | 6728                 | 99         |
| 327        | AF198532         | Homo sapiens   | lymphoid enhancer binding factor-1                                   | 2173                 | 100        |
| 328        | Z78013           | Caenorhabditis elegans   | Similarity to Drosophila Cadherin-related tumor suppressor           | 569                  | 33         |
| 329        | AF212921         | Mus musculus   | MMTV receptor variant 1  | 484                  | 94         |
| 330        | Z75330           | Homo sapiens]<br>>R65207<br>R65207 02-MAR-1995 27-AUG-1993<br>Human stromalin-1. (Homo sapiens | nuclear protein SA-1   | 6492                 | 99         |
| 331        | AL008583         | Homo sapiens   | dJ327J16.3 (supported by GENSCAN, FGENES and GENEWISE)               | 2133                 | 99         |
| 332        | Y36104           | Homo sapiens   | Extended human secreted protein sequence, SEQ ID NO. 489.            | 310                  | 41         |
| 333        | AJ271669         | Homo sapiens   | putative sialoglycoprotease  | 1747                 | 100        |
| 334        | AF156598         | Mus musculus   | p53-regulated DDA3   | 997                  | 64         |
| 335        | M99058           | Eimeria maxima   | em100 gene is homologous the Eimeria tenella gene et100              | 154                  | 26         |
| 336        | Y85564           | Homo sapiens   | Human homologue of UNC-53 (Hs-UNC-53/1) sequence.                    | 3386                 | 97         |
| 337        | Y85564           | Homo sapiens   | Human homologue of UNC-53 (Hs-UNC-53/1) . sequence.                  | 2602                 | 94         |
| 338        | Y85564           | Homo sapiens   | Human homologue of UNC-53 (Hs-UNC-53/1) sequence.                    | 3447                 | 98         |
| 339        | Z66561           | Caenorhabditis elegans   | Similarity to Human rab13 protein (PIR Acc. No. A49647).             | 716                  | 34         |
| 340        | AB021643         | Homo sapiens   | gonadotropin inducible transcription repressor-3                     | 2761                 | 99         |
| 341        | G01946           | Homo sapiens   | Human secreted protein, SEQ ID NO: 6027.                             | 465                  | 98         |
| 342        | AF020591         | Homo sapiens   | zinc finger protein  | 1091                 | 48         |
| 343        | L29154           | Homo sapiens   | immunoglobulin heavy chain   | 439                  | 84         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                 | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
|            |                  |                         | VDJ region  |                      |            |
| 344        | U10281           | Sus scrofa              | gastric mucin   |                      |            |
| 345        | AK000404         | Homo sapiens            | unnamed protein product   | 279                  | 24         |
| 346        | L22557           | Rattus norvegicus       | calmodulin-binding protein  | 1177                 | 99         |
| 347        | L22557           | Rattus norvegicus       | calmodulin-binding protein  | 1949                 | 84         |
| 348        | AL049481         | Arabidopsis thaliana    | AIG1-like protein   | 2363                 | 91         |
| 350        | AJ251516         | Mus musculus            | cysteine and histidine-rich protein                                 | 316                  | 30         |
| 351        | AK024477         | Homo sapiens            | FLJ00070 protein  | 1460                 | 99         |
| 352        | U50133           | Homo sapiens            | ankyrin   | 1773                 | 100        |
| 353        | AK000625         | Homo sapiens            | unnamed protein product   | 502                  | 33         |
| 354        | AF161420         | Homo sapiens            | HSPC302   | 721                  | 100        |
| 355        | AJ010014         | Homo sapiens            | M96A protein  | 2623                 | 97         |
| 356        | AF151029         | Homo sapiens            | HSPC195   | 1269                 | 47         |
| 357        | AL022327         | Homo sapiens            | dj355c18.1 (KIAA0027)   | 941                  | 91         |
| 358        | W78128           | Homo sapiens            | Human secreted protein encoded by gene 3 clone HOSBI96.             | 1911                 | 100        |
|            |                  |                         |   | 1117                 | 100        |
| 359        | X03414           | Drosophila melanogaster | Kr polypeptide  | 316                  | 45         |
| 360        | AF151079         | Homo sapiens            | HSPC245   | 643                  | 100        |
| 361        | Y53886           | Homo sapiens            | A suppressor of cytokine signalling protein designated HSCOP-6.     | 530                  | 41         |
| 362        | AF254741         | Drosophila melanogaster | Centaurin Gamma 1A  | 681                  | 46         |
| 363        | AF213465         | Homo sapiens            | dual oxidase  | 2016                 | 100        |
| 364        | AF181562         | Homo sapiens            | proSAAS   | 1319                 | 100        |
| 365        | AF181562         | Homo sapiens            | proSAAS   | 1024                 | 99         |
| 366        | U73200           | Mus musculus            | pl16Rip   | 884                  | 82         |
| 367        | AP263744         | Homo sapiens            | erbB2-interacting protein ERBIN                                     | 4973                 | 99         |
| 368        | U37501           | Mus musculus            | laminin alpha 5 chain   | 5867                 | 72         |
| 369        | AF043695         | Caenorhabditis elegans  | similar to the protein phosphates 2c family                         | 549                  | 36         |
| 370        | Y73440           | Homo sapiens            | Human secreted protein clone yj23.1 protein sequence SEQ ID NO:102. | 1484                 | 99         |
| 371        | AF272833         | Homo sapiens            | misato  | 2869                 | 97         |
| 372        | AF198454         | Homo sapiens            | epithelial protein lost in neoplasm beta                            | 3927                 | 100        |
| 373        | Y73345           | Homo sapiens            | HTRM clone 438283 protein sequence.                                 | 273                  | 80         |
| 374        | AF169017         | Homo sapiens            | formiminotransferase cyclodeaminase                                 | 2717                 | 98         |
| 375        | A95106           | unidentified            | RED ALPHA   | 1202                 | 99         |
| 376        | W74828           | Homo sapiens            | Human secreted protein encoded by gene 100 clone HLQA352.           | 1012                 | 99         |
| 377        | Y32131           | Homo sapiens            | Human LYST-2 protein.   | 3556                 | 99         |
| 378        | M14912           | Homo sapiens            | pol   | 132                  | 86         |
| 379        | AF090934         | Homo sapiens            | PRO0518   | 382                  | 100        |
| 380        | X66363           | Homo sapiens            | serine/threonine protein kinase                                     | 2499                 | 100        |
| 381        | Y41699           | Homo sapiens            | Human PRO703 protein sequence.                                      | 2362                 | 100        |
| 382        | AF174498         | Homo sapiens            | GR AF-1 specific protein phosphatase                                | 7008                 | 98         |
| 383        | U64608           | Caenorhabditis elegans  | coded for by C. elegans cDNA yk173c12.5                             | 246                  | 36         |
| 384        | U50133           | Homo sapiens            | ankyrin   | 502                  | 33         |
| 385        | AJ238520         | Homo sapiens            | putative transcription factor-like nuclear regulator                | 4123                 | 97         |



TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 387        | AF208845         | Homo sapiens              | BM-003   | 1375                 | 99         |
| 389        | X57821           | Homo sapiens              | immunoglobulin lambda light chain  | 797                  | 76         |
| 390        | AF182404         | Homo sapiens              | mitochondrial uncoupling protein 1   | 1670                 | 99         |
| 391        | Y85564           | Homo sapiens              | Human homologue of UNC-53 (Hs-UNC-53/1) sequence.                          | 3386                 | 97         |
| 393        | AF178432         | Homo sapiens              | SH3 protein  | 3700                 | 100        |
| 394        | AF229928         | Drosophila melanogaster   | cytoplasmic protein 89BC   | 1616                 | 62         |
| 395        | AF181721         | Homo sapiens              | RU2S   | 2254                 | 100        |
| 396        | Y69197           | Homo sapiens              | Amino acid sequence of a human betaIV-spectrin protein.                    | 1626                 | 98         |
| 397        | U48238           | Mus musculus              | zinc finger protein neuro-d4   | 749                  | 60         |
| 398        | AL390137         | Homo sapiens              | hypothetical protein   | 263                  | 51         |
| 399        | AF217525         | Homo sapiens              | Down syndrome cell adhesion molecule                                       | 5337                 | 60         |
| 400        | AL022599         | Schizosaccharomyces pombe | WD repeat protein  | 447                  | 27         |
| 401        | AC004859         | Homo sapiens              | similar to 2-oxoglutarate dehydrogenase ; similar to Q02218 (PID:q1352618) | 4176                 | 78         |
| 402        | AB010266         | Mus musculus              | tenascin-X   | 10246                | 62         |
| 403        | AL133288         | Homo sapiens              | dJ671D7.1 (similar to D.melanogaster CG5986 protein)                       | 761                  | 100        |
| 404        | Z68753           | Caenorhabditis elegans    | ZCS18.3b   | 888                  | 48         |
| 405        | Z78013           | Caenorhabditis elegans    | Similarity to Drosophila Cadherin-related tumor suppressor                 | 569                  | 33         |
| 406        | AB031230         | Homo sapiens              | protein containing CXXC domain-2   | 1196                 | 97         |
| 407        | AF155106         | Homo sapiens              | NY-REN-36 antigen  | 1168                 | 100        |
| 408        | Y57945           | Homo sapiens              | Human transmembrane protein HTMPN-69.                                      | 1538                 | 99         |
| 409        | Z18361           | Ovis aries                | trichohyalin   | 184                  | 30         |
| 410        | AF249744         | Homo sapiens              | RhoGEF   | 2733                 | 100        |
| 411        | AF176529         | Mus musculus              | F-box protein FBX13  | 2072                 | 94         |
| 412        | AF210842         | Homo sapiens              | HARP   | 4880                 | 100        |
| 413        | AL031658         | Homo sapiens              | dJ310013.7 (novel protein similar to H. roretzi HRPET-3)                   | 776                  | 98         |
| 414        | X57398           | Homo sapiens              | pm5 protein  | 6131                 | 99         |
| 415        | AB029826         | Homo sapiens              | 3-methylcrotonyl-CoA carboxylase biotin-containing subunit                 | 2961                 | 99         |
| 416        | U43503           | Saccharomyces cerevisiae  | Lph1p  | 115                  | 42         |
| 417        | AL160493         | Leishmania major          | possible t26f17.21   | 239                  | 35         |
| 418        | Y08100           | Homo sapiens              | Human PRO331 protein.  | 330                  | 29         |
| 419        | U15131           | Homo sapiens              | p126   | 2228                 | 54         |
| 420        | AF117946         | Homo sapiens              | Link guanine nucleotide exchange factor II                                 | 2363                 | 100        |
| 421        | AF190635         | Drosophila melanogaster   | ankyrin 2  | 755                  | 30         |
| 422        | AF302150         | Homo sapiens              | phosphoinositol 3-phosphate-binding protein-2                              | 1962                 | 100        |
| 423        | AL137530         | Homo sapiens              | hypothetical protein   | 433                  | 94         |
| 424        | X63753           | Homo sapiens              | son-a  | 7269                 | 100        |
| 425        | AB027249         | Homo sapiens              | MAPKK like protein kinase  | 1693                 | 100        |
| 426        | AF279144         | Homo sapiens              | tumor endothelial marker 7 precursor                                       | 1084                 | 55         |

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| SEQ ID NO: | ACCESSION NUMBER | SPECIES                 | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 427        | AF279144         | Homo sapiens            | tumor endothelial marker 7 precursor                                | 1259                 | 56         |
| 428        | AE003683         | Drosophila melanogaster | CG8312 gene product   | 149                  | 29         |
| 429        | Y07829           | Homo sapiens            | RING finger protein   | 2201                 | 99         |
| 430        | AF096897         | Drosophila melanogaster | pushover  | 4442                 | 47         |
| 431        | U41387           | Homo sapiens            | Gu protein  | 4021                 | 99         |
| 432        | AF023674         | Homo sapiens            | nephrocystin  | 3783                 | 100        |
| 433        | AF146760         | Homo sapiens            | septin 2-like cell division control protein                         | 2284                 | 100        |
| 434        | AB006697         | Arabidopsis thaliana    | cleft lip and palate associated transmembrane protein-like          | 886                  | 42         |
| 437        | Y94247           | Homo sapiens            | Human calcium binding protein hCBP.                                 | 1704                 | 100        |
| 438        | AB040672         | Homo sapiens            | UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase           | 1075                 | 63         |
| 439        | AF105228         | Bos taurus              | tuftelin  | 285                  | 33         |
| 440        | R06463           | Homo sapiens            | Derived protein of clone ICA13 (ATCC 40553).                        | 3073                 | 95         |
| 441        | X14971           | Mus musculus            | alpha-adaptin (A) (AA 1-977)  | 4897                 | 98         |
| 442        | X53773           | Rattus norvegicus       | alpha-c large chain (AA 1-938)                                      | 3979                 | 81         |
| 443        | Y66689           | Homo sapiens            | Membrane-bound protein PRO1136.                                     | 3299                 | 99         |
| 444        | AC067754         | Arabidopsis thaliana    | unknown protein; 20348-23707  | 114                  | 33         |
| 445        | AF229032         | Mus musculus            | pIL   | 2077                 | 93         |
| 446        | AF056035         | Rattus norvegicus       | s-nexilin   | 2662                 | 85         |
| 447        | AF132484         | Mus musculus            | unknown   | 478                  | 51         |
| 448        | W89024           | Homo sapiens            | Polypeptide fragment encoded by gene 156.                           | 528                  | 45         |
| 449        | AF161445         | Homo sapiens            | HSPC327   | 1606                 | 100        |
| 450        | Z68753           | Caenorhabditis elegans  | ZC518.3b  | 951                  | 49         |
| 451        | W39160           | Homo sapiens            | Human partial complement factor H protein fragment 3.               | 155                  | 32         |
| 452        | W85727           | Homo sapiens            | Novel protein (Clone BM46.10).                                      | 2799                 | 99         |
| 453        | Y53629           | Homo sapiens            | A bone marrow secreted protein designated BMS115.                   | 2810                 | 100        |
| 454        | D87438           | Homo sapiens            | Similar to a C.elegans protein in cosmid C14H10                     | 4069                 | 100        |
| 455        | AF240468         | Homo sapiens            | nicastatin  | 3687                 | 100        |
| 456        | Z15005           | Homo sapiens            | CENP-E  | 13305                | 99         |
| 457        | M59216           | Homo sapiens            | gamma-aminobutyric acid receptor beta-1 subunit                     | 2477                 | 100        |
| 458        | Y73467           | Homo sapiens            | Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156. | 966                  | 100        |
| 459        | W67824           | Homo sapiens            | Human secreted protein encoded by gene 18 clone HSLFM29.            | 535                  | 100        |
| 460        | AF163151         | Homo sapiens            | dentin sialophosphoprotein precursor                                | 279                  | 19         |
| 461        | D87446           | Homo sapiens            | Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)     | 9196                 | 99         |
| 462        | G04044           | Homo sapiens            | Human secreted protein, SEQ ID NO: 8125.                            | 486                  | 93         |
| 463        | AC002398         | Homo sapiens            | F25965_1  | 1018                 | 100        |
| 464        | AF064856         | Rattus sp.              | 7acomp protein  | 1845                 | 84         |
| 465        | AF223408         | Homo sapiens            | B99   | 3686                 | 99         |

TABLE 2

| SEQ ID NO. | ACCESSION NUMBER | SPECIES                   | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|---|----------------------|------------|
| 466        | AF223408         | Homo sapiens              | B99   | 2878                 | 87         |
| 467        | AF104415         | Mus musculus              | gene trap locus-13  | 6336                 | 91         |
| 468        | U53450           | Rattus norvegicus         | Jun dimerization protein 1 JDP-1  | 196                  | 49         |
| 469        | AL031297         | Homo sapiens              | dJ97P20.1 (novel gene)  | 3564                 | 99         |
| 470        | AF257077         | Homo sapiens              | eukaryotic translation initiation factor EIF2B subunit 3                        | 1274                 | 95         |
| 471        | L28125           | Podospora anserina        | beta transducin-like protein  | 284                  | 38         |
| 472        | Y84903           | Homo sapiens              | A human proliferation and apoptosis related protein.                            | 2337                 | 100        |
| 473        | AF144237         | Homo sapiens              | LOMP protein  | 252                  | 44         |
| 474        | Y71213           | Homo sapiens              | Human irritable bowel disease related polypeptide IMX39.                        | 838                  | 100        |
| 475        | Y95006           | Homo sapiens              | Human secreted protein vel3_1, SEQ ID NO:52.                                    | 3411                 | 100        |
| 476        | D38549           | Homo sapiens              | hal025 is new   | 6533                 | 99         |
| 477        | AF241230         | Homo sapiens              | TAK1-binding protein 2  | 3656                 | 100        |
| 478        | AL031534         | Schizosaccharomyces pombe | putative asparagine synthase  | 482                  | 40         |
| 479        | L28125           | Podospora anserina        | beta transducin-like protein  | 233                  | 26         |
| 480        | AF161544         | Homo sapiens              | HSPC059   | 434                  | 77         |
| 481        | AJ238248         | Homo sapiens              | centaurin beta2   | 3986                 | 99         |
| 482        | Z38061           | Saccharomyces cerevisiae  | mal5, stal, len: 1367, CAI: 0.3, AMYH YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3) | 295                  | 23         |
| 483        | AF161381         | Homo sapiens              | HSPC263   | 1404                 | 100        |
| 484        | AF223468         | Homo sapiens              | AD021 protein   | 1314                 | 100        |
| 486        | X57527           | Homo sapiens              | alpha 1(VIII) collagen  | 4166                 | 99         |
| 487        | Y19062           | Homo sapiens              | 39k3 protein  | 2475                 | 100        |
| 488        | Y73373           | Homo sapiens              | HTRM clone 921803 protein sequence.   | 555                  | 56         |
| 489        | AL021918         | Homo sapiens              | B34Y8.1 (Kruppel related Zinc Finger protein 184)                               | 4184                 | 100        |
| 490        | X53773           | Rattus norvegicus         | alpha-c large chain (AA 1-938)  | 4675                 | 97         |
| 491        | U52426           | Homo sapiens              | GOK   | 1459                 | 59         |
| 492        | AL359773         | Leishmania major          | possible threonine synthase   | 702                  | 45         |
| 493        | AF226614         | Homo sapiens              | ferroportin1  | 2929                 | 100        |
| 494        | Z93241           | Homo sapiens              | dJ222E13.1 (novel protein with some similarity to Drosophila KRAXEN)            | 513                  | 96         |
| 495        | AF036977         | Homo sapiens              | unknown   | 1812                 | 100        |
| 496        | U93564           | Homo sapiens              | p40   | 133                  | 45         |
| 497        | Y91405           | Homo sapiens              | Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.                | 357                  | 100        |
| 498        | AF069781         | Drosophila melanogaster   | Bem46-like protein  | 653                  | 43         |
| 499        | Y16601           | Homo sapiens              | Human cell-cycle phosphoprotein CECYP-2.  | 1658                 | 98         |
| 500        | X70944           | Homo sapiens              | PTB-associated splicing factor  | 3883                 | 100        |
| 501        | AF027503         | Mus musculus              | putative membrane-associated guanylate kinase 1                                 | 205                  | 36         |
| 502        | AF282874         | Homo sapiens              | nectin 3; PRR3  | 2856                 | 99         |
| 503        | AJ249732         | Homo sapiens              | G8 protein  | 669                  | 100        |
| 504        | AF208861         | Homo sapiens              | BM-019  | 1629                 | 100        |
| 505        | L09708           | Homo sapiens              | complement component C2   | 4022                 | 100        |
| 507        | X66285           | Mus musculus              | HCl ORF   | 115                  | 43         |
| 508        | D00189           | Rattus norvegicus         | Na+,K+-ATPase alpha-subunit   | 5227                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                              | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|---|----------------------|------------|
| 509        | Y94971           | Homo sapiens                         | Human secreted protein clone fa171_1 protein sequence SEQ ID NO:148.                          | 2176                 | 100        |
| 510        | AB019038         | Homo sapiens                         | beta-1,4 mannosyltransferase  | 781                  | 77         |
| 511        | AB019038         | Homo sapiens                         | beta-1,4 mannosyltransferase  | 1347                 | 100        |
| 512        | AB019038         | Homo sapiens                         | beta-1,4 mannosyltransferase  | 1520                 | 99         |
| 513        | X84908           | Homo sapiens                         | phosphorylase kinase  | 5729                 | 99         |
| 514        | X52851           | Homo sapiens                         | peptidylprolyl isomerase  | 650                  | 76         |
| 515        | AF186084         | Homo sapiens                         | epidermal growth factor repeat containing protein   | 3046                 | 99         |
| 516        | G03602           | Homo sapiens                         | Human secreted protein, SEQ ID NO: 7683.  | 505                  | 99         |
| 517        | U04706           | Bos taurus                           | 50 kDa protein  | 1749                 | 77         |
| 518        | G00653           | Homo sapiens                         | Human secreted protein, SEQ ID NO: 4734.  | 530                  | 100        |
| 519        | AF161475         | Homo sapiens                         | HSPC126   | 1368                 | 100        |
| 520        | Y99366           | Homo sapiens                         | Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88.                                      | 3394                 | 97         |
| 521        | AF266852         | Homo sapiens                         | PTPLA   | 1295                 | 100        |
| 522        | AE000995         | Archaeoglobus fulgidus               | chromosome segregation protein (smc1)   | 153                  | 20         |
| 523        | AF062249         | Homo sapiens                         | immunoglobulin heavy chain variable region  | 605                  | 97         |
| 524        | AJ223830         | Rattus norvegicus                    | ARE1  | 2950                 | 98         |
| 525        | W01535           | Homo sapiens                         | Cellular homologue of the SV40 large T antigen.   | 1276                 | 83         |
| 526        | AF145658         | Drosophila melanogaster              | BcDNA.GH10229   | 320                  | 33         |
| 527        | AF112213         | Homo sapiens                         | putative Rab5-interacting protein   | 524                  | 79         |
| 528        | D49387           | Homo sapiens                         | NADP dependent leukotriene b4 12-hydroxydehydrogenase   | 1616                 | 100        |
| 529        | Y30819           | Homo sapiens                         | Human secreted protein encoded from gene 9.   | 328                  | 32         |
| 530        | AL079335         | Homo sapiens                         | dJ132F21.3 (72.1 kDa protein (DKFZP564A032, SBB188) similar to mouse IFN-gamma induce MG11. ) | 1059                 | 99         |
| 531        | Y91506           | Homo sapiens                         | Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.                             | 1159                 | 98         |
| 532        | X76116           | Caenorhabditis elegans               | carrier protein (c2)  | 576                  | 50         |
| 533        | X76116           | Caenorhabditis elegans               | carrier protein (c2)  | 506                  | 50         |
| 534        | X12966           | Homo sapiens                         | 3-oxoacyl-CoA thiolase propeptide (424 AA)  | 1972                 | 100        |
| 535        | Y09267           | Homo sapiens                         | flavin-containing monooxygenase 2   | 2486                 | 100        |
| 536        | Z11773           | Homo sapiens                         | SRE-ZBP   | 2201                 | 99         |
| 537        | D84224           | Homo sapiens                         | methionyl tRNA synthetase   | 4741                 | 99         |
| 538        | D84224           | Homo sapiens                         | methionyl tRNA synthetase   | 3887                 | 99         |
| 539        | D84224           | Homo sapiens                         | methionyl tRNA synthetase   | 2933                 | 96         |
| 540        | D84224           | Homo sapiens                         | methionyl tRNA synthetase   | 4529                 | 99         |
| 541        | J03244           | Bos taurus                           | H+ ATPase 31kDa subunit (EC 3.6.1.3)  | 848                  | 77         |
| 542        | Y92514           | Homo sapiens                         | Human OXRE-11.  | 2301                 | 99         |
| 543        | AF221712         | Homo sapiens                         | Smad- and Olf-interacting zinc finger protein   | 2151                 | 61         |
| 544        | AE000919         | Methanobacterium thermoautotrophicum | conserved protein   | 207                  | 38         |
| 545        | A06669           | synthetic construct                  | preTGF-beta1  | 2070                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                 | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 546        | Y02698           | Homo sapiens            | Human secreted protein encoded by gene 49 clone HTPCS60.      | 854                  | 98         |
| 547        | AF112205         | Homo sapiens            | WSB-1 protein   | 2275                 | 100        |
| 548        | X60271           | Mus musculus            | c-rel   | 2264                 | 74         |
| 549        | AC016827         | Arabidopsis thaliana    | putative GTPase   | 810                  | 42         |
| 550        | Y70400           | Homo sapiens            | Human cell-signalling protein-2.                              | 429                  | 68         |
| 551        | AB048365         | Homo sapiens            | NEDD4-like ubiquitin ligase 1                                 | 8290                 | 99         |
| 552        | Y57880           | Homo sapiens            | Human transmembrane protein HTPMN-4.                          | 1112                 | 95         |
| 553        | AF119855         | Homo sapiens            | PRO1847   | 265                  | 67         |
| 554        | M17236           | Homo sapiens            | MHC HLA-DQ alpha precursor                                    | 1332                 | 100        |
| 555        | AL078468         | Arabidopsis thaliana    | putative protein  | 540                  | 40         |
| 556        | AC006963         | Homo sapiens            | similar to Kelch proteins; similar to BAA77027 (PID:g4650844) | 515                  | 44         |
| 557        | AK024487         | Homo sapiens            | PLJ00086 protein  | 1623                 | 98         |
| 558        | M12140           | Homo sapiens            | pol gene protein; Xxx   | 117                  | 48         |
| 559        | W74825           | Homo sapiens            | Human secreted protein encoded by gene 97 clone HAQBF73.      | 225                  | 56         |
| 560        | X56581           | Homo sapiens            | jund protein  | 373                  | 88         |
| 561        | AF093136         | Caenorhabditis elegans  | contains weak similarity to an AMP-binding motif              | 2926                 | 54         |
| 562        | AL109839         | Homo sapiens            | dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)          | 877                  | 100        |
| 563        | AF181640         | Drosophila melanogaster | BcDNA.GH09817   | 289                  | 42         |
| 564        | AF052723         | Feline leukemia virus   | gag-pol precursor polyprotein gPr80                           | 1547                 | 43         |
| 565        | AF161472         | Homo sapiens            | HSPC123   | 439                  | 44         |
| 566        | Y28817           | Homo sapiens            | pt326_4 secreted protein.                                     | 3338                 | 100        |
| 567        | U09848           | Homo sapiens            | zinc finger protein   | 1738                 | 100        |
| 569        | AF155113         | Homo sapiens            | NY-REN-55 antigen   | 3603                 | 93         |
| 570        | AF155113         | Homo sapiens            | NY-REN-55 antigen   | 3951                 | 99         |
| 571        | AL032821         | Homo sapiens            | dJ55C23.1 (vanin 1)   | 1821                 | 98         |
| 572        | M69181           | Homo sapiens            | non-muscle myosin B   | 7350                 | 99         |
| 573        | M69181           | Homo sapiens            | non-muscle myosin B   | 7311                 | 98         |
| 574        | Y59678           | Homo sapiens            | Secreted protein 108-008-5-0-E6-FL.                           | 772                  | 100        |
| 575        | AL365234         | Arabidopsis thaliana    | putative protein  | 788                  | 40         |
| 576        | AL365234         | Arabidopsis thaliana    | putative protein  | 788                  | 40         |
| 577        | X06745           | Homo sapiens            | DNA polymerase alpha-subunit (AA 1 - 1462)                    | 7619                 | 99         |
| 578        | AB041642         | Homo sapiens            | PAR-6   | 1342                 | 100        |
| 579        | D86984           | Homo sapiens            | similar to yeast adenylate cyclase (S56776)                   | 2446                 | 100        |
| 580        | AF165124         | Homo sapiens            | gamma-aminobutyric acid A receptor gamma 2                    | 2499                 | 99         |
| 581        | W88812           | Homo sapiens            | Polypeptide fragment encoded by gene 58.                      | 2339                 | 99         |
| 582        | U82319           | Homo sapiens            | novel ORF   | 342                  | 100        |
| 583        | P92219           | Homo sapiens (human)    | CR1 protein.  | 11425                | 99         |
| 584        | AJ223948         | Homo sapiens            | RNA helicase  | 6608                 | 99         |
| 585        | Y08612           | Homo sapiens            | 88kDa nuclear pore complex protein                            | 3874                 | 99         |
| 586        | Y42384           | Homo sapiens            | Amino acid sequence of 1v310_7.                               | 1007                 | 37         |
| 587        | AF129756         | Homo sapiens            | BAT4  | 1873                 | 98         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---|--|----------------------|------------|
| 588        | AF131775         | Homo sapiens  | Unknown  | 1929                 | 99         |
| 589        | AJ250865         | Homo sapiens  | TESS 2   | 2348                 | 100        |
| 591        | Z98885           | Homo sapiens  | dJ522J7.2 (bromodomain-containing 1 (similar to peregrin, BR140))  | 4167                 | 100        |
| 592        | L76571           | Homo sapiens  | nuclear hormone receptor   | 1355                 | 100        |
| 593        | AF091622         | Homo sapiens  | PHD finger protein 3   | 9054                 | 100        |
| 594        | X56807           | Homo sapiens  | desmocollin type 2a  | 4443                 | 100        |
| 595        | AL137802         | Homo sapiens  | dJ798A10.1 (novel protein)   | 212                  | 55         |
| 596        | AL022329         | Homo sapiens  | bK407F11.2 (adrenergic, beta, receptor kinase 2)                   | 3653                 | 100        |
| 597        | AF226048         | Homo sapiens  | GL003  | 2009                 | 99         |
| 598        | AJ278112         | Homo sapiens<br>>Y49635<br>Y49635 21-<br>OCT-1999 15-<br>APR-1998<br>Human sdp3.5<br>protein.<br>[Homo sapiens] | putative cell cycle control protein                                | 335                  | 23         |
| 599        | Y59741           | Homo sapiens  | Human normal ovarian tissue derived protein 10.                    | 1574                 | 99         |
| 600        | L36531           | Homo sapiens  | integrin alpha 8 subunit   | 5386                 | 99         |
| 601        | Y38458           | Homo sapiens  | Human secreted protein encoded by gene No. 20.                     | 895                  | 100        |
| 602        | AF218584         | Homo sapiens  | GGAI   | 3265                 | 100        |
| 603        | Y13115           | Homo sapiens  | serine/threonine protein kinase                                    | 5071                 | 99         |
| 604        | AL132776         | Homo sapiens  | dJ393D12.1 (KIAA0776)  | 2413                 | 99         |
| 605        | AL034452         | Homo sapiens  | dJ682J15.1 (novel Collagen triple helix repeat containing protein) | 1979                 | 100        |
| 606        | Y14494           | Homo sapiens  | aralar1  | 3465                 | 99         |
| 607        | AJ001981         | Homo sapiens  | OXAIL  | 2603                 | 100        |
| 608        | X86098           | Homo sapiens  | binds directly to adenovirus type 5 E1A protein                    | 3069                 | 100        |
| 610        | AF163572         | Homo sapiens  | Forssman glycolipid synthetase                                     | 1865                 | 99         |
| 611        | AF161503         | Homo sapiens  | HSPC154  | 1261                 | 97         |
| 612        | L41834           | Ensis minor   | nuclear protein  | 345                  | 30         |
| 613        | Y91954           | Homo sapiens  | Human cytoskeleton associated protein 9 (CYSKP-9).                 | 3668                 | 100        |
| 614        | AL022327         | Homo sapiens  | dJ355C18.1 (KIAA0027)  | 361                  | 94         |
| 615        | X85786           | Homo sapiens  | binding regulatory factor  | 3203                 | 100        |
| 616        | Y08319           | Homo sapiens  | kinesin-2  | 3487                 | 99         |
| 617        | D12644           | Mus musculus  | KIF2 protein   | 3609                 | 97         |
| 618        | U28789           | Mus musculus  | PACT   | 5936                 | 89         |
| 619        | Y35914           | Homo sapiens  | Extended human secreted protein sequence, SEQ ID NO. 163.          | 1684                 | 99         |
| 620        | A5046382         | Mus musculus  | testis-abundant finger protein                                     | 199                  | 23         |
| 621        | Y00062           | Homo sapiens  | precursor polypeptide (AA -23 to 1120)                             | 3440                 | 99         |
| 622        | AF068286         | Homo sapiens  | HDCMD38P   | 861                  | 100        |
| 623        | X98248           | Homo sapiens  | sortilin   | 4436                 | 99         |
| 624        | X61100           | Homo sapiens  | 75 kDa subunit NADH dehydrogenase precursor                        | 3734                 | 99         |
| 625        | S58544           | Homo sapiens  | 75 kDa infertility-related sperm protein                           | 2125                 | 99         |
| 626        | AF151027         | Homo sapiens  | HSPC193  | 582                  | 93         |
| 627        | X14968           | Homo sapiens  | R11-alpha subunit (AA 1-404)                                       | 2079                 | 100        |
| 628        | Y50911           | Homo sapiens  | Human fetal brain cDNA clone vb7_1 derived protein                 | 1983                 | 100        |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                 | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 629        | Y50911           | Homo sapiens            | Human fetal brain cDNA clone vb7.1 derived protein  | 1694                 | 100        |
| 630        | AF098786         | Homo sapiens            | 17 beta-hydroxysteroid dehydrogenase type VII   | 1754                 | 100        |
| 631        | AL034555         | Homo sapiens            | dJ134019.3 (zinc finger protein 151 (pHZ-67))   | 4273                 | 100        |
| 632        | W74826           | Homo sapiens            | Human secreted protein encoded by gene 98 clone HAQBT94.  | 794                  | 96         |
| 633        | AF288288         | Homo sapiens            | HPT protein   | 2236                 | 100        |
| 634        | AF041429         | Homo sapiens            | PRGR1   | 823                  | 99         |
| 635        | X66357           | Homo sapiens            | serine/threonine protein kinase   | 1589                 | 100        |
| 636        | Y11284           | Homo sapiens            | AFX1  | 2571                 | 98         |
| 637        | AR004884         | Homo sapiens            | PKU-alpha   | 3718                 | 99         |
| 638        | AJ002303         | Homo sapiens            | synaptogyrin 1c   | 1020                 | 100        |
| 639        | AJ002304         | Homo sapiens            | synaptogyrin 1b   | 1002                 | 100        |
| 640        | AJ002303         | Homo sapiens            | synaptogyrin 1c   | 933                  | 94         |
| 641        | D87682           | Homo sapiens            | similar to a C.elegans protein encoded in cosmid T26A5.   | 2676                 | 100        |
| 642        | M14660           | Homo sapiens            | ISG-K54   | 2473                 | 99         |
| 643        | X06661           | Homo sapiens            | calbindin (AA 1-261)  | 1358                 | 100        |
| 644        | AF119900         | Homo sapiens            | PRO2822   | 185                  | 76         |
| 645        | AB031048         | Drosophila melanogaster | microtubule associated-protein orbit  | 738                  | 27         |
| 646        | AF250842         | Drosophila melanogaster | multiple asters   | 834                  | 29         |
| 647        | X86691           | Homo sapiens            | M1-2 protein  | 10110                | 99         |
| 648        | U67934           | Homo sapiens            | 44.9 kDa protein C18B11 homolog   | 827                  | 96         |
| 649        | AF236061         | Oryctolagus cuniculus   | RING-finger binding protein   | 3930                 | 91         |
| 650        | AL034553         | Homo sapiens            | dJ914P20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp)) | 5708                 | 100        |
| 653        | X14766           | Homo sapiens            | GABA-A receptor alpha 1 subunit   | 2388                 | 99         |
| 654        | AC004614         | Homo sapiens            | similar to f-spondin proteins AB006086 (PID:g2529225)   | 3026                 | 99         |
| 655        | Y57908           | Homo sapiens            | Human transmembrane protein HTMPN-32.   | 608                  | 99         |
| 656        | Z34975           | Homo sapiens            | IdlCp   | 3733                 | 100        |
| 658        | AL050306         | Homo sapiens            | dJ475B7.2 (novel protein)   | 1942                 | 99         |
| 659        | W76734           | Homo sapiens            | Human mDia Rho targeting protein.   | 781                  | 34         |
| 660        | AF202724         | Homo sapiens            | Sad1 unc-84 domain protein 1  | 2172                 | 100        |
| 661        | Z21966           | Homo sapiens            | mPOU homeobox protein   | 1529                 | 100        |
| 662        | AJ242954         | Mus musculus            | dysferlin   | 4752                 | 59         |
| 663        | AF182316         | Homo sapiens            | myoferlin   | 6232                 | 99         |
| 665        | AL161516         | Arabidopsis thaliana    | hypothetical protein  | 209                  | 30         |
| 667        | X59303           | Homo sapiens            | valyl-tRNA synthetase   | 3393                 | 99         |
| 668        | Y13355           | Homo sapiens            | Amino acid sequence of protein PRO220.  | 3692                 | 100        |
| 669        | AB010692         | Arabidopsis thaliana    | contains similarity to endo-beta-N-acetylglucosaminidase gene   | 611                  | 52         |
| 671        | X56123           | Mus musculus            | talin   | 4474                 | 76         |
| 672        | AB039371         | Homo sapiens            | mitochondrial ABC transporter 3   | 2902                 | 99         |
| 673        | AF269223         | Homo sapiens            | TCP11   | 806                  | 42         |
| 674        | AF229633         | Mus musculus            | groucho-related protein 4   | 4053                 | 99         |
| 675        | L14463           | Rattus                  | *transducin   | 3619                 | 92         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES               | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-----------------------|---|----------------------|------------|
|            |                  | norvegicus            |   |                      |            |
| 676        | AC005757         | Homo sapiens          | R32611.1  | 2779                 | 100        |
| 677        | S61069           | Homo sapiens          | reverse transcriptase homolog=pol (retroviral element)                                  | 252                  | 65         |
| 678        | AF271388         | Homo sapiens          | CMP-N-acetylneuraminic acid synthase  | 2273                 | 100        |
| 679        | X79066           | Homo sapiens          | ERF-1   | 1783                 | 100        |
| 680        | AF118566         | Mus musculus          | hematopoietic zinc finger protein   | 769                  | 50         |
| 681        | Y51415           | Homo sapiens          | Human wild type pKs83 protein.  | 2621                 | 99         |
| 682        | AL133545         | Homo sapiens          | hA386N14.1 (novel protein similar to a dual specificity phosphatase)                    | 700                  | 68         |
| 683        | Y86214           | Homo sapiens          | Nuclear transport protein clone hfb341 protein sequence.                                | 5888                 | 99         |
| 684        | Y94952           | Homo sapiens          | Human secreted protein clone fh116_11 protein sequence SEQ ID NO:110.                   | 354                  | 98         |
| 685        | AL021878         | Homo sapiens          | dJ257I20.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))                       | 154                  | 67         |
| 686        | AE000198         | Escherichia coli      | orf, hypothetical protein   | 628                  | 100        |
| 687        | M58378           | Homo sapiens          | synapsin I  | 3730                 | 99         |
| 688        | AF039697         | Homo sapiens          | antigen NY-CO-31  | 508                  | 98         |
| 689        | U09355           | Oryctolagus cuniculus | protein phosphatase 2A1 B gamma subunit   | 2356                 | 99         |
| 690        | AF155106         | Homo sapiens          | NY-REN-36 antigen   | 265                  | 50         |
| 691        | AC004774         | Homo sapiens          | Dlx-5   | 1542                 | 100        |
| 692        | X90530           | Homo sapiens          | ragB  | 1926                 | 99         |
| 693        | X90530           | Homo sapiens          | ragB  | 1405                 | 99         |
| 694        | X90530           | Homo sapiens          | ragB  | 1590                 | 85         |
| 695        | G01563           | Homo sapiens          | Human secreted protein, SEQ ID NO: 5644.  | 330                  | 100        |
| 696        | AC011810         | Arabidopsis thaliana  | Putative methionine aminopeptidase  | 669                  | 52         |
| 697        | AJ250425         | Rattus norvegicus     | Collybistin I   | 2455                 | 98         |
| 698        | AB037901         | Homo sapiens          | gene amplified in squamous cell carcinoma-1   | 5364                 | 99         |
| 699        | Y99401           | Homo sapiens          | Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.                               | 1386                 | 100        |
| 701        | AF221712         | Homo sapiens          | Smad- and Olf-interacting zinc finger protein   | 6705                 | 100        |
| 702        | X83573           | Homo sapiens          | ARSE  | 3184                 | 99         |
| 703        | AJ243274         | Homo sapiens          | AP-2rep protein   | 2078                 | 99         |
| 704        | Y71262           | Homo sapiens          | Human chondromodulin-like protein, Zchm1.   | 1697                 | 94         |
| 705        | Y71262           | Homo sapiens          | Human chondromodulin-like protein, Zchm1.   | 1736                 | 99         |
| 706        | Y41257           | Homo sapiens          | Amino acid sequence of long human FAIM.   | 1060                 | 100        |
| 707        | AL022237         | Homo sapiens          | bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1)) | 2030                 | 100        |
| 708        | AJ006266         | Homo sapiens          | AND-1 protein   | 5942                 | 100        |
| 709        | G01571           | Homo sapiens          | Human secreted protein, SEQ ID NO: 5652.  | 777                  | 99         |
| 710        | Y08698           | Homo sapiens          | ranbp3  | 2849                 | 98         |
| 711        | Y68770           | Homo sapiens          | Amino acid sequence of a human phosphorylation effector PHSP-2.                         | 754                  | 99         |



TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES   | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---|---|----------------------|------------|
| 712        | U93574           | Homo sapiens  | putative p150   | 799                  | 59         |
| 713        | AC004531         | Homo sapiens  | Gene with similaity to DEAD box helicases   | 2715                 | 99         |
| 714        | D89016           | Homo sapiens  | Neuroblastoma   | 538                  | 48         |
| 715        | Y92175           | Homo sapiens  | Human cardiovascular system associated protein tyrosine phosphatase 2.                            | 734                  | 98         |
| 716        | AL137013         | Homo sapiens  | bA311P8.3 (probable uracil phosphoribosyltransferase)   | 862                  | 100        |
| 717        | AB035123         | Mus musculus  | GD1 alpha/GT1a alpha/GQ1b alpha synthase  | 1696                 | 93         |
| 718        | Y96290           | Homo sapiens<br>>P40254<br>P40254 25-<br>OCT-1984 09-<br>APR-1983<br>Human IgD.<br>[Homo sapiens]                       | Human IGFAM-2 immunoglobulin.   | 2345                 | 85         |
| 719        | X07979           | Homo sapiens  | integrin beta 1 subunit precursor   | 4347                 | 99         |
| 720        | AJ224819         | Homo sapiens  | tumor suppressor  | 2149                 | 99         |
| 721        | Y07595           | Homo sapiens  | transcription factor TFIIH  | 2373                 | 100        |
| 722        | W41565           | Homo sapiens<br>[Homo sapiens]<br>>W41564<br>W41564 08-<br>OCT-1997 05-<br>APR-1996<br>Human calpain.<br>[Homo sapiens] | Human calpain.  | 1591                 | 99         |
| 723        | AF161341         | Homo sapiens  | HSPC078   | 1097                 | 98         |
| 724        | AF187318         | Homo sapiens  | F-box protein Fbx2  | 1607                 | 100        |
| 725        | AC006708         | Caenorhabditis elegans  | contains similarity to Saccharomyces cerevisiae pre-mRNA splicing protein PRP31 (GB:Z72876)       | 1143                 | 46         |
| 726        | AC006708         | Caenorhabditis elegans  | contains similarity to Saccharomyces cerevisiae pre-mRNA splicing protein PRP31 (GB:Z72876)       | 988                  | 46         |
| 727        | AC024818         | Caenorhabditis elegans  | contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 | 950                  | 44         |
| 728        | AJ005897         | Homo sapiens  | JM5   | 831                  | 47         |
| 729        | Y45377           | Homo sapiens  | Human secreted protein fragment encoded from gene 27.   | 908                  | 97         |
| 730        | G03931           | Homo sapiens  | Human secreted protein, SEQ ID NO: 8012.  | 578                  | 100        |
| 731        | AB012720         | Oncorhynchus masou  | GTP-binding protein   | 3865                 | 76         |
| 732        | W73404           | Homo sapiens  | Human secreted protein encoded by Gene No. 8.   | 862                  | 97         |
| 733        | G02650           | Homo sapiens  | Human secreted protein, SEQ ID NO: 6731.  | 644                  | 97         |
| 734        | AC024813         | Caenorhabditis elegans  | Hypothetical protein Y54F10AL.a   | 152                  | 24         |
| 735        | AL035461         | Homo sapiens  | dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)                      | 1562                 | 98         |
| 736        | U00033           | Caenorhabditis elegans  | similar to S. cerevisiae YJU2 protein   | 605                  | 41         |
| 737        | AF079098         | Homo sapiens  | arginine-tRNA-protein transferase 1-1p; ATE1-1p   | 2733                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|------------------------|--|----------------------|------------|
| 738        | AJ131712         | Homo sapiens           | nucleolar RNA-helicase   | 2793                 | 100        |
| 739        | AJ133115         | Homo sapiens           | TSC-22-like protein  | 2054                 | 99         |
| 740        | X98258           | Homo sapiens           | M-phase phosphoprotein 9   | 953                  | 100        |
| 741        | X98258           | Homo sapiens           | M-phase phosphoprotein 9   | 564                  | 74         |
| 742        | U97191           | Caenorhabditis elegans | strong similarity to the YPT1 sub-family of RAS proteins           | 960                  | 85         |
| 743        | X76057           | Homo sapiens           | phosphomannose isomerase   | 2191                 | 100        |
| 744        | G03209           | Homo sapiens           | Human secreted protein, SEQ ID NO: 7290.                           | 496                  | 98         |
| 745        | X97064           | Homo sapiens           | Sec23 protein  | 4034                 | 99         |
| 746        | W93946           | Homo sapiens           | Human regulatory molecule HRM-2 protein.                           | 994                  | 100        |
| 747        | Y73388           | Homo sapiens           | HTRM clone 3376404 protein sequence.                               | 1565                 | 99         |
| 748        | M19529           | Sus scrofa             | folliculin A   | 1906                 | 98         |
| 749        | AJ249457         | Trichomonas vaginalis  | centrin, putative  | 183                  | 28         |
| 750        | AC004410         | Homo sapiens           | fos39554_1   | 2094                 | 100        |
| 751        | AF074968         | Homo sapiens           | p47ING3 protein  | 2167                 | 100        |
| 752        | AF252284         | Homo sapiens           | transcription specificity factor Spl                               | 4005                 | 100        |
| 753        | AB049629         | Homo sapiens           | phospholysine phosphohistidine inorganic pyrophosphate phosphatase | 1375                 | 99         |
| 754        | D79205           | Homo sapiens           | ribosomal protein L39  | 160                  | 77         |
| 755        | AB008430         | Homo sapiens           | CDEP   | 142                  | 29         |
| 758        | L32162           | Homo sapiens           | transcription factor   | 574                  | 80         |
| 759        | AF037204         | Homo sapiens           | RING zinc finger protein   | 295                  | 54         |
| 760        | Y44250           | Homo sapiens           | Human cell signalling protein-13.                                  | 625                  | 100        |
| 761        | AF218586         | Homo sapiens           | Cide-b   | 1136                 | 100        |
| 762        | U38934           | Gallus gallus          | histone H2A  | 625                  | 97         |
| 763        | AF226053         | Homo sapiens           | HSKM-B   | 606                  | 32         |
| 764        | X13403           | Homo sapiens           | Oct-1 protein (AA 1 - 743)   | 3626                 | 100        |
| 765        | D87446           | Homo sapiens           | Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)    | 568                  | 38         |
| 766        | AL023828         | Caenorhabditis elegans | Y17G7B.14  | 200                  | 27         |
| 767        | Y82777           | Homo sapiens           | Human chordin related protein (Clone dw665_4).                     | 2551                 | 99         |
| 768        | X92475           | Homo sapiens           | ITBA1  | 1429                 | 100        |
| 769        | Y42752           | Homo sapiens           | Human calcium binding protein 3 (CaBP-3).                          | 1426                 | 100        |
| 770        | X51416           | Homo sapiens           | hormone receptor hERR1 (AA 1-521)                                  | 2641                 | 97         |
| 771        | AJ006591         | Homo sapiens           | cysteine-rich protein  | 1793                 | 100        |
| 772        | A08695           | Homo sapiens           | rap2   | 935                  | 100        |
| 773        | Z12173           | Homo sapiens           | N-acetylglucosamine-6-sulphatase                                   | 2970                 | 100        |
| 774        | Y91950           | Homo sapiens           | Human cytoskeleton associated protein 5 (CYSKP-5).                 | 565                  | 43         |
| 776        | AL023799         | Homo sapiens           | dJ322P7.1 (zinc finger)  | 855                  | 56         |
| 777        | AL023799         | Homo sapiens           | dJ322P7.1 (zinc finger)  | 855                  | 56         |
| 778        | G01880           | Homo sapiens           | Human secreted protein, SEQ ID NO: 5961.                           | 849                  | 98         |
| 779        | AJ012590         | Homo sapiens           | glucose 1-dehydrogenase  | 4155                 | 99         |
| 780        | AL078582         | Homo sapiens           | dJ130E4.2 (KIAA0796)   | 1321                 | 68         |
| 781        | Z75955           | Caenorhabditis elegans | similar to mitochondrial carrier protein                           | 384                  | 34         |
| 782        | AL109965         | Homo sapiens           | dJ1121G12.2 (SCAN domain-containing 1 protein)                     | 900                  | 100        |
| 783        | AF061262         | Mus musculus           | semaF cytoplasmic domain associated protein 2                      | 1316                 | 83         |
| 784        | G03873           | Homo sapiens           | Human secreted protein, SEQ  | 649                  | 95         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                    | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|----------------------------|---|----------------------|------------|
|            |                  |                            | ID NO: 7954.  |                      |            |
| 785        | Y84441           | Homo sapiens               | Amino acid sequence of a human RNA-associated protein.                                    | 2074                 | 100        |
| 785        | Y00918           | Homo sapiens               | Human Rab protein, RABP-1, protein sequence.  | 1048                 | 99         |
| 787        | Z97029           | Homo sapiens               | ribonuclease HI large subunit   | 1548                 | 99         |
| 788        | AB035384         | Homo sapiens               | SRp25 nuclear protein   | 962                  | 94         |
| 789        | AF024631         | Homo sapiens               | ANG2  | 2644                 | 100        |
| 790        | AJ006710         | Rattus norvegicus          | phosphatidylinositol 3-kinase   | 4508                 | 97         |
| 792        | V00638           | bacteriophage lambda       | reading frame ea10  | 600                  | 100        |
| 793        | AF049103         | Homo sapiens               | Huntingtin interacting protein  | 819                  | 100        |
| 795        | Z26317           | Homo sapiens               | desmoglein 2  | 4810                 | 99         |
| 796        | Y76884           | Homo sapiens               | Retinoblastoma binding protein-7 sequence.  | 5080                 | 99         |
| 797        | U15155           | Gallus gallus              | trypsinogen   | 372                  | 37         |
| 798        | U97189           | Caenorhabditis elegans     | strong similarity to the P13/P14 family of kinases  | 227                  | 28         |
| 799        | AF112201         | Homo sapiens               | neuronal protein NP25   | 1053                 | 100        |
| 800        | AF234765         | Rattus norvegicus          | serine-arginine-rich splicing regulatory protein SRRP86                                   | 958                  | 63         |
| 801        | AF267852         | Homo sapiens               | placental protein 13-like protein   | 743                  | 99         |
| 802        | AF208851         | Homo sapiens               | BM-009  | 766                  | 80         |
| 803        | Z81097           | Caenorhabditis elegans     | Similarity to Human retinoblastoma-binding protein RBAP46 yk662d12.5 comes from this gene | 152                  | 27         |
| 804        | G02113           | Homo sapiens               | Human secreted protein, SEQ ID NO: 6194.  | 496                  | 98         |
| 805        | AL121673         | Homo sapiens               | BA305P22.1 (novel protein)  | 1160                 | 100        |
| 806        | AC013483         | Arabidopsis thaliana       | putative GTPase activator protein   | 264                  | 30         |
| 807        | AC013483         | Arabidopsis thaliana       | putative GTPase activator protein   | 264                  | 30         |
| 808        | AB013885         | Homo sapiens               | beta-ureidopropionase   | 1494                 | 100        |
| 809        | AF078842         | Homo sapiens               | HOTTL protein   | 1581                 | 99         |
| 810        | AF161421         | Homo sapiens               | HSPC303   | 2134                 | 96         |
| 811        | AF261689         | Homo sapiens               | DNA polymerase epsilon p17 subunit  | 734                  | 100        |
| 812        | Z74029           | Caenorhabditis elegans     | Similarity to C.elegans alcohol dehydrogenase comes from this gene                        | 610                  | 71         |
| 813        | Z73497           | Homo sapiens               | cU240C2.2 (Core histone H2A/H2B/H3/H4)  | 324                  | 100        |
| 814        | W87689           | Homo sapiens               | Human HTXFT19 polypeptide.  | 1484                 | 99         |
| 815        | X16282           | Homo sapiens               | zinc finger protein (217 AA) (1 is 2nd base in codon)                                     | 1109                 | 99         |
| 816        | Z92539           | Mycobacterium tuberculosis | pth   | 300                  | 36         |
| 818        | AB030483         | Mus musculus               | B9  | 197                  | 27         |
| 819        | AL117555         | Homo sapiens               | hypothetical protein  | 321                  | 94         |
| 820        | AC005328         | Homo sapiens               | R26660_2, partial CDS   | 865                  | 97         |
| 821        | G03951           | Homo sapiens               | Human secreted protein, SEQ ID NO: 8032.  | 700                  | 99         |
| 822        | L34807           | Musca domestica            | transposase   | 174                  | 20         |
| 823        | G02928           | Homo sapiens               | Human secreted protein, SEQ ID NO: 7009.  | 558                  | 78         |
| 824        | Z99531           | Schizosaccharomyces pombe  | caffeine-induced death  | 184                  | 29         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                 | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
|            |                  | romyces pombe           | protein 1   |                      |            |
| 825        | AJ006692         | Homo sapiens            | ultra high sulfur keratin   | 693                  | 68         |
| 826        | U23037           | Oryctolagus cuniculus   | eIF-2Bepsilon   | 3406                 | 90         |
| 827        | G03412           | Homo sapiens            | Human secreted protein, SEQ ID NO: 7493.                          | 464                  | 100        |
| 828        | Y30327           | Homo sapiens            | Human secreted protein encoded from gene 17.                      | 113                  | 44         |
| 829        | Y32199           | Homo sapiens            | Human receptor molecule (REC) encoded by Incyte clone 2022379.    | 1012                 | 100        |
| 830        | W78279           | Homo sapiens            | Fragment of human secreted protein encoded by gene 33.            | 1264                 | 99         |
| 832        | AB011542         | Homo sapiens            | MEGF9   | 2097                 | 100        |
| 833        | G02639           | Homo sapiens            | Human secreted protein, SEQ ID NO: 6720.                          | 223                  | 70         |
| 834        | AF119664         | Homo sapiens            | transcriptional regulator protein HCNGP                           | 1574                 | 100        |
| 835        | AF119664         | Homo sapiens            | transcriptional regulator protein HCNGP                           | 1144                 | 89         |
| 836        | AF119664         | Homo sapiens            | transcriptional regulator protein HCNGP                           | 1448                 | 94         |
| 837        | X12517           | Homo sapiens            | C protein (AA 1-159)  | 918                  | 100        |
| 838        | U32865           | Drosophila melanogaster | linotte protein   | 164                  | 24         |
| 839        | AF067730         | Homo sapiens            | TLS-associated protein TASR-2                                     | 631                  | 56         |
| 840        | U27831           | Homo sapiens            | striatum-enriched phosphatase                                     | 2840                 | 98         |
| 841        | AF286366         | Homo sapiens            | CamKI-like protein kinase   | 1796                 | 100        |
| 842        | G02309           | Homo sapiens            | Human secreted protein, SEQ ID NO: 6390.                          | 278                  | 98         |
| 843        | AE003615         | Drosophila melanogaster | ade3 gene product   | 113                  | 48         |
| 844        | G01350           | Homo sapiens            | Human secreted protein, SEQ ID NO: 5431.                          | 629                  | 100        |
| 845        | U27838           | Mus musculus            | glycosyl-phosphatidyl-inositol-anchored protein homolog           | 3305                 | 96         |
| 847        | Y87788           | Homo sapiens            | Human RBP-26 protein.   | 2026                 | 100        |
| 848        | AF164794         | Homo sapiens            | Diff33 protein homolog  | 2398                 | 100        |
| 849        | U41315           | Homo sapiens            | ZNF127-Xp   | 2458                 | 93         |
| 850        | AF192784         | Homo sapiens            | makorin 1   | 2062                 | 97         |
| 851        | Y58628           | Homo sapiens            | Protein regulating gene expression PRGZ-21.                       | 1548                 | 100        |
| 852        | Z22968           | Homo sapiens            | M130 antigen  | 6205                 | 100        |
| 853        | Z22971           | Homo sapiens            | M130 antigen extracellular variant                                | 6380                 | 100        |
| 854        | G03362           | Homo sapiens            | Human secreted protein, SEQ ID NO: 7443.                          | 330                  | 96         |
| 855        | G03362           | Homo sapiens            | Human secreted protein, SEQ ID NO: 7443.                          | 203                  | 100        |
| 856        | AF285118         | Homo sapiens            | CGI-203   | 452                  | 100        |
| 857        | AC006069         | Arabidopsis thaliana    | putative cleavage and polyadenylation specificity factor          | 1383                 | 55         |
| 858        | AL021546         | Homo sapiens            | Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1) | 593                  | 100        |
| 859        | L02956           | Xenopus laevis          | ribonucleoprotein   | 1664                 | 85         |
| 860        | AF201947         | Homo sapiens            | MEK binding partner 1   | 616                  | 100        |
| 861        | L31783           | Mus musculus            | uridine kinase  | 1266                 | 92         |
| 862        | AF161472         | Homo sapiens            | HSPC123   | 602                  | 73         |
| 863        | Z49068           | Caenorhabditis elegans  | mitochondrial carrier protein                                     | 370                  | 43         |
| 864        | AF154108         | Homo sapiens            | tumor necrosis factor type 1                                      | 3559                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                  | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------|--|----------------------|------------|
|            |                  |                          | receptor associated protein  |                      |            |
| 865        | AE001530         | Helicobacter pylori J99  | putative   | 230                  | 32         |
| 866        | X57807           | Homo sapiens             | immunoglobulin lambda light chain  | 699                  | 91         |
| 867        | AL031673         | Homo sapiens             | dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains)                         | 4066                 | 99         |
| 868        | Y11652           | Homo sapiens             | phosphate cyclase  | 238                  | 100        |
| 869        | AF192968         | Homo sapiens             | high-glucose-regulated protein 8   | 3041                 | 99         |
| 870        | AB020648         | Homo sapiens             | KIAA0841 protein   | 3237                 | 99         |
| 871        | AL031427         | Homo sapiens             | dJ167A19.1 (novel protein)   | 1608                 | 100        |
| 872        | AF151534         | Homo sapiens             | core histone macroH2A2.2   | 1866                 | 100        |
| 873        | AL021331         | Homo sapiens             | dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F11.1) LIKE protein)                                 | 1129                 | 100        |
| 874        | X14608           | Homo sapiens             | propionyl-CoA carboxylase  | 3579                 | 100        |
| 875        | AL117334         | Homo sapiens             | dJ687F11.1 (novel protein (part of translation of cDNA DKFZp434N061, Em:AL110249))                         | 306                  | 100        |
| 876        | X79489           | Saccharomyces cerevisiae | E-925 protein  | 446                  | 35         |
| 877        | Y53501           | Homo sapiens             | Human secreted protein clone dn834.1 protein sequence SEQ ID NO:8.   | 811                  | 100        |
| 878        | AF281064         | Homo sapiens             | CHMP1.5  | 957                  | 100        |
| 879        | X79417           | Sus scrofa               | 40S ribosomal protein S12  | 687                  | 100        |
| 880        | AF001317         | Saccharomyces cerevisiae | Soilp  | 478                  | 28         |
| 881        | Y87275           | Homo sapiens             | Human signal peptide containing protein HSPP-52 SEQ ID NO:52.  | 2547                 | 100        |
| 882        | M14036           | Homo sapiens             | C1-inhibitor   | 598                  | 77         |
| 883        | AB041261         | Homo sapiens             | calcium-independent phospholipase A2   | 2903                 | 100        |
| 884        | AF020313         | Mus musculus             | proline-rich protein 48  | 999                  | 84         |
| 885        | Y10936           | Homo sapiens             | hypothetical protein   | 1104                 | 99         |
| 886        | AF073997         | Mus musculus             | myotubularin related protein 1   | 866                  | 36         |
| 887        | Y57893           | Homo sapiens             | Human transmembrane protein HTMPN-17.  | 1099                 | 94         |
| 888        | AL117635         | Homo sapiens             | hypothetical protein   | 929                  | 99         |
| 889        | AF210317         | Homo sapiens             | facilitative glucose transporter family member GLUT9   | 2046                 | 99         |
| 890        | Y36031           | Homo sapiens             | Extended human secreted protein sequence, SEQ ID NO. 416.  | 583                  | 100        |
| 891        | Y36031           | Homo sapiens             | Extended human secreted protein sequence, SEQ ID NO. 416.  | 192                  | 57         |
| 892        | AF237631         | Homo sapiens             | ubiquitous tropomodulin U-Tmod   | 1798                 | 100        |
| 893        | AF090929         | Homo sapiens             | PRO0477p   | 653                  | 99         |
| 894        | AL031228         | Homo sapiens             | dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)) | 3196                 | 100        |
| 895        | AL031228         | Homo sapiens             | dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)) | 2825                 | 96         |
| 896        | AF171102         | Homo sapiens             | retinal degeneration B beta  | 1302                 | 95         |
| 897        | AE003551         | Drosophila melanogaster  | CG18176 gene product   | 633                  | 33         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES  | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--|---|----------------------|------------|
| 898        | AJ237946         | Homo sapiens   | DEAD Box Protein 5  | 2443                 | 100        |
| 899        | Z97184           | Homo sapiens   | EKE2  | 624                  | 100        |
| 900        | Z97184           | Homo sapiens   | EKE2  | 409                  | 98         |
| 901        | AJ245587         | Homo sapiens   | Kruppel-type zinc finger  | 1942                 | 100        |
| 902        | AF091034         | Homo sapiens   | GTP-binding protein RAB22A  | 1011                 | 100        |
| 903        | R95953           | Homo sapiens   | Eukaryotic cell growth inhibiting factor.                                       | 414                  | 96         |
| 904        | L04733           | Homo sapiens   | kinesin light chain   | 1936                 | 72         |
| 905        | AE003540         | Drosophila melanogaster  | CG10984 gene product  | 446                  | 33         |
| 906        | M55542           | Homo sapiens   | guanylate binding protein isoform I   | 2993                 | 98         |
| 907        | M55542           | Homo sapiens   | guanylate binding protein isoform I   | 2901                 | 96         |
| 908        | N84085           | Homo sapiens   | Human membrane fusion protein WDProl.   | 1889                 | 100        |
| 909        | AF168676         | Homo sapiens   | TNF intracellular domain-interacting protein                                    | 647                  | 100        |
| 910        | AB029150         | Homo sapiens   | KRAB zinc finger protein HFB101L  | 2196                 | 100        |
| 911        | G02871           | Homo sapiens   | Human secreted protein, SEQ ID NO: 6952.  | 521                  | 100        |
| 912        | G03162           | Homo sapiens   | Human secreted protein, SEQ ID NO: 7243.  | 387                  | 87         |
| 913        | AJ243721         | Homo sapiens<br>>Y92508<br>Y92508 13-<br>APR-2000 06-<br>OCT-1998<br>Human OXRE-<br>5. (Homo sapiens | dTDP-4-keto-6-deoxy-D-glucose 4-reductase                                       | 1710                 | 100        |
| 914        | U24189           | Caenorhabditis elegans   | hypothetical protein 1207-1; Method: conceptual translation supplied by authors | 244                  | 41         |
| 915        | Y02591           | Homo sapiens   | A human progesterone receptor complex p23-like protein.                         | 843                  | 99         |
| 916        | AE000984         | Archaeoglobus fulgidus   | dinitrogenase reductase activating glycohydrolase (draG)                        | 171                  | 26         |
| 918        | M23159           | Cricetus cricetus  | DHFR-coamplified protein  | 163                  | 30         |
| 919        | L12018           | Caenorhabditis elegans   | putative  | 1232                 | 41         |
| 920        | AF102177         | Homo sapiens   | tumor antigen SLP-8p  | 1260                 | 97         |
| 921        | AL096712         | Homo sapiens   | dJ744I24.2 (similar to a novel human gene mapping to Activator)                 | 1017                 | 78         |
| 922        | AL161495         | Arabidopsis thaliana   | putative WD-repeat protein  | 866                  | 42         |
| 923        | AL161495         | Arabidopsis thaliana   | putative WD-repeat protein  | 442                  | 36         |
| 924        | U97001           | Caenorhabditis elegans   | similar to Schizosaccharomyces pombe  | 605                  | 51         |
| 925        | X71978           | Mus musculus   | Fif   | 1503                 | 95         |
| 926        | M92288           | Drosophila melanogaster  | beta-spectrin   | 290                  | 51         |
| 927        | Y27575           | Homo sapiens   | Human secreted protein encoded by gene No. 9.                                   | 1392                 | 100        |
| 928        | Y22499           | Homo sapiens   | Human secreted protein sequence clone mh703.1.                                  | 2249                 | 100        |
| 930        | AJ224326         | Homo sapiens   | ribulose-5-phosphate-epimerase  | 912                  | 100        |
| 931        | U28991           | Caenorhabditis   | coded for by C. elegans cDNA  | 660                  | 55         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                        | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------|--|----------------------|------------|
|            |                  | <i>is elegans</i>              | cm21c7   |                      |            |
| 932        | AL080065         | <i>Homo sapiens</i>            | hypothetical protein   | 210                  | 25         |
| 933        | G01884           | <i>Homo sapiens</i>            | Human secreted protein, SEQ ID NO: 5965.   | 767                  | 98         |
| 934        | AJ276485         | <i>Homo sapiens</i>            | integral membrane transporter protein  | 1200                 | 100        |
| 935        | AL035681         | <i>Homo sapiens</i>            | dJ756G23.3 (novel protein similar to drosophila transcriptional repressor)                     | 1142                 | 80         |
| 936        | AB026808         | <i>Mus musculus</i>            | synaptotagmin XI   | 2142                 | 95         |
| 937        | AB015345         | <i>Homo sapiens</i>            | HRIHFB2216   | 2601                 | 99         |
| 938        | X65724           | <i>Homo sapiens</i>            | ORF2   | 498                  | 100        |
| 939        | W89024           | <i>Homo sapiens</i>            | Polypeptide fragment encoded by gene 156.  | 1487                 | 100        |
| 940        | G04047           | <i>Homo sapiens</i>            | Human secreted protein, SEQ ID NO: 8128.   | 117                  | 100        |
| 941        | AF094583         | <i>Homo sapiens</i>            | putative HIV-1 infection related protein   | 452                  | 100        |
| 942        | AC024200         | <i>Caenorhabditis elegans</i>  | contains similarity to several zinc finger proteins but not to the zinc finger domains         | 350                  | 69         |
| 943        | AF129756         | <i>Homo sapiens</i>            | G5c  | 273                  | 100        |
| 944        | M23765           | <i>Rattus norvegicus</i>       | alpha-tropomyosin  | 133                  | 96         |
| 945        | AC009917         | <i>Arabidopsis thaliana</i>    | Contains similarity to   | 583                  | 47         |
| 946        | AF223468         | <i>Homo sapiens</i>            | AD021 protein  | 551                  | 44         |
| 947        | AF055473         | <i>Homo sapiens</i>            | GAGE-8   | 273                  | 51         |
| 948        | X75756           | <i>Homo sapiens</i>            | protein kinase C mu  | 2019                 | 68         |
| 949        | AF143956         | <i>Mus musculus</i>            | corrin-2   | 2300                 | 93         |
| 950        | Y36729           | <i>Homo sapiens</i>            | Human PGI protein sequence.  | 1861                 | 99         |
| 951        | W49041           | <i>Homo sapiens</i>            | Human low density lipoprotein binding protein LBP-2.   | 202                  | 67         |
| 952        | AB016881         | <i>Arabidopsis thaliana</i>    | gene_id:MXC17.7-   | 203                  | 46         |
| 953        | Y01785           | <i>Homo sapiens</i>            | Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL-1999 12-AUG-1998 Human NCE-2 protein. | 365                  | 100        |
| 954        | AF145615         | <i>Drosophila melanogaster</i> | BcDNA.GH03377  | 823                  | 46         |
| 955        | U09410           | <i>Homo sapiens</i>            | zinc finger protein ZNF131   | 2483                 | 99         |
| 956        | U09410           | <i>Homo sapiens</i>            | zinc finger protein ZNF131   | 1853                 | 99         |
| 957        | AF195623         | <i>Homo sapiens</i>            | cholinephosphotransferase 1 alpha  | 2126                 | 99         |
| 958        | X94917           | <i>Drosophila melanogaster</i> | head-elevated expression in 0.9 kb   | 155                  | 32         |
| 959        | U54807           | <i>Rattus norvegicus</i>       | GTP-binding protein  | 1167                 | 97         |
| 960        | AF058807         | <i>Bos taurus</i>              | GTP-binding protein rah  | 606                  | 97         |
| 961        | G03244           | <i>Homo sapiens</i>            | Human secreted protein, SEQ ID NO: 7325.   | 471                  | 100        |
| 962        | AF078850         | <i>Homo sapiens</i>            | steroid dehydrogenase homolog  | 583                  | 40         |
| 963        | AP001754         | <i>Homo sapiens</i>            | transient receptor potential-related channel 7, a novel putative Ca2+ channel protein          | 317                  | 30         |
| 964        | AL035419         | <i>Homo sapiens</i>            | dJ1100H13.1 (putative novel protein)   | 1129                 | 100        |
| 965        | X61381           | <i>Rattus rattus</i>           | interferon-induced protein   | 202                  | 46         |
| 966        | D38169           | <i>Homo sapiens</i>            | inositol 1,4,5-trisphosphate 3-kinase isoenzyme  | 3278                 | 100        |
| 967        | AL031432         | <i>Homo sapiens</i>            | dJ465W24.2.1 (PUTATIVE novel protein) (isoform 1)  | 893                  | 100        |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 968        | U79275           | Homo sapiens              | unknown  | 611                  | 100        |
| 969        | AJ011306         | Homo sapiens              | guanine nucleotide exchange factor (long isoform)  | 2752                 | 99         |
| 970        | AF281134         | Homo sapiens              | exosome component Rrp46  | 1186                 | 100        |
| 971        | U53336           | Caenorhabditis elegans    | weak similarity over a short region to myosin heavy chain  | 536                  | 23         |
| 972        | AC018749         | Leishmania major          | L8840.12   | 589                  | 53         |
| 973        | AF188504         | Mus musculus              | LNV  | 544                  | 85         |
| 974        | U25801           | Homo sapiens              | Tax1 binding protein   | 852                  | 98         |
| 975        | AF049523         | Homo sapiens              | huntingtin-interacting protein HYP/FPB11   | 1390                 | 97         |
| 976        | AF161530         | Homo sapiens              | HSPC182  | 1040                 | 100        |
| 977        | G04020           | Homo sapiens              | Human secreted protein, SEQ ID NO: 8101.   | 626                  | 100        |
| 978        | AF164797         | Homo sapiens              | ribosomal protein L17 isolog   | 908                  | 100        |
| 979        | U94991           | Xenopus laevis            | transcription factor XLMO1   | 795                  | 97         |
| 980        | S73775           | Homo sapiens              | calmitine; calsequestrine  | 2029                 | 100        |
| 981        | Y94888           | Homo sapiens              | Human protein clone HP01462.   | 2501                 | 100        |
| 982        | AJ243191         | Homo sapiens              | heat shock protein   | 827                  | 96         |
| 983        | X65020           | Bos taurus                | PSST subunit of the NADH: ubiquinone oxidoreductase complex  | 964                  | 85         |
| 984        | AJ249207         | Rhodococcus sp. AD45      | putative racemase  | 351                  | 43         |
| 985        | Z30093           | Homo sapiens              | basic transcription factor 2, 35 kD subunit  | 1576                 | 99         |
| 986        | AB030835         | Homo sapiens              | contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3) | 4697                 | 99         |
| 987        | AF227258         | Bos taurus                | RPR-interacting protein-1  | 1262                 | 38         |
| 988        | AL022238         | Homo sapiens              | dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)  | 4048                 | 99         |
| 989        | AL022238         | Homo sapiens              | dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)  | 2321                 | 99         |
| 990        | AF161426         | Homo sapiens              | HSPC308  | 448                  | 92         |
| 991        | AF161426         | Homo sapiens              | HSPC308  | 448                  | 92         |
| 992        | AF161426         | Homo sapiens              | HSPC308  | 453                  | 92         |
| 993        | AL023859         | Schizosaccharomyces pombe | trna-splicing endonuclease subunit   | 172                  | 42         |
| 994        | AL049631         | Homo sapiens              | dJ513M9.1 (novel Homeobox domain protein)  | 241                  | 47         |
| 995        | AC005253         | Homo sapiens              | R26445_1   | 902                  | 100        |
| 996        | AF265206         | Homo sapiens              | MOG1 isoform A   | 974                  | 100        |
| 997        | AJ248285         | Pyrococcus abyssi         | sarcosine oxidase, subunit beta (soxB)   | 195                  | 28         |
| 998        | AE003641         | Drosophila melanogaster   | BG:DS00941.3 gene product  | 218                  | 58         |
| 999        | W69343           | Homo sapiens              | Secreted protein of clone CR930_1.   | 1340                 | 98         |
| 1000       | AY007135         | Homo sapiens              | similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1                   | 1543                 | 100        |
| 1001       | Y73381           | Homo sapiens              | HTRM clone 1877278 protein sequence.   | 1668                 | 100        |
| 1002       | AF208844         | Homo sapiens              | BM-002   | 428                  | 100        |
| 1003       | AE004944         | Pseudomonas aeruginosa    | hypothetical protein   | 134                  | 35         |
| 1004       | AL031431         | Homo sapiens              | dJ462023.2 (novel protein)   | 2058                 | 100        |
| 1005       | S45367           | Canis familiaris          | centractin   | 1949                 | 100        |



TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|---|----------------------|------------|
| 1006       | S45367           | Canis familiaris          | centractin  | 1315                 | 98         |
| 1007       | AB022158         | Mus musculus              | chaperonin containing TCP-1 epsilon subunit   | 2649                 | 96         |
| 1008       | Y76332           | Homo sapiens              | Fragment of human secreted protein encoded by gene 38.                                    | 1282                 | 97         |
| 1009       | AB011414         | Homo sapiens              | Kruppel-type zinc finger protein  | 1671                 | 58         |
| 1010       | Z58218           | Caenorhabditis elegans    | K01H12.1  | 269                  | 67         |
| 1011       | AB011414         | Homo sapiens              | Kruppel-type zinc finger protein  | 1671                 | 58         |
| 1012       | Z14000           | Homo sapiens              | RING1   | 2017                 | 100        |
| 1013       | G02841           | Homo sapiens              | Human secreted protein, SEQ ID NO: 6922.  | 332                  | 93         |
| 1014       | AF145659         | Drosophila melanogaster   | BcDNA.GH10333   | 1244                 | 52         |
| 1015       | Y02860           | Homo sapiens              | Fragment of human secreted protein encoded by gene 65.                                    | 664                  | 67         |
| 1016       | Y02591           | Homo sapiens              | A human progesterone receptor complex p23-like protein.                                   | 772                  | 97         |
| 1017       | Y99448           | Homo sapiens              | Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374.                                 | 2323                 | 100        |
| 1018       | X67250           | Rattus norvegicus         | n-chimaerin   | 1710                 | 97         |
| 1019       | AF183417         | Homo sapiens              | microtubule-associated proteins 1A/1B light chain 3.                                      | 631                  | 100        |
| 1020       | AF164795         | Homo sapiens              | sex-regulated protein janus-a   | 674                  | 100        |
| 1021       | AF190625         | Coturnix coturnix         | qdg1-1  | 638                  | 96         |
| 1022       | AL133363         | Arabidopsis thaliana      | putative protein  | 155                  | 37         |
| 1023       | AB034912         | Homo sapiens              | WD-repeat like sequence   | 2483                 | 100        |
| 1024       | AY007091         | Homo sapiens              | similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with Ge | 2243                 | 100        |
| 1025       | X69910           | Homo sapiens              | P63 protein   | 2958                 | 99         |
| 1026       | U80736           | Homo sapiens              | CAGF9   | 1657                 | 100        |
| 1027       | AB029333         | Halocynthia roretzi       | HrPET-1   | 1048                 | 54         |
| 1028       | AB032931         | Homo sapiens              | ubiquitin-conjugating enzyme isolog   | 1045                 | 100        |
| 1029       | G01797           | Homo sapiens              | Human secreted protein, SEQ ID NO: 5878.  | 749                  | 98         |
| 1030       | G01797           | Homo sapiens              | Human secreted protein, SEQ ID NO: 5878.  | 749                  | 98         |
| 1031       | AF193795         | Homo sapiens              | vacuolar sorting protein VPS29/PEP11  | 960                  | 100        |
| 1032       | AJ222968         | Mus musculus              | L-periaxin  | 120                  | 30         |
| 1033       | Z81317           | Schizosaccharomyces pombe | DNA2-NAM7 helicase family protein   | 685                  | 31         |
| 1034       | Y41519           | Homo sapiens              | Fragment of human secreted protein encoded by gene 75.                                    | 1321                 | 99         |
| 1035       | AJ276004         | Mus musculus              | Paxneb protein  | 1709                 | 77         |
| 1036       | AF025459         | Caenorhabditis elegans    | H14A12.3 gene product   | 190                  | 30         |
| 1037       | U37251           | Homo sapiens              | Description: KRAB zinc finger protein; this is a splicing supplied by author              | 196                  | 43         |
| 1038       | W74580           | Homo sapiens              | Human membrane protein BA0306.  | 1921                 | 97         |
| 1039       | U88173           | Caenorhabditis elegans    | weak similarity to Arabidopsis thaliana ubiquitin-like protein 8                          | 331                  | 80         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                        | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------|---|----------------------|------------|
| 1040       | AF290204         | Homo sapiens                   | blood group carrier molecule DOK1   | 1637                 | 99         |
| 1041       | Y96730           | Homo sapiens                   | PRO539, a Costal-2 homologue.   | 162                  | 22         |
| 1042       | AF140683         | Mus musculus                   | F-box protein FWD2  | 2397                 | 98         |
| 1043       | AF151023         | Homo sapiens                   | HSPC189   | 1104                 | 100        |
| 1044       | AF181631         | Drosophila melanogaster        | BcDNA.GH04929   | 204                  | 37         |
| 1045       | Y77985           | Homo sapiens                   | Human collectin amino acid sequence.  | 1940                 | 100        |
| 1046       | AJ243972         | Homo sapiens                   | 6-phosphogluconolactonase   | 1317                 | 100        |
| 1047       | AB035863         | Homo sapiens                   | ATP specific succinyl CoA synthetase beta subunit precursor                         | 2324                 | 99         |
| 1048       | AL034550         | Homo sapiens                   | dJ1184F4.2 (novel protein similar to nucleolar protein 4 (NOLA) (NOLP))             | 981                  | 92         |
| 1049       | AF163825         | Homo sapiens                   | pre-B lymphocyte protein 3  | 634                  | 100        |
| 1050       | AF201949         | Homo sapiens                   | 60S ribosomal protein L30 isolog  | 868                  | 100        |
| 1051       | AF190624         | Mus musculus                   | mdgl-1  | 236                  | 85         |
| 1052       | AE003529         | Drosophila melanogaster        | CG6151 gene product   | 160                  | 44         |
| 1053       | G01191           | Homo sapiens                   | Human secreted protein, SEQ ID NO: 5272.  | 646                  | 98         |
| 1054       | AL162756         | Neisseria meningitidis         | Glu-tRNA(Gln) amidotransferase subunit A  | 682                  | 44         |
| 1055       | AF181856         | Rattus norvegicus              | tRNA selenocysteine associated protein  | 1525                 | 99         |
| 1056       | U89649           | Chlamydomonas reinhardtii      | Mr19,000 outer arm dynein light chain   | 244                  | 34         |
| 1057       | AF159141         | Homo sapiens                   | breast cancer metastasis-suppressor 1   | 663                  | 53         |
| 1058       | AF230929         | Homo sapiens                   | keratinocyte annexin-like protein pemphaxin   | 1710                 | 99         |
| 1059       | AJ270952         | Homo sapiens                   | putative membrane protein   | 1363                 | 100        |
| 1060       | AF224263         | Heterodontus francisci         | HoxD8   | 742                  | 83         |
| 1061       | X63417           | Homo sapiens                   | IRLB  | 1037                 | 100        |
| 1062       | AL079345         | Streptomyces coelicolor A3 (2) | hypothetical protein  | 143                  | 27         |
| 1063       | Y71112           | Homo sapiens                   | Human Hydrolase protein-10 (HYDRL-10).  | 2547                 | 100        |
| 1064       | AF263614         | Homo sapiens                   | acetyl-CoA synthetase   | 3493                 | 99         |
| 1065       | Y13356           | Homo sapiens                   | Amino acid sequence of protein PRO221.  | 1363                 | 100        |
| 1066       | AC006153         | Homo sapiens                   | similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292) | 662                  | 98         |
| 1067       | Y18930           | Sulfolobus solfataricus        | hypothetical protein  | 162                  | 29         |
| 1068       | R65969           | Homo sapiens T98G              | Glioblastoma-derived polypeptide.   | 887                  | 100        |
| 1069       | Y07964           | Homo sapiens                   | Human secreted protein fragment   | 863                  | 96         |
| 1070       | AF177476         | Rattus norvegicus              | CDK5 activator-binding protein  | 1995                 | 85         |
| 1071       | AF245505         | Homo sapiens                   | adlcan  | 3109                 | 99         |
| 1072       | U92794           | Mus musculus                   | alpha glucosidase II, beta subunit  | 147                  | 36         |
| 1073       | G03889           | Homo sapiens                   | Human secreted protein, SEQ ID NO: 7970.  | 698                  | 98         |
| 1074       | U15779           | Homo sapiens                   | p70   | 380                  | 28         |
| 1075       | Y13392           | Homo sapiens                   | Amino acid sequence of  | 1271                 | 91         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                 | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
|            |                  |                         | protein PRO328.   |                      |            |
| 1076       | AF161457         | Homo sapiens            | HSPC339   | 571                  | 100        |
| 1077       | Y79509           | Homo sapiens            | Human carbohydrate-associated protein CRBAP-5.                    | 2151                 | 98         |
| 1078       | AF223466         | Homo sapiens            | HT015 protein   | 831                  | 66         |
| 1079       | AL132965         | Arabidopsis thaliana    | putative WD-40 repeat-protein                                     | 286                  | 29         |
| 1080       | AB024937         | Homo sapiens            | LUNX  | 1284                 | 100        |
| 1081       | Y14768           | Homo sapiens            | V-ATPase G-subunit like protein                                   | 579                  | 100        |
| 1082       | AF016416         | Caenorhabditis elegans  | F29A7.4 gene product  | 141                  | 31         |
| 1083       | L13291           | Homo sapiens            | ADP-ribosylarginine hydrolase                                     | 802                  | 45         |
| 1084       | AB041541         | Mus musculus            | unnamed protein product   | 151                  | 44         |
| 1085       | G01922           | Homo sapiens            | Human secreted protein, SEQ ID NO: 6003.                          | 202                  | 97         |
| 1086       | AB030814         | Homo sapiens            | H-REV107 protein homolog  | 833                  | 100        |
| 1087       | AF151638         | Homo sapiens            | phosphatidylcholine transfer protein                              | 1142                 | 100        |
| 1088       | Y84432           | Homo sapiens            | Amino acid sequence of a human RNA-associated protein.            | 2783                 | 100        |
| 1089       | Y94867           | Homo sapiens            | Human protein clone HP10563.                                      | 613                  | 100        |
| 1090       | AK023982         | Homo sapiens            | unnamed protein product   | 130                  | 49         |
| 1091       | AB041586         | Mus musculus            | unnamed protein product   | 1103                 | 81         |
| 1092       | Y71277           | Homo sapiens            | Human Zlipo3 protein.   | 606                  | 100        |
| 1093       | G34973           | Mus musculus            | protein tyrosine phosphatase-like                                 | 1131                 | 95         |
| 1094       | Y66677           | Homo sapiens            | Membrane-bound protein PRO828.                                    | 522                  | 56         |
| 1095       | Y87276           | Homo sapiens            | Human signal peptide containing protein HSPP-53 SEQ ID NO:53.     | 1029                 | 99         |
| 1096       | Y87276           | Homo sapiens            | Human signal peptide containing protein HSPP-53 SEQ ID NO:53.     | 863                  | 98         |
| 1097       | AF161455         | Homo sapiens            | HSPC337   | 742                  | 98         |
| 1098       | U80029           | Caenorhabditis elegans  | similar to thioredoxin  | 242                  | 39         |
| 1099       | AJ005866         | Homo sapiens            | Sqv-7-like protein  | 1321                 | 99         |
| 1100       | AJ005866         | Homo sapiens            | Sqv-7-like protein  | 1118                 | 99         |
| 1101       | AJ005866         | Homo sapiens            | Sqv-7-like protein  | 891                  | 99         |
| 1102       | AJ005866         | Homo sapiens            | Sqv-7-like protein  | 1016                 | 99         |
| 1103       | AL110244         | Homo sapiens            | hypothetical protein  | 299                  | 31         |
| 1104       | AF242194         | Drosophila melanogaster | brakeless-B   | 147                  | 52         |
| 1105       | AL031010         | Homo sapiens            | dJ422F24.1 (PUTATIVE novel protein similar to C. elegans C02C2.5) | 968                  | 100        |
| 1106       | U28016           | Mus musculus            | parathion hydrolase (phosphotriesterase)-related protein          | 1624                 | 87         |
| 1107       | AJ278150         | Homo sapiens            | putative lipid kinase   | 2207                 | 99         |
| 1108       | G03733           | Homo sapiens            | Human secreted protein, SEQ ID NO: 7814.                          | 495                  | 98         |
| 1109       | AF217287         | Drosophila melanogaster | G protein Rho8TB  | 834                  | 54         |
| 1110       | Y28921           | Homo sapiens            | Human regulatory protein HRGP-7.                                  | 941                  | 48         |
| 1111       | Y28921           | Homo sapiens            | Human regulatory protein HRGP-7.                                  | 1331                 | 51         |
| 1112       | AF176704         | Homo sapiens            | F-box protein FBX9  | 2027                 | 99         |
| 1113       | AF182076         | Homo sapiens            | glioma tumor suppressor candidate region protein 2                | 2418                 | 100        |
| 1114       | G04039           | Homo sapiens            | Human secreted protein, SEQ                                       | 475                  | 96         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|---|----------------------|------------|
|            |                  |                           | ID NO: 8120.  |                      |            |
| 1115       | AF229439         | Mus musculus              | zinc finger protein 289   | 1697                 | 91         |
| 1116       | L40357           | Homo sapiens              | thyroid receptor interactor   | 509                  | 100        |
| 1117       | L40357           | Homo sapiens              | thyroid receptor interactor   | 404                  | 85         |
| 1118       | AL2155           | Homo sapiens              | Human XSL cDNA.   | 1673                 | 100        |
| 1119       | AL161542         | Arabidopsis thaliana      | isomerase like protein  | 607                  | 53         |
| 1120       | AL023754         | Homo sapiens              | dJ272L16.1 (Rat Ca2+/Calmodulin dependent Protein Kinase LIKE protein)    | 2341                 | 98         |
| 1121       | Y57901           | Homo sapiens              | Human transmembrane protein ETMPN-25.                                     | 321                  | 36         |
| 1122       | Z14122           | Xenopus laevis            | XLCL2   | 455                  | 77         |
| 1123       | AF225418         | Homo sapiens              | lipase  | 1531                 | 97         |
| 1124       | Y06518           | Homo sapiens              | Zen GTPase interacting protein ZIP.                                       | 3227                 | 100        |
| 1125       | AL035690         | Homo sapiens              | dJ202I21.1 (novel protein)  | 952                  | 100        |
| 1126       | AJ000217         | Homo sapiens              | CLIC2   | 1286                 | 99         |
| 1127       | AB030505         | Mus musculus              | UBE-1c2   | 1069                 | 79         |
| 1128       | Y73375           | Homo sapiens              | HTRM clone 1427838 protein sequence.                                      | 874                  | 100        |
| 1129       | Y78941           | Homo sapiens              | Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence. | 877                  | 100        |
| 1130       | AL023553         | Homo sapiens              | dJ347H13.4 (novel protein)  | 557                  | 100        |
| 1131       | Y91945           | Homo sapiens              | Human chaperone protein 6 (HCHP-6).                                       | 1408                 | 100        |
| 1132       | Z68197           | Schizosaccharomyces pombe | putative nuclear pore protein   | 596                  | 39         |
| 1133       | Z68197           | Schizosaccharomyces pombe | putative nuclear pore protein   | 389                  | 35         |
| 1134       | AF180681         | Homo sapiens              | guanine nucleotide exchange factor  | 3597                 | 100        |
| 1135       | AF079765         | Mus musculus              | enhancer of polycomb  | 264                  | 41         |
| 1136       | M62419           | Mus musculus              | clathrin-associated protein   | 2189                 | 99         |
| 1137       | AJ006219         | Drosophila melanogaster   | clathrin-associated protein   | 1254                 | 78         |
| 1138       | Y76218           | Homo sapiens              | Human secreted protein encoded by gene 95.                                | 440                  | 98         |
| 1139       | W88104           | Homo sapiens              | A Rab protein designated HRAB5-2.   | 1065                 | 99         |
| 1140       | Y13401           | Homo sapiens              | Amino acid sequence of protein PRO339.                                    | 3979                 | 98         |
| 1141       | W85026           | Chimeric - Homo sapiens   | Green fluorescent protein-Zap70 fusion product.                           | 3309                 | 100        |
| 1142       | Y13402           | Homo sapiens              | Amino acid sequence of protein PRO310.                                    | 1694                 | 99         |
| 1143       | G03875           | Homo sapiens              | Human secreted protein, SEQ ID NO: 7956.                                  | 660                  | 99         |
| 1144       | Y12917           | Homo sapiens              | Amino acid sequence of a human secreted peptide.                          | 750                  | 98         |
| 1145       | Y12917           | Homo sapiens              | Amino acid sequence of a human secreted peptide.                          | 1096                 | 100        |
| 1146       | AL022157         | Homo sapiens              | SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))                                   | 1233                 | 100        |
| 1147       | AL022157         | Homo sapiens              | SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))                                   | 1233                 | 100        |
| 1148       | G02548           | Homo sapiens              | Human secreted protein, SEQ ID NO: 6629.                                  | 370                  | 98         |
| 1149       | Y73338           | Homo sapiens              | HTRM clone 2019742 protein sequence.                                      | 1492                 | 100        |
| 1150       | W74841           | Homo sapiens              | Human secreted protein encoded by gene 113 clone                          | 228                  | 55         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---|--|----------------------|------------|
|            |                  |   | HEAAR60.   |                      |            |
| 1151       | AF044201         | Rattus norvegicus   | neural membrane protein 35; NMP35  | 1570                 | 92         |
| 1152       | AF156774         | Homo sapiens  | lysophosphatidic acid acyltransferase-gammal                                       | 1855                 | 99         |
| 1153       | AL118501         | Homo sapiens  | dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069)) | 872                  | 64         |
| 1154       | AF131852         | Homo sapiens  | Unknown  | 473                  | 100        |
| 1155       | Y41705           | Homo sapiens  | Human PRO352 protein sequence.   | 1381                 | 97         |
| 1156       | G04036           | Homo sapiens  | Human secreted protein, SEQ ID NO: 8117.   | 607                  | 99         |
| 1157       | AF112444         | Lupinus luteus  | L-asparaginase   | 287                  | 43         |
| 1158       | AF151848         | Homo sapiens  | CGI-90 protein   | 232                  | 32         |
| 1159       | AJ272267         | Homo sapiens  | choline dehydrogenase  | 2449                 | 100        |
| 1160       | AB001773         | Ciona savignyi  | PEM-6  | 196                  | 33         |
| 1161       | Y87330           | Homo sapiens  | Human signal peptide containing protein HSPP-107 SEQ ID NO:107.                    | 746                  | 83         |
| 1162       | Y87330           | Homo sapiens  | Human signal peptide containing protein HSPP-107 SEQ ID NO:107.                    | 746                  | 83         |
| 1163       | AF113534         | Homo sapiens  | HP1-BP74 protein   | 2723                 | 96         |
| 1164       | AF232226         | Danio rerio   | Deddl  | 191                  | 41         |
| 1165       | AL118501         | Homo sapiens  | dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069)) | 1051                 | 71         |
| 1166       | AL118501         | Homo sapiens  | dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069)) | 945                  | 75         |
| 1167       | AF187733         | Homo sapiens  | syntaphilin  | 831                  | 42         |
| 1168       | AB019435         | Homo sapiens  | phospholipase  | 951                  | 55         |
| 1169       | AF064604         | Homo sapiens  | KE03 protein   | 324                  | 33         |
| 1170       | Y01164           | Homo sapiens  | Polypeptide fragment encoded by gene 6.  | 1191                 | 100        |
| 1171       | L03188           | Saccharomyces cerevisiae  | putative   | 180                  | 22         |
| 1172       | AF113751         | Mus musculus  | nuclear pore membrane glycoprotein POM210  | 3941                 | 81         |
| 1173       | AJ245417         | Homo sapiens  | G5b protein  | 794                  | 100        |
| 1174       | AL022238         | Homo sapiens  | dJ1042K10.3 (novel protein)  | 1285                 | 100        |
| 1175       | U41278           | Caenorhabditis elegans  | F33G12.3 gene product  | 332                  | 28         |
| 1176       | M35617           | Homo sapiens  | T-cell receptor V-alpha-J-alpha region   | 284                  | 83         |
| 1177       | AC012680         | Arabidopsis thaliana  | putative protein phosphatase 2C; 55455-56414                                       | 209                  | 37         |
| 1178       | G01345           | Homo sapiens  | Human secreted protein, SEQ ID NO: 5426.   | 692                  | 99         |
| 1179       | AL096767         | Homo sapiens  | dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)          | 1342                 | 100        |
| 1180       | AF039716         | Caenorhabditis elegans  | similar to ATP synthase B chain  | 496                  | 55         |
| 1181       | Y11710           | Homo sapiens  | collagen type XIV  | 1048                 | 97         |
| 1182       | X82240           | Homo sapiens<br>>R94974<br>R94974 09-MAY-1996 27-OCT-1994<br>Human TCL-1 polypeptide. | T cell leukemia/lymphoma 1   | 617                  | 100        |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
|            |                  | [Homo sapiens             |  |                      |            |
| 1183       | U42841           | Caenorhabditis elegans    | short region of weak similarity to collagen  | 161                  | 33         |
| 1185       | AJ131613         | Homo sapiens              | dicarboxylate carrier protein  | 1470                 | 99         |
| 1186       | L27645           | Danio rerio               | growth-associated protein  | 130                  | 36         |
| 1187       | Y02738           | Homo sapiens              | Human secreted protein encoded by gene 89 clone HLHFP03.                           | 636                  | 100        |
| 1188       | AF217544         | Xenopus laevis            | ornithine decarboxylase-2  | 1459                 | 60         |
| 1189       | AL136307         | Homo sapiens              | dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)                   | 182                  | 33         |
| 1190       | X89602           | Homo sapiens              | rTSbeta  | 197                  | 100        |
| 1191       | U32828           | Haemophilus influenzae Rd | ribosomal protein S6 modification protein (rimK)                                   | 268                  | 31         |
| 1192       | AF154831         | Rattus norvegicus         | PV-1   | 1403                 | 60         |
| 1193       | Y50926           | Homo sapiens              | Human fetal brain cDNA clone vcl6.1 derived protein.                               | 918                  | 100        |
| 1194       | AF026530         | Rattus norvegicus         | stathmin-like-protein splice variant RB3''   | 1093                 | 97         |
| 1195       | U35244           | Rattus norvegicus         | vacuolar protein sorting homolog r-vps33a  | 2981                 | 96         |
| 1196       | Y70470           | Homo sapiens              | Human p53 target molecule, PRG3 protein.   | 1680                 | 100        |
| 1197       | AF157318         | Homo sapiens              | AD-017 protein   | 912                  | 47         |
| 1198       | AF125443         | Caenorhabditis elegans    | contains similarity to S. pombe phosphatidyl synthase (GB:Z28295)                  | 460                  | 39         |
| 1199       | AF201934         | Homo sapiens              | DC12   | 1649                 | 88         |
| 1200       | AL031775         | Homo sapiens              | dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)                            | 1902                 | 100        |
| 1201       | M21103           | Ovis aries                | BIIIR4 high-sulfur keratin   | 484                  | 82         |
| 1202       | Z85986           | Homo sapiens              | dJ108K11.3 (similar to yeast suppressor protein SRP40)                             | 1143                 | 75         |
| 1203       | U18762           | Rattus norvegicus         | retinol dehydrogenase type I   | 890                  | 52         |
| 1204       | U35730           | Mus musculus              | jerky  | 2235                 | 76         |
| 1205       | AB002327         | Homo sapiens              | KIAA0329   | 151                  | 24         |
| 1206       | AB019233         | Arabidopsis thaliana      | ubiquinone/menaquinone biosynthesis methyltransferase-like                         | 762                  | 56         |
| 1207       | AL136307         | Homo sapiens              | dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)                   | 742                  | 100        |
| 1208       | AF207989         | Homo sapiens              | orphan G-protein coupled receptor  | 2326                 | 100        |
| 1209       | Z97630           | Homo sapiens              | dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G))) | 181                  | 44         |
| 1210       | U21549           | Mus musculus              | Ac39/physophilin   | 1280                 | 68         |
| 1211       | Y27700           | Homo sapiens              | Human secreted protein encoded by gene No. 12.                                     | 1267                 | 100        |
| 1212       | AF117814         | Mus musculus              | odd-skipped related 1 protein  | 945                  | 66         |
| 1213       | AF277233         | Naegleria fowleri         | calcineurin B  | 222                  | 39         |
| 1214       | D14849           | Mus musculus              | meiosis-specific nuclear structural protein 1                                      | 1950                 | 77         |
| 1215       | G03022           | Homo sapiens              | Human secreted protein, SEQ ID NO: 7103.   | 590                  | 100        |
| 1216       | Z72510           | Caenorhabditis            | similarity to yeast UTR3   | 634                  | 49         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                  | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------|---|----------------------|------------|
|            |                  | is elegans               | protein (Swiss Prot accession yk677h11.5 comes from this gene                                 |                      |            |
| 1217       | Z49703           | Saccharomyces cerevisiae | unknown   | 134                  | 22         |
| 1218       | AC013430         | Arabidopsis thaliana     | F3F9.18   | 199                  | 29         |
| 1219       | L10910           | Homo sapiens             | splicing factor   | 1026                 | 71         |
| 1220       | Z70750           | Caenorhabditis elegans   | similar to vanadate resistance protein transmembranous comes from this gene                   | 965                  | 58         |
| 1221       | AL163815         | Arabidopsis thaliana     | putative protein  | 653                  | 61         |
| 1222       | AF155100         | Homo sapiens             | zinc finger protein NY-REN-21 antigen   | 2261                 | 100        |
| 1223       | J05071           | Bos taurus               | GTP-binding regulatory protein gamma-6 subunit  | 356                  | 100        |
| 1224       | Y73364           | Homo sapiens             | HTRM clone 2765991 protein sequence.  | 1169                 | 99         |
| 1225       | AL050170         | Homo sapiens             | hypothetical protein  | 714                  | 100        |
| 1226       | X64002           | Homo sapiens             | RAP74   | 2661                 | 99         |
| 1227       | X04085           | Homo sapiens             | catalase  | 2846                 | 100        |
| 1228       | AJ005620         | Mus musculus             | skeletal muscle-specific gene   | 1416                 | 90         |
| 1229       | AF045564         | Rattus norvegicus        | development-related protein   | 1715                 | 93         |
| 1230       | X97571           | Mus musculus             | HCMV-interacting protein  | 479                  | 96         |
| 1231       | L08239           | Homo sapiens             | located at OATL1  | 2274                 | 100        |
| 1232       | AF121863         | Homo sapiens             | sorting nexin 14  | 1964                 | 100        |
| 1233       | AF121863         | Homo sapiens             | sorting nexin 14  | 1203                 | 84         |
| 1234       | AC024805         | Caenorhabditis elegans   | contains similarity to TR:004595  | 744                  | 31         |
| 1235       | AC006634         | Caenorhabditis elegans   | contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162) | 357                  | 33         |
| 1236       | Y18101           | Mus musculus             | macrophage actin-associated-tyrosine-phosphorylated protein                                   | 1559                 | 87         |
| 1237       | AB042646         | Homo sapiens             | TGIF2   | 1224                 | 100        |
| 1238       | AB026264         | Homo sapiens             | IMPACT  | 1694                 | 100        |
| 1239       | AB026264         | Homo sapiens             | IMPACT  | 1123                 | 100        |
| 1240       | G00429           | Homo sapiens             | Human secreted protein, SEQ ID NO: 4510.  | 324                  | 100        |
| 1241       | Y76144           | Homo sapiens             | Human secreted protein encoded by gene 21.  | 1363                 | 53         |
| 1242       | AL035602         | Arabidopsis thaliana     | putative protein  | 499                  | 28         |
| 1243       | X76483           | Gallus gallus            | Yes-associated protein (65kDa)  | 574                  | 48         |
| 1244       | AF220186         | Homo sapiens             | uncharacterized hypothalamus protein HT012  | 503                  | 100        |
| 1245       | AL021453         | Homo sapiens             | dJ821D11.3 (PUTATIVE protein)   | 856                  | 100        |
| 1246       | AJ276003         | Homo sapiens             | GARI protein  | 1216                 | 100        |
| 1247       | Y57910           | Homo sapiens             | Human transmembrane protein HTPN-34.  | 1369                 | 98         |
| 1248       | AC004874         | Homo sapiens             | similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989)                | 957                  | 100        |
| 1249       | AF199597         | Homo sapiens             | A-type potassium channel modulatory protein 1   | 1139                 | 100        |
| 1250       | Y13148           | Rattus norvegicus        | PAG608  | 1350                 | 88         |
| 1251       | M24852           | Rattus norvegicus        | neuron-specific protein PEP-19  | 124                  | 46         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                 | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 1252       | AF146738         | Rattus norvegicus       | testis specific protein   | 771                  | 83         |
| 1253       | G02725           | Homo sapiens            | Human secreted protein, SEQ ID NO: 68C6.                                    | 419                  | 97         |
| 1254       | W44375           | Homo sapiens            | Human ubiquitin-conjugating enzyme polypeptide.                             | 1045                 | 99         |
| 1255       | AC006538         | Homo sapiens            | BC41195.1   | 831                  | 78         |
| 1256       | AB004316         | Bos taurus              | mitochondrial methionyl-tRNA transformylase                                 | 1556                 | 88         |
| 1257       | Z35094           | Homo sapiens            | SURF-2  | 1354                 | 97         |
| 1258       | Y13362           | Homo sapiens            | Amino acid sequence of protein PRO214.                                      | 2383                 | 100        |
| 1259       | AC006014         | Homo sapiens            | similar to RFP transforming protein; similar to P14373 (PID:g132517)        | 1299                 | 100        |
| 1260       | AC005099         | Homo sapiens            | match to A1222572 (NID:g3804775)  | 469                  | 100        |
| 1261       | V00507           | Homo sapiens            | coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon) | 984                  | 100        |
| 1262       | X15443           | Rattus sp.              | gamma-glutamyltranspeptidase (AA 1-568)                                     | 697                  | 32         |
| 1263       | AF173871         | Mus musculus            | neuronal PAS3   | 977                  | 94         |
| 1264       | AF178983         | Homo sapiens            | Ras-associated protein Rap1   | 433                  | 97         |
| 1265       | Y70473           | Homo sapiens            | Human cyclic nucleotide-associated protein-1 (CNAP-1).                      | 2785                 | 99         |
| 1266       | Y41738           | Homo sapiens            | Human PRO541 protein sequence.  | 1622                 | 100        |
| 1267       | AF061346         | Mus musculus            | Edp1 protein  | 1077                 | 64         |
| 1268       | U97006           | Caenorhabditis elegans  | C13F10.4 gene product   | 154                  | 23         |
| 1269       | AF233582         | Mus musculus            | GTPase Rab37  | 942                  | 95         |
| 1270       | AF195951         | Homo sapiens            | signal recognition particle 68  | 3127                 | 98         |
| 1271       | AL031177         | Homo sapiens            | dJ889M15.3 (novel protein)  | 1150                 | 55         |
| 1272       | AF201933         | Homo sapiens            | DC11  | 650                  | 100        |
| 1273       | AF201933         | Homo sapiens            | DC11  | 346                  | 98         |
| 1274       | AL021710         | Arabidopsis thaliana    | putative protein  | 348                  | 49         |
| 1275       | AC004449         | Homo sapiens            | R33683_3  | 556                  | 100        |
| 1276       | Y86295           | Homo sapiens            | Human secreted protein HL2AG87, SEQ ID NO:210.                              | 1920                 | 100        |
| 1277       | Y71111           | Homo sapiens            | Human Hydrolase protein-9 (HYDRL-9).  | 1576                 | 99         |
| 1278       | S94421           | Homo sapiens            | T cell receptor eta-exon  | 478                  | 100        |
| 1279       | Y66695           | Homo sapiens            | Membrane-bound protein PRO1344.   | 1909                 | 100        |
| 1280       | AF161380         | Homo sapiens            | HSPC262   | 772                  | 100        |
| 1281       | Y48610           | Homo sapiens            | Human breast tumour-associated protein 71.                                  | 779                  | 100        |
| 1282       | AC015446         | Arabidopsis thaliana    | Similar to AIG1 protein   | 406                  | 35         |
| 1283       | AK024432         | Homo sapiens            | FLJ00022 protein  | 403                  | 35         |
| 1284       | W96153           | Homo sapiens            | Human FADD-interacting protein (FIP).                                       | 1825                 | 81         |
| 1285       | AJ001019         | Homo sapiens            | ring finger protein   | 1301                 | 100        |
| 1286       | AE003823         | Drosophila melanogaster | CG13178 gene product  | 195                  | 29         |
| 1287       | AF178632         | Homo sapiens            | FEM-1-like death receptor binding protein                                   | 3261                 | 100        |
| 1288       | AC006033         | Homo sapiens            | similar to MLN 64; similar to I38027 (PID:g2135214)                         | 1195                 | 100        |
| 1289       | AC006033         | Homo sapiens            | similar to MLN 64; similar to I38027 (PID:g2135214)                         | 668                  | 93         |
| 1290       | AB023811         | Homo sapiens            | TU3A  | 351                  | 54         |



TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---|--|----------------------|------------|
| 1291       | Z73424           | Caenorhabditis elegans  | C44B9.1  | 235                  | 36         |
| 1292       | Y94871           | Homo sapiens  | Human protein clone HP02551.                                     | 1222                 | 100        |
| 1293       | AF190425         | Homo sapiens  | retinoblastoma-associated protein RAP140                         | 489                  | 29         |
| 1294       | G03856           | Homo sapiens  | Human secreted protein, SEQ ID NO: 7937.                         | 538                  | 99         |
| 1295       | AF133670         | Mus musculus  | ARL-6 interacting protein-2                                      | 367                  | 51         |
| 1296       | AJ249735         | Homo sapiens  | claudin-6  | 1142                 | 100        |
| 1297       | X57560           | Escherichia coli  | pspE protein   | 535                  | 100        |
| 1298       | AF169284         | Homo sapiens  | LIM and cysteine-rich domains protein 1                          | 1997                 | 100        |
| 1299       | U41023           | Caenorhabditis elegans  | coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5 | 324                  | 29         |
| 1300       | AB024523         | Homo sapiens  | basic kruppel like factor  | 1206                 | 100        |
| 1301       | X55989           | Homo sapiens  | eosinophil cationic-related protein                              | 737                  | 99         |
| 1302       | AF007151         | Homo sapiens  | unknown  | 1481                 | 100        |
| 1303       | X52904           | Escherichia coli  | open reading frame (AA 1-65)                                     | 359                  | 100        |
| 1304       | U19577           | Escherichia coli  | galactonate dehydratase  | 242                  | 93         |
| 1305       | AF266508         | Mus musculus  | NELF protein   | 1409                 | 97         |
| 1306       | Y57901           | Homo sapiens  | Human transmembrane protein HTPN-25.                             | 932                  | 100        |
| 1307       | U58750           | Caenorhabditis elegans  | similar to the mitochondrial carrier family                      | 365                  | 54         |
| 1308       | AF044774         | Homo sapiens  | breakpoint cluster region protein 2                              | 2681                 | 99         |
| 1309       | AL078593         | Homo sapiens  | dJ210B1.1 (KIAA0680)   | 267                  | 34         |
| 1310       | X82693           | Homo sapiens  | E48 antigen  | 620                  | 96         |
| 1311       | Z82263           | Caenorhabditis elegans  | C47A4.1  | 283                  | 35         |
| 1312       | AF131218         | Homo sapiens  | chromosome 16 open reading frame 5                               | 1493                 | 100        |
| 1313       | Y41763           | Homo sapiens  | Human PRO938 protein sequence.                                   | 1636                 | 100        |
| 1314       | AF196972         | Homo sapiens  | JM24 protein   | 2239                 | 100        |
| 1315       | AF053356         | Homo sapiens  | insulin receptor substrate like protein                          | 228                  | 97         |
| 1316       | Y66695           | Homo sapiens  | Membrane-bound protein PRO1344.                                  | 1909                 | 100        |
| 1317       | AF153127         | Gallus gallus   | SAPK interacting protein   | 2442                 | 89         |
| 1318       | AF153127         | Gallus gallus   | SAPK interacting protein   | 1477                 | 83         |
| 1319       | AF153127         | Gallus gallus   | SAPK interacting protein   | 1651                 | 86         |
| 1320       | X56932           | Homo sapiens  | 23 kD highly basic protein                                       | 1044                 | 100        |
| 1321       | AF174605         | Homo sapiens<br>>Y83086<br>Y83086 09-MAR-2000 28-AUG-1998 F-box protein FBP-18.<br>[Homo sapiens] | F-box protein Fbx25  | 467                  | 70         |
| 1322       | M61732           | Trypanosoma cruzi   | neuraminidase  | 214                  | 24         |
| 1323       | Y17013           | porcine endogenous  | pol  | 304                  | 64         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                              | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|---|----------------------|------------|
|            |                  | retrovirus                           |   |                      |            |
| 1324       | AL138655         | Arabidopsis thaliana                 | putative protein  | 1174                 | 37         |
| 1325       | AL138655         | Arabidopsis thaliana                 | putative protein  | 946                  | 35         |
| 1326       | AL133215         | Homo sapiens                         | bA108L7.2 (novel protein similar to rat tricarboxylate carrier)     | 1322                 | 99         |
| 1327       | AF161541         | Homo sapiens                         | HSPC056   | 1357                 | 99         |
| 1328       | Y73346           | Homo sapiens                         | HTRM clone 619699 protein sequence.                                 | 785                  | 96         |
| 1329       | L10910           | Homo sapiens                         | splicing factor   | 912                  | 82         |
| 1330       | AF146568         | Homo sapiens                         | MIL1 protein  | 1936                 | 100        |
| 1331       | W87772           | Homo sapiens                         | Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.   | 232                  | 39         |
| 1332       | Y41741           | Homo sapiens                         | Human PRO704 protein sequence.                                      | 1860                 | 100        |
| 1333       | AF295096         | Homo sapiens                         | zinc-finger protein ZBRK1   | 411                  | 91         |
| 1334       | Z82271           | Caenorhabditis elegans               | Similarity to Mouse kinensin-like protein KI74 comes from this gene | 578                  | 44         |
| 1335       | AE000810         | Methanobacterium thermoautotrophicum | conserved protein   | 290                  | 43         |
| 1336       | Y68779           | Homo sapiens                         | Amino acid sequence of a human phosphorylation effector PHSP-11.    | 1019                 | 91         |
| 1337       | AB027003         | Mus musculus                         | protein phosphatase   | 378                  | 84         |
| 1338       | U64856           | Caenorhabditis elegans               | weak similarity to TPR domains                                      | 215                  | 40         |
| 1339       | AE001394         | Plasmodium falciparum                | protein of the YMR7 family  | 170                  | 29         |
| 1340       | X76717           | Homo sapiens                         | MT-11 protein   | 204                  | 89         |
| 1341       | AC011914         | Arabidopsis thaliana                 | putative mutT protein; 68398-67881                                  | 289                  | 45         |
| 1342       | AJ276171         | Homo sapiens                         | ASPIC   | 2122                 | 100        |
| 1343       | AF187016         | Homo sapiens                         | myosin regulatory light chain interacting protein MIR               | 2303                 | 99         |
| 1344       | AC006963         | Homo sapiens                         | similar to Kelch proteins; similar to BAA77027 (PID:g4650844)       | 894                  | 35         |
| 1345       | AF257466         | Homo sapiens                         | N-acetylneuraminic acid phosphate synthase                          | 1880                 | 99         |
| 1346       | Y25896           | Homo sapiens                         | Human secreted protein fragment encoded from gene 64.               | 1148                 | 100        |
| 1347       | AJ272073         | Torpedo marmorata                    | male sterility protein 2-like protein                               | 1664                 | 58         |
| 1348       | AF161548         | Homo sapiens                         | HSPC063   | 1018                 | 98         |
| 1349       | W78128           | Homo sapiens                         | Human secreted protein encoded by gene 3 clone HOSBI96.             | 1117                 | 100        |
| 1351       | G02144           | Homo sapiens                         | Human secreted protein, SEQ ID NO: 6225.                            | 418                  | 100        |
| 1352       | D90869           | Escherichia coli                     | similar to  | 2047                 | 100        |
| 1353       | A12029           | Homo sapiens                         | MRP-14  | 613                  | 100        |
| 1354       | AC005328         | Homo sapiens                         | R26660_1, partial CDS   | 870                  | 74         |
| 1355       | AC024876         | Caenorhabditis elegans               | contains similarity to SW:RPB1 CRIGR                                | 829                  | 61         |
| 1356       | AF077226         | Homo sapiens                         | copine III  | 1876                 | 64         |
| 1359       | AF217188         | Mus musculus                         | YIP1B   | 801                  | 63         |
| 1360       | AC074331         | Homo sapiens                         | ZNF234  | 3869                 | 100        |
| 1361       | AL163279         | Homo sapiens                         | homolog to cAMP response  | 5035                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                  | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------|--|----------------------|------------|
|            |                  |                          | element binding and beta transducin family proteins  |                      |            |
| 1362       | Z48475           | Homo sapiens             | glucokinase regulator  | 3160                 | 99         |
| 1363       | Z48475           | Homo sapiens             | glucokinase regulator  | 2682                 | 97         |
| 1364       | AF195764         | Homo sapiens             | megakaryocyte-enhanced gene transcript 1 protein; MEGT1 protein  | 2055                 | 99         |
| 1365       | AF116609         | Homo sapiens             | PRO0915  | 581                  | 100        |
| 1366       | AF116609         | Homo sapiens             | PRO0915  | 581                  | 100        |
| 1367       | AL117352         | Homo sapiens             | dJ876B10.3 (novel protein similar to C. elegans T19B10.6 (Tr:Q22557))                                      | 2581                 | 99         |
| 1368       | Y34124           | Homo sapiens             | Human potassium channel K+Hnov15.  | 1342                 | 100        |
| 1369       | AJ245621         | Homo sapiens             | CTL2 protein   | 3728                 | 99         |
| 1370       | AF008220         | Bacillus subtilis        | YtaG   | 429                  | 45         |
| 1371       | X05562           | Homo sapiens             | alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)                                      | 5908                 | 99         |
| 1372       | Z98048           | Homo sapiens             | dJ408N23.4 (novel DnaJ domain protein)   | 1296                 | 99         |
| 1373       | AF154415         | Homo sapiens             | FLASH  | 10253                | 100        |
| 1374       | U20286           | Rattus norvegicus        | lamina associated polypeptide 1C   | 1567                 | 69         |
| 1375       | U53445           | Homo sapiens             | DOC1   | 1645                 | 46         |
| 1376       | AL117337         | Homo sapiens             | BA393J16.1 (zinc finger protein 33a (KOX 31))  | 250                  | 60         |
| 1377       | AC005328         | Homo sapiens             | R26660_1, partial CDS  | 1126                 | 100        |
| 1378       | U35113           | Homo sapiens             | metastasis-associated gene   | 1823                 | 69         |
| 1379       | L15313           | Caenorhabditis elegans   | putative   | 858                  | 58         |
| 1380       | Y25756           | Homo sapiens             | Human secreted protein encoded from gene 46.   | 1508                 | 100        |
| 1381       | AB037360         | Homo sapiens             | ANKHZN   | 5734                 | 95         |
| 1382       | AB037360         | Homo sapiens             | ANKHZN   | 959                  | 97         |
| 1383       | AF237676         | Mus musculus             | G beta-like protein GBL  | 1721                 | 96         |
| 1384       | AF237676         | Mus musculus             | G beta-like protein GBL  | 1043                 | 70         |
| 1385       | Y58793           | Homo sapiens             | Human calcium regulatory protein CaREG-1.  | 715                  | 100        |
| 1386       | AF212162         | Homo sapiens             | nina1n   | 10369                | 99         |
| 1387       | AL031585         | Homo sapiens             | dJ963K23.2 (novel protein)   | 337                  | 33         |
| 1388       | AC004890         | Homo sapiens             | similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein. | 542                  | 86         |
| 1389       | AF187989         | Homo sapiens             | zinc finger protein ZNF223   | 2665                 | 99         |
| 1390       | AC035150         | Homo sapiens             | Zinc finger protein ZNF221   | 3459                 | 100        |
| 1391       | AF287894         | Homo sapiens             | PIST   | 1410                 | 97         |
| 1392       | AF282265         | Homo sapiens             | inner centromere protein INCENP  | 1794                 | 99         |
| 1393       | X90840           | Homo sapiens             | axonal transporter of synaptic vesicles  | 4584                 | 99         |
| 1394       | AF076249         | Homo sapiens             | zinc finger protein SBBIZ1   | 3208                 | 99         |
| 1395       | G02224           | Homo sapiens             | Human secreted protein, SEQ ID NO: 6305.   | 299                  | 75         |
| 1396       | AC004809         | Arabidopsis thaliana     | Similar to   | 130                  | 34         |
| 1398       | AF242519         | Homo sapiens             | zinc finger protein SBZF3  | 181                  | 66         |
| 1399       | AL133396         | Homo sapiens             | dJ1068H6.4 (prion protein like protein doppel)   | 962                  | 100        |
| 1400       | Y48611           | Homo sapiens             | Human breast tumour-associated protein 72.   | 817                  | 99         |
| 1401       | AC004472         | Homo sapiens             | Pl.11659_5   | 280                  | 54         |
| 1402       | X91489           | Saccharomyces cerevisiae | putative HMG box   | 164                  | 27         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                 | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 1403       | Y79222           | Homo sapiens            | Human transferase TRNSPS-14.  | 2842                 | 100        |
| 1404       | X81058           | Mus musculus            | tex261  | 1010                 | 99         |
| 1405       | AB012084         | Mus musculus            | ITM   | 194                  | 29         |
| 1406       | AB030251         | Homo sapiens            | GTPase activating protein   | 3233                 | 99         |
| 1407       | AJ010585         | Rattus rattus           | PTB-like protein  | 2684                 | 99         |
| 1408       | X75760           | Drosophila melanogaster | LRR47   | 364                  | 29         |
| 1409       | U76618           | Mus musculus            | N-RAP   | 804                  | 48         |
| 1410       | AC005578         | Homo sapiens            | P20887_1, partial CDS   | 835                  | 63         |
| 1411       | AE000284         | Escherichia coli        | orf, hypothetical protein.  | 360                  | 100        |
| 1412       | X01563           | Escherichia coli        | L5 (rplE) (aa 1-179)  | 911                  | 100        |
| 1413       | W78279           | Homo sapiens            | Fragment of human secreted protein encoded by gene 33.                                    | 1264                 | 99         |
| 1414       | AB031051         | Homo sapiens            | organic anion transporter OATP-E  | 3832                 | 100        |
| 1415       | M17466           | Homo sapiens            | coagulation factor XII  | 3455                 | 100        |
| 1416       | AF097994         | Homo sapiens            | L-kynurenine/alpha-aminoadipate aminotransferase  | 2202                 | 99         |
| 1417       | AF151077         | Homo sapiens            | HSPC243   | 1262                 | 99         |
| 1418       | Y09945           | Rattus norvegicus       | putative integral membrane transport protein  | 1098                 | 61         |
| 1419       | U13152           | Mesocricetus auratus    | guanine nucleotide-binding protein beta 5   | 2179                 | 76         |
| 1420       | AL162458         | Homo sapiens            | ba465L10.5 (KIAA1176 (novel protein, presumed ortholog of mouse K-CI cotransporter KCC2)) | 5696                 | 100        |
| 1421       | Y99426           | Homo sapiens            | Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.                                 | 152                  | 29         |
| 1422       | Y94923           | Homo sapiens            | Human secreted protein clone qs14_3 protein sequence SEQ ID NO:52.                        | 4039                 | 99         |
| 1423       | AF177388         | Homo sapiens            | cancer-amplified transcriptional coactivator ASC-2  | 10748                | 99         |
| 1424       | Y48517           | Homo sapiens            | Human breast tumour-associated protein 62.  | 1851                 | 99         |
| 1425       | AF208848         | Homo sapiens            | BM-006  | 1454                 | 89         |
| 1426       | AF208848         | Homo sapiens            | BM-006  | 853                  | 79         |
| 1427       | AF112886         | Bos taurus              | differentiation enhancing factor 1  | 4693                 | 95         |
| 1428       | U41387           | Homo sapiens            | Gu protein  | 1372                 | 63         |
| 1429       | AF161534         | Homo sapiens            | HSPC049   | 2853                 | 78         |
| 1430       | AF125043         | Mus musculus            | bisphosphate 3'-nucleotidase  | 275                  | 30         |
| 1431       | Y66718           | Homo sapiens            | Membrane-bound protein PRO1106.   | 1886                 | 100        |
| 1432       | AF193613         | Homo sapiens            | cell recognition molecule Caspr2  | 568                  | 100        |
| 1433       | AB044560         | Mus musculus            | Gliacolin   | 192                  | 34         |
| 1434       | R99900           | Homo sapiens            | NTII-1 nerve protein, facilitates regeneration of nerve cells.                            | 707                  | 51         |
| 1435       | AF220530         | Homo sapiens            | myo-inositol 1-phosphate synthase A1  | 2904                 | 100        |
| 1436       | X70944           | Homo sapiens            | PTB-associated splicing factor  | 1261                 | 72         |
| 1437       | AF271732         | Homo sapiens            | bridging integrator-3   | 1282                 | 100        |
| 1438       | Y30811           | Homo sapiens            | Human secreted protein encoded from gene 1.   | 595                  | 98         |
| 1439       | AJ293659         | Homo sapiens            | mucolipidin   | 628                  | 97         |
| 1440       | AF219138         | Homo sapiens            | GGA3 long isoform   | 3083                 | 100        |
| 1441       | AF219138         | Homo sapiens            | GGA3 long isoform   | 3346                 | 100        |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|---|----------------------|------------|
| 1442       | AB039669         | Homo sapiens              | ALEX3   | 1944                 | 100        |
| 1443       | AF237711         | Drosophila melanogaster   | Diablo  | 191                  | 27         |
| 1444       | AJ011896         | Homo sapiens              | Naf1 beta protein   | 439                  | 39         |
| 1445       | X73874           | Homo sapiens              | phosphorylase kinase  | 6233                 | 98         |
| 1446       | AF214114         | Homo sapiens              | breast carcinoma-associated antigen BCAA  | 3999                 | 99         |
| 1447       | AF003924         | Homo sapiens              | ANC 2H01  | 2645                 | 99         |
| 1448       | AF003136         | Caenorhabditis elegans    | contains weak similarity to an AMP-binding motif  | 2843                 | 52         |
| 1449       | AF155112         | Homo sapiens              | NY-REN-50 antigen   | 1184                 | 89         |
| 1450       | Y95004           | Homo sapiens              | Human secreted protein vc54_1, SEQ ID NO:48.  | 985                  | 100        |
| 1451       | AF107203         | Homo sapiens              | ataxin 2-binding protein  | 688                  | 57         |
| 1452       | AF107203         | Homo sapiens              | ataxin 2-binding protein  | 456                  | 78         |
| 1453       | Z38011           | Mus musculus              | DMR-N9  | 882                  | 56         |
| 1454       | X90568           | Homo sapiens              | Protein sequence and annotation available soon via LABELIT@EMBL-Heidelberg.DE             | 510                  | 28         |
| 1455       | AL035409         | Homo sapiens              | dJ564M11.3 (similar to sialyltransferase)   | 1356                 | 100        |
| 1456       | D44480           | Mus musculus              | MATH-2 protein  | 272                  | 100        |
| 1458       | AF141326         | Homo sapiens              | RNA helicase HDB/DICE1  | 478                  | 45         |
| 1459       | AF242552         | Gallus gallus             | retinovin   | 945                  | 34         |
| 1460       | U11036           | Homo sapiens              | Ibd1  | 724                  | 84         |
| 1461       | AB025258         | Mus musculus              | granuphillin-a  | 545                  | 39         |
| 1462       | Y08134           | Homo sapiens              | acid sphingomyelinase-like phosphodiesterase  | 2428                 | 99         |
| 1463       | AC004997         | Homo sapiens              | match to ESTs 243979 (NID:g573097), R19699 (NID:g774333)                                  | 869                  | 98         |
| 1464       | AC004997         | Homo sapiens              | match to ESTs 243979 (NID:g573097), R19699 (NID:g774333)                                  | 869                  | 98         |
| 1465       | U32743           | Haemophilus influenzae Rd | fucose operon protein (fucU)  | 315                  | 50         |
| 1466       | Y09022           | Homo sapiens              | Not56-like protein  | 2342                 | 100        |
| 1467       | AC003034         | Homo sapiens              | Homolog of rat kidney-specific (KS) gene  | 1072                 | 99         |
| 1468       | AF071544         | Spinacia oleracea         | ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I       | 333                  | 26         |
| 1469       | Y57930           | Homo sapiens              | Human transmembrane protein HTPN-54.  | 1053                 | 100        |
| 1470       | AF032666         | Rattus norvegicus         | rsec5   | 4504                 | 93         |
| 1471       | Y70467           | Homo sapiens              | Human membrane channel protein-17 (MECHP-17).   | 452                  | 74         |
| 1472       | AL031033         | Homo sapiens              | C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)                         | 1694                 | 100        |
| 1473       | AF177292         | Homo sapiens              | genethonin 3  | 4026                 | 98         |
| 1474       | S45936           | Homo sapiens              | HTS1  | 1101                 | 50         |
| 1475       | Y86241           | Homo sapiens              | Human secreted protein HOABR60, SEQ ID NO:156.  | 1879                 | 98         |
| 1476       | AJ010317         | Fugu rubripes             | Sand  | 1278                 | 68         |
| 1477       | U42831           | Caenorhabditis elegans    | coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) | 846                  | 44         |
| 1478       | X62447           | Homo sapiens              | PR 264  | 543                  | 61         |
| 1479       | X82209           | Homo sapiens              | MN1   | 7116                 | 100        |
| 1480       | U10536           | Pan paniscus              | MHC class I A   | 675                  | 84         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 1481       | AL078599         | Homo sapiens              | dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:P91086))         | 1274                 | 65         |
| 1482       | 298977           | Schizosaccharomyces pombe | putative vacuolar protein  | 256                  | 29         |
| 1483       | AB005662         | Mus musculus              | JNK/SAPK-associated protein-1  | 4968                 | 92         |
| 1484       | AL050120         | Homo sapiens              | hypothetical protein   | 716                  | 100        |
| 1485       | M27878           | Homo sapiens              | DNA binding protein  | 1006                 | 53         |
| 1486       | Y69161           | Homo sapiens              | Amino acid sequence of a partial protein kinase.                             | 575                  | 99         |
| 1487       | X84156           | Saccharomyces cerevisiae  | ATH1   | 341                  | 29         |
| 1488       | AF038963         | Homo sapiens              | RNA helicase   | 446                  | 34         |
| 1489       | U56966           | Caenorhabditis elegans    | coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 | 620                  | 42         |
| 1490       | AE000989         | Archaeoglobus fulgidus    | enoyl-CoA hydratase (fad-4)  | 533                  | 46         |
| 1491       | M80633           | Rattus norvegicus         | adenylyl cyclase type IV   | 707                  | 95         |
| 1492       | Y73342           | Homo sapiens              | HTRM clone 2709055 protein sequence.   | 3513                 | 99         |
| 1493       | Y17220           | Homo sapiens              | Human secreted protein (clone fj283-11).                                     | 462                  | 37         |
| 1494       | AF133670         | Mus musculus              | ARL-6 interacting protein-2  | 701                  | 97         |
| 1495       | Y94897           | Homo sapiens              | Human protein clone HP10574.   | 1371                 | 100        |
| 1496       | AL049699         | Homo sapiens              | dJ747H23.2 (novel protein)   | 1550                 | 100        |
| 1497       | AF037447         | Homo sapiens              | ribosomal S6 protein kinase  | 2427                 | 100        |
| 1498       | AL445067         | Thermoplasma acidophilum  | putative target YPL207w of the HAP2 transcriptional complex related protein  | 269                  | 35         |
| 1499       | AB039947         | Homo sapiens              | X11L-binding protein 51  | 227                  | 36         |
| 1500       | AJ277750         | Homo sapiens              | UBASH3A protein  | 3509                 | 100        |
| 1501       | AL050333         | Homo sapiens              | dJ93K22.1 (novel protein (contains DKFZF564B116))                            | 2439                 | 100        |
| 1502       | AF179896         | Homo sapiens              | TAL1 homeobox protein Meis2b   | 1140                 | 100        |
| 1503       | AF178948         | Homo sapiens              | TAL1 homeobox protein Meis2a   | 1177                 | 100        |
| 1504       | Y53005           | Homo sapiens              | Human secreted protein clone pm749.8 protein sequence SEQ ID NO:16.          | 1442                 | 99         |
| 1505       | X82494           | Homo sapiens              | fibulin-2  | 3580                 | 99         |
| 1506       | X98296           | Homo sapiens              | ubiquitin hydrolase  | 783                  | 42         |
| 1507       | AL034548         | Homo sapiens              | dJ1103G7.6 (novel protein)   | 1098                 | 100        |
| 1508       | Y76144           | Homo sapiens              | Human secreted protein encoded by gene 21.                                   | 1736                 | 100        |
| 1509       | AF220182         | Homo sapiens              | uncharacterized hypothalamus protein HT008                                   | 1181                 | 98         |
| 1510       | U64601           | Caenorhabditis elegans    | Gene probably begins in the next cosmid                                      | 415                  | 58         |
| 1511       | AL356192         | Neurospora crassa         | related to MDM1 protein  | 196                  | 29         |
| 1512       | D17629           | Homo sapiens              | N-acetylgalactosamine 6-sulfate sulfatase (GALNS)                            | 1829                 | 100        |
| 1513       | AF168717         | Homo sapiens              | x 009 protein  | 694                  | 99         |
| 1514       | AJ243531         | Homo sapiens              | nM15 protein   | 735                  | 100        |
| 1515       | AC003672         | Arabidopsis thaliana      | putative C3HC4-type RING zinc finger protein                                 | 407                  | 30         |
| 1516       | AF115435         | Rattus norvegicus         | syntaxin 17  | 1374                 | 90         |
| 1517       | AF003140         | Caenorhabditis elegans    | C44E4.5 gene product   | 274                  | 31         |
| 1518       | AB002584         | Rattus norvegicus         | beta-alanine-pyruvate aminotransferase                                       | 2238                 | 82         |
| 1519       | AL121764         | Schizosaccharomyces       | yeast atp12 protein precursor  | 270                  | 30         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
|            |                  | romyces pombe             | homolog  |                      |            |
| 1520       | AF255910         | Homo sapiens              | vascular endothelial junction-associated molecule                                  | 547                  | 100        |
| 1521       | D31764           | Homo sapiens              | KIAA0064   | 170                  | 27         |
| 1522       | Y66634           | Homo sapiens              | Membrane-bound protein PRO190.   | 985                  | 100        |
| 1523       | Y94450           | Homo sapiens              | Human inflammation associated protein  | 250                  | 43         |
| 1524       | AC000107         | Arabidopsis thaliana      | F17F8.22   | 277                  | 37         |
| 1525       | AF109377         | Mus musculus              | ldlBp  | 1277                 | 83         |
| 1526       | AL031427         | Homo sapiens              | dJ167A19.4 (novel protein)   | 1432                 | 99         |
| 1527       | Y08135           | Mus musculus              | acid sphingomyelinase-like phosphodiesterase                                       | 1496                 | 79         |
| 1528       | AK024423         | Homo sapiens              | FLJ00012 protein   | 611                  | 100        |
| 1529       | AF154502         | Homo sapiens              | quiescent cell proline dipeptidase   | 679                  | 100        |
| 1530       | AF205598         | Homo sapiens              | transposase-like protein   | 1368                 | 100        |
| 1531       | AF251039         | Homo sapiens              | putative zinc finger protein   | 1420                 | 50         |
| 1532       | W74805           | Homo sapiens              | Human secreted protein encoded by gene 77 clone HOEAS24.                           | 493                  | 57         |
| 1533       | AF039023         | Homo sapiens              | Ran-GTP binding protein; RanBP6  | 5707                 | 99         |
| 1534       | AC007190         | Arabidopsis thaliana      | F23N19.9   | 374                  | 37         |
| 1535       | AB027564         | Homo sapiens              | DINB1  | 4482                 | 100        |
| 1536       | Y36178           | Homo sapiens              | Human secreted protein   | 377                  | 87         |
| 1537       | Y50907           | Homo sapiens              | Human fetal brain cDNA clone vb3_1 derived protein.                                | 3593                 | 99         |
| 1538       | AF017368         | Mus musculus              | faciogenital dysplasia protein 2   | 177                  | 47         |
| 1539       | AF266756         | Homo sapiens              | sphingosine kinase   | 2011                 | 99         |
| 1540       | Z48804           | Homo sapiens              | OAL  | 2238                 | 100        |
| 1541       | AF000195         | Caenorhabditis elegans    | Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1 | 379                  | 42         |
| 1542       | Y71159           | Homo sapiens              | Human phosphodiesterase interacting protein, myomegalin.                           | 9415                 | 99         |
| 1543       | X76092           | Homo sapiens              | DNA binding protein RFX3   | 3327                 | 100        |
| 1544       | AB015330         | Homo sapiens              | HRIHFB2007   | 631                  | 50         |
| 1545       | AF198487         | Homo sapiens              | transcription factor LBP-1b  | 2822                 | 100        |
| 1546       | AF016417         | Caenorhabditis elegans    | Similar to BZIP transcription factor   | 518                  | 42         |
| 1547       | X55885           | Homo sapiens              | KDEL receptor  | 1106                 | 100        |
| 1548       | AB035495         | Carassius auratus         | ubiquitin-activating enzyme E1   | 836                  | 42         |
| 1549       | AL021707         | Homo sapiens              | dJ508I15.4 (KIAA0668)  | 3688                 | 100        |
| 1550       | AJ223978         | Bacillus subtilis         | YvqK protein   | 292                  | 42         |
| 1551       | AF145615         | Drosophila melanogaster   | BcDNA.GH03377  | 822                  | 44         |
| 1552       | AL157734         | Schizosaccharomyces pombe | putative mannosyltransferase involved in N-glycosylation                           | 435                  | 37         |
| 1553       | AF079527         | Mus musculus              | IER5   | 691                  | 63         |
| 1554       | AB026291         | Rattus norvegicus         | acetoacetyl-CoA synthetase   | 1099                 | 88         |
| 1555       | Y44722           | Homo sapiens              | Human immune system molecule, ISMO-3.  | 1780                 | 99         |
| 1556       | AF116553         | Drosophila melanogaster   | antennal-specific short-chain dehydrogenase/reductase                              | 277                  | 32         |
| 1557       | Y71056           | Homo sapiens              | Human membrane transport   | 1975                 | 99         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                             | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------------------|--|----------------------|------------|
|            |                  |                                     | protein, MTRP-1.   |                      |            |
| 1558       | Y71056           | Homo sapiens                        | Human membrane transport protein, MTRP-1.  | 1975                 | 99         |
| 1559       | Y71056           | Homo sapiens                        | Human membrane transport protein, MTRP-1.  | 1894                 | 97         |
| 1560       | AF092050         | Mus musculus                        | beta-1,3-N-acetylglucosaminyltransferase   | 262                  | 44         |
| 1561       | AL109827         | Homo sapiens                        | dJ309K20.2 (acrosomal protein ACR55 (similar to rat sperm antigen 4 (SPAG4)))      | 1607                 | 97         |
| 1562       | AJ131890         | Homo sapiens                        | DNA polymerase lambda  | 3002                 | 100        |
| 1563       | AL035424         | Homo sapiens                        | dA22D12.1 (novel protein similar to Drosophila Kelch proteins)                     | 3015                 | 100        |
| 1564       | AC002400         | Homo sapiens                        | Gene product with similarity to Ubiquitin binding enzyme                           | 2790                 | 100        |
| 1565       | AC005306         | Homo sapiens                        | R27216_1   | 919                  | 82         |
| 1566       | AF000195         | Caenorhabditis elegans              | Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1 | 550                  | 45         |
| 1567       | AB033281         | Homo sapiens                        | F-box and WD-repeats protein beta-TRCP2 isoform C                                  | 2879                 | 100        |
| 1568       | D49473           | Mus musculus                        | truncated form of Sox17  | 1047                 | 78         |
| 1569       | AK025270         | Homo sapiens                        | unnamed protein product  | 210                  | 91         |
| 1570       | X75756           | Homo sapiens                        | protein kinase C mu  | 4797                 | 99         |
| 1571       | AF145713         | Homo sapiens                        | SCHIP-1  | 2388                 | 100        |
| 1572       | AE003831         | Drosophila melanogaster             | CG18445 gene product   | 180                  | 31         |
| 1573       | AF074603         | Streptomyces griseus subsp. griseus | NonF   | 205                  | 38         |
| 1574       | U28993           | Caenorhabditis elegans              | F22D3.3 gene product   | 144                  | 27         |
| 1575       | AF129507         | Homo sapiens                        | transcription factor ICBP90  | 287                  | 68         |
| 1576       | X64878           | Homo sapiens                        | oxytocin receptor  | 2002                 | 100        |
| 1577       | AF237711         | Drosophila melanogaster             | Diablo   | 421                  | 54         |
| 1578       | G00975           | Homo sapiens                        | Human secreted protein, SEQ ID NO: 5056.   | 480                  | 100        |
| 1579       | AF248744         | Cryptosporidium parvum              | thrombospondin-related adhesive protein  | 123                  | 33         |
| 1580       | AL121782         | Homo sapiens                        | dJ585I14.2 (novel protein (translation of cDNA Em:AK000219))                       | 663                  | 100        |
| 1581       | AF041853         | Homo sapiens                        | kinesin family member protein KIF3A  | 345                  | 33         |
| 1582       | AF025441         | Homo sapiens                        | Opa-interacting protein OIP5   | 1198                 | 100        |
| 1583       | AE001803         | Thermotoga maritima                 | glycerate kinase, putative   | 349                  | 34         |
| 1584       | AF252283         | Homo sapiens                        | Kelch-like 1 protein   | 3973                 | 100        |
| 1585       | AF169675         | Homo sapiens                        | leucine-rich repeat transmembrane protein FLRT1                                    | 3494                 | 99         |
| 1586       | AF118274         | Homo sapiens                        | DND-5  | 2628                 | 97         |
| 1587       | X79440           | Homo sapiens                        | NADP+-dependent malic enzyme   | 3167                 | 99         |
| 1588       | X99802           | Homo sapiens                        | ZYG homologue  | 3966                 | 99         |
| 1589       | AF169803         | Homo sapiens                        | flavohemoprotein b5+b5R  | 2563                 | 100        |
| 1590       | Y29861           | Homo sapiens                        | Human secreted protein clone cb98.4.   | 181                  | 47         |
| 1591       | Z25535           | Homo sapiens                        | nuclear pore complex protein hnup153   | 7567                 | 99         |
| 1592       | X13293           | Homo sapiens                        | B-myb protein (AA 1-700)   | 3678                 | 99         |
| 1593       | M74027           | Homo sapiens                        | mucin  | 242                  | 27         |
| 1594       | AL139314         | Schizosaccharomyces                 | hypothetical protein   | 235                  | 54         |



TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
|            |                  | pombe                     |  |                      |            |
| 1595       | W78324           | Homo sapiens              | Fragment of human secreted protein encoded by gene 81.   | 1318                 | 98         |
| 1596       | Y94906           | Homo sapiens              | Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18.                              | 2236                 | 98         |
| 1597       | AF174605         | Homo sapiens              | F-box protein Fbx25  | 1408                 | 99         |
| 1598       | AB032254         | Homo sapiens              | bromodomain adjacent to zinc finger domain 2A  | 9676                 | 98         |
| 1599       | X73114           | Homo sapiens              | slow MyBP-C  | 5568                 | 95         |
| 1600       | X82200           | Homo sapiens              | gpStat50   | 2305                 | 100        |
| 1601       | Y00876           | Homo sapiens              | Human LAPH-1 protein sequence.   | 1149                 | 98         |
| 1602       | AJ223351         | Homo sapiens              | HIRA-interacting protein 3   | 2821                 | 99         |
| 1603       | AJ222801         | Homo sapiens              | neutral sphingomyelinase   | 2268                 | 99         |
| 1604       | AJ222801         | Homo sapiens              | neutral sphingomyelinase   | 1601                 | 99         |
| 1605       | AF185576         | Mus musculus              | POZ/zinc finger transcription factor ODA-8   | 3435                 | 97         |
| 1606       | AF093744         | Homo sapiens              | unknown  | 131                  | 100        |
| 1607       | A12142           | synthetic construct       | IFN-pseudo-omega 2   | 800                  | 98         |
| 1608       | Y57949           | Homo sapiens              | Human transmembrane protein HTPN-73.   | 1868                 | 100        |
| 1609       | AF151044         | Homo sapiens              | HSPC210  | 681                  | 97         |
| 1610       | X15218           | Homo sapiens              | ski protein (AA 1 - 728)   | 3765                 | 100        |
| 1611       | Y08200           | Homo sapiens              | rab geranylgeranyl transferase   | 2976                 | 100        |
| 1612       | AF220560         | Homo sapiens              | B/K protein  | 2486                 | 99         |
| 1613       | AC004481         | Arabidopsis thaliana      | nodulin-like protein   | 371                  | 26         |
| 1614       | Y09501           | Homo sapiens              | NADH-cytochrome-b5 reductase   | 1607                 | 100        |
| 1615       | Y15521           | Homo sapiens              | start position 1   | 3150                 | 97         |
| 1616       | AJ010750         | Rattus norvegicus         | Castration induced prostatic apoptosis related protein-1, (CIPAR-1)                              | 890                  | 62         |
| 1617       | X58079           | Homo sapiens              | SI00 alpha protein   | 481                  | 100        |
| 1618       | Y66678           | Homo sapiens              | Membrane-bound protein PRO1009.  | 967                  | 100        |
| 1619       | AJ242973         | Homo sapiens              | peptide methionine sulfoxide reductase   | 929                  | 100        |
| 1620       | AF150733         | Homo sapiens              | AD-014 protein   | 288                  | 100        |
| 1621       | AJ007509         | Homo sapiens              | E1B-55kDa-associated protein   | 4646                 | 98         |
| 1622       | X64177           | Homo sapiens              | metallothionein  | 380                  | 100        |
| 1623       | AE001045         | Archaeoglobus fulgidus    | A. fulgidus predicted coding region AF0859   | 240                  | 36         |
| 1624       | AL355013         | Schizosaccharomyces pombe | mitochondrial carrier protein  | 403                  | 34         |
| 1625       | Y66746           | Homo sapiens              | Membrane-bound protein PRO1198.  | 1184                 | 100        |
| 1626       | D90053           | Sus scrofa                | destrin  | 853                  | 100        |
| 1627       | Y35954           | Homo sapiens              | Extended human secreted protein sequence, SEQ ID NO. 203.  | 756                  | 100        |
| 1628       | AL031775         | Homo sapiens              | dJ30M3.2 (novel protein)   | 470                  | 100        |
| 1629       | AF132484         | Mus musculus              | unknown  | 286                  | 68         |
| 1630       | AF017096         | Drosophila melanogaster   | similar to C. elegans R10H10.6 and S. cerevisiae YD8419.03c                                      | 493                  | 61         |
| 1631       | X03077           | Homo sapiens              | lactate dehydrogenase-A  | 1704                 | 100        |
| 1632       | AF151084         | Homo sapiens              | HSPC250  | 763                  | 100        |
| 1633       | AJ001874         | Homo sapiens              | orf  | 255                  | 97         |
| 1634       | AC012187         | Arabidopsis thaliana      | Contains weak similarity to GATA-6 DNA-binding protein gb H36135, gb Z26200 come from this gene. | 143                  | 38         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES  | DESCRIPTION   | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--|---|----------------------|------------|
| 1635       | AF026246         | Homo sapiens   | HERV-E integrase  | 411                  | 90         |
| 1636       | Y50943           | Homo sapiens   | Human adult brain cDNA clone ve8_1 derived protein.                 | 1126                 | 95         |
| 1637       | AF134593         | Homo sapiens   | L-pipecolic acid oxidase  | 2068                 | 99         |
| 1638       | AJ238247         | Mus musculus   | putative phosphatase subunit  | 1948                 | 96         |
| 1639       | Y94942           | Homo sapiens   | Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90. | 1320                 | 100        |
| 1640       | AF235030         | Homo sapiens   | BM88 antigen  | 766                  | 99         |
| 1641       | AF233288         | Drosophila melanogaster  | WDS   | 358                  | 26         |
| 1642       | M19351           | Mus musculus   | immunoglobulin heavy chain binding protein                          | 145                  | 34         |
| 1643       | Y70452           | Homo sapiens   | Human membrane channel protein-2 (MECHP-2).                         | 1352                 | 100        |
| 1644       | AF176520         | Mus musculus   | WD repeat-containing F-box protein FBW5                             | 2676                 | 88         |
| 1645       | W67816           | Homo sapiens   | Human secreted protein encoded by gene 10 clone HCEMU42.            | 1156                 | 100        |
| 1646       | X67155           | Homo sapiens   | mitotic kinase-like protein-1                                       | 4456                 | 99         |
| 1647       | M63180           | Homo sapiens   | threonyl-tRNA synthetase  | 1040                 | 61         |
| 1648       | Y87342           | Homo sapiens   | Human signal peptide containing protein HSPP-119 SEQ ID NO:119.     | 1566                 | 93         |
| 1649       | R95332           | Homo sapiens   | Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).   | 4137                 | 100        |
| 1650       | AC007136         | Homo sapiens   | Putative map kinase interacting kinase                              | 856                  | 99         |
| 1651       | AB015346         | Homo sapiens   | Eps15R  | 4464                 | 99         |
| 1652       | AL161576         | Arabidopsis thaliana   | putative protein  | 1341                 | 48         |
| 1653       | AC005313         | Arabidopsis thaliana   | putative calmodulin   | 288                  | 28         |
| 1654       | AL031428         | Homo sapiens   | dJ184J9.1 (KIAA0601 protein)  | 3526                 | 100        |
| 1655       | AL031428         | Homo sapiens   | dJ184J9.1 (KIAA0601 protein)  | 3526                 | 100        |
| 1656       | AB017910         | Dictyostelium discoideum   | mycM  | 297                  | 32         |
| 1657       | Y28919           | Homo sapiens   | Human regulatory protein HRGP-5.                                    | 2251                 | 99         |
| 1658       | AF056191         | Homo sapiens   | TPA inducible protein   | 2744                 | 98         |
| 1659       | U76846           | Arabidopsis thaliana   | ubiquitin-specific protease   | 137                  | 35         |
| 1660       | AL078627         | Schizosaccharomyces pombe  | actin-like protein; (2 actin domains)                               | 320                  | 34         |
| 1662       | X52022           | Homo sapiens   | collagen type VI, alpha 3 chain                                     | 16274                | 99         |
| 1663       | AF300648         | Homo sapiens   | guanine nucleotide binding protein beta subunit 4                   | 1811                 | 100        |
| 1664       | AF214736         | Homo sapiens   | EH domain containing protein 2                                      | 2774                 | 100        |
| 1665       | Z48613           | Saccharomyces cerevisiae   | unknown   | 138                  | 26         |
| 1666       | AF177385         | Homo sapiens   | cytochrome c oxidase assembly protein isoform 2                     | 1395                 | 99         |
| 1667       | AC007842         | Homo sapiens   | BC331191_1  | 1581                 | 47         |
| 1668       | S67513           | Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Peptide, 370 | p40   | 397                  | 43         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                   | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
|            |                  | aa                        |  |                      |            |
| 1669       | Z99753           | Schizosaccharomyces pombe | putative NOL1-NOP2-sun family nucleolar protein    | 569                  | 47         |
| 1670       | G03130           | Homo sapiens              | Human secreted protein, SEQ ID NO: 7211.           | 427                  | 97         |
| 1671       | M96625           | Gallus gallus             | cardiac muscle tensin                              | 1185                 | 54         |
| 1672       | AF174482         | Homo sapiens              | polycomb 3   | 2005                 | 99         |
| 1673       | Y51946           | Homo sapiens              | Human 18.1 homolog protein fragment.               | 233                  | 29         |
| 1674       | AF255334         | Homo sapiens              | EXP35  | 152                  | 29         |
| 1675       | Y94867           | Homo sapiens              | Human protein clone HP10563.                       | 109                  | 30         |
| 1676       | Y25712           | Homo sapiens              | Human secreted protein encoded from gene 2.        | 3043                 | 99         |
| 1677       | Y25712           | Homo sapiens              | Human secreted protein encoded from gene 2.        | 1580                 | 91         |
| 1678       | AF163151         | Homo sapiens              | dentin sialophosphoprotein precursor               | 170                  | 17         |
| 1679       | AF163151         | Homo sapiens              | dentin sialophosphoprotein precursor               | 170                  | 17         |
| 1680       | AK024453         | Homo sapiens              | FLJ00045 protein                                   | 1349                 | 100        |
| 1681       | AF019236         | Dictyostellium discoideum | TipD   | 613                  | 34         |
| 1682       | AJ243459         | Leishmania major          | proteophosphoglycan                                | 153                  | 26         |
| 1683       | Z69369           | Schizosaccharomyces pombe | putative GTP-binding protein                       | 560                  | 46         |
| 1684       | X94910           | Homo sapiens              | ERp28  | 1334                 | 100        |
| 1685       | AF286475         | Takifugu rubripes         | retinitis pigmentosa GTPase regulator-like protein | 196                  | 19         |
| 1686       | AF191298         | Homo sapiens              | vacuolar sorting protein 35                        | 4087                 | 100        |
| 1687       | AJ275986         | Homo sapiens              | transcription factor                               | 2958                 | 100        |
| 1688       | AJ275986         | Homo sapiens              | transcription factor                               | 1886                 | 88         |
| 1689       | X07311           | Drosophila melanogaster   | heat shock protein                                 | 138                  | 43         |
| 1690       | AF240463         | Rattus norvegicus         | LIS1-interacting protein NUDE1                     | 1383                 | 83         |
| 1691       | AJ272078         | Homo sapiens              | APOBEC-1 stimulating protein                       | 1256                 | 68         |
| 1692       | AJ272079         | Homo sapiens              | APOBEC-1 stimulating protein                       | 1336                 | 60         |
| 1693       | AF177942         | Xenopus laevis            | katanin p60  | 1664                 | 66         |
| 1694       | AF263539         | Homo sapiens              | arginine N-methyltransferase                       | 1774                 | 100        |
| 1695       | AF222689         | Homo sapiens              | protein arginine N-methyltransferase 1-variant 2   | 1182                 | 81         |
| 1696       | AK000193         | Homo sapiens              | unnamed protein product                            | 1060                 | 100        |
| 1697       | AB041035         | Homo sapiens              | kidney superoxide-producing NADPH oxidase          | 3122                 | 100        |
| 1698       | AB041035         | Homo sapiens              | kidney superoxide-producing NADPH oxidase          | 2181                 | 100        |
| 1699       | AF025772         | Homo sapiens              | C2H2 zinc finger protein                           | 488                  | 54         |
| 1700       | Y44676           | Homo sapiens              | Human ARF-Related Protein-1 (HARP-1).              | 938                  | 97         |
| 1701       | AK022407         | Homo sapiens              | unnamed protein product                            | 315                  | 98         |
| 1702       | AB024574         | Homo sapiens              | GTP-binding like protein 2                         | 1172                 | 100        |
| 1703       | AF055078         | Homo sapiens              | zinc finger protein 42                             | 421                  | 52         |
| 1704       | AF198092         | Mus musculus              | RP42   | 1057                 | 77         |
| 1705       | AE003573         | Drosophila melanogaster   | CG12474 gene product                               | 161                  | 33         |
| 1706       | AB036345         | Drosophila melanogaster   | aquaporin  | 164                  | 24         |
| 1707       | Y55927           | Homo sapiens              | Human STK2 protein.                                | 2146                 | 100        |
| 1708       | U27121           | Danio rerio               | G12  | 212                  | 47         |
| 1709       | AL391710         | Arabidopsis               | putative protein                                   | 505                  | 50         |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|------------------------|--|----------------------|------------|
|            |                  | thaliana               |  |                      |            |
| 1710       | B01311           | Homo sapiens           | Human PRO241 polypeptide.  | 1649                 | 97         |
| 1711       | U40750           | Mus musculus           | formin binding protein 30  | 4561                 | 85         |
| 1712       | AJ011118         | Mus musculus           | skeletal muscle and cardiac protein  | 1490                 | 89         |
| 1713       | AF255303         | Homo sapiens           | membrane-associated nucleic acid binding protein                                       | 4416                 | 99         |
| 1714       | AF255303         | Homo sapiens           | membrane-associated nucleic acid binding protein                                       | 2960                 | 100        |
| 1715       | U08227           | Rattus norvegicus      | Ras-related protein  | 511                  | 51         |
| 1716       | AF168795         | Rattus norvegicus      | schlafen-4   | 1129                 | 44         |
| 1717       | AF196304         | Homo sapiens           | SUMO-1-specific protease   | 5804                 | 99         |
| 1718       | AL355737         | Homo sapiens           | HMG20A   | 1782                 | 100        |
| 1719       | AB029333         | Halocynthia roretzi    | HrPET-1  | 1069                 | 46         |
| 1720       | AF071317         | Mus musculus           | COP9 complex subunit 7b  | 1297                 | 97         |
| 1721       | AJ272215         | Homo sapiens           | HEYL protein   | 1681                 | 99         |
| 1722       | G01982           | Homo sapiens           | Human secreted protein, SEQ ID NO: 6063.   | 718                  | 100        |
| 1723       | AL032643         | Caenorhabditis elegans | similar to Uncharacterized protein family UPF0034,                                     | 825                  | 41         |
| 1724       | G01972           | Homo sapiens           | Human secreted protein, SEQ ID NO: 6053.   | 586                  | 92         |
| 1725       | Y94441           | Homo sapiens           | Human Adipose Specific Protein 1.  | 1231                 | 100        |
| 1726       | AF255443         | Homo sapiens           | CGI-201 protein  | 4397                 | 99         |
| 1727       | AF183426         | Homo sapiens           | HT004 protein  | 1810                 | 99         |
| 1728       | D10884           | Bos taurus             | neurocalcin  | 1002                 | 99         |
| 1729       | Z18529           | Gallus gallus          | tensin   | 1411                 | 84         |
| 1730       | Z73423           | Caenorhabditis elegans | cDNA EST EMBL:Z14908 comes from this gene-cDNA EST this gene                           | 233                  | 41         |
| 1732       | AF090891         | Homo sapiens           | PRO0105  | 470                  | 30         |
| 1733       | AJ277724         | Homo sapiens           | histone deacetylase 8  | 2015                 | 100        |
| 1734       | G04050           | Homo sapiens           | Human secreted protein, SEQ ID NO: 8131.   | 503                  | 95         |
| 1735       | D45913           | Mus musculus           | leucine-rich-repeat protein  | 3531                 | 94         |
| 1736       | AF096709         | Drosophila virilis     | failed axon connections protein  | 276                  | 32         |
| 1737       | AF195120         | Homo sapiens           | dynactin p62 subunit   | 2417                 | 99         |
| 1738       | L15314           | Caenorhabditis elegans | contains similarity to Pfam family PF01772 N=1   | 206                  | 37         |
| 1739       | X54618           | Listeria monocytogenes | phosphatidylinositol specific phospholipase C  | 134                  | 27         |
| 1740       | AL031658         | Homo sapiens           | dJ310013.4 (novel protein similar to predicted C. elegans an C. intestinalis proteins) | 123                  | 31         |
| 1741       | Y35924           | Homo sapiens           | Extended human secreted protein sequence, SEQ ID NO. 173.                              | 1013                 | 99         |
| 1742       | AC013354         | Arabidopsis thaliana   | F15H18.15  | 202                  | 32         |
| 1743       | W75771           | Homo sapiens           | Human GTP binding protein APD08.   | 1932                 | 59         |
| 1744       | W75771           | Homo sapiens           | Human GTP binding protein APD08.   | 1854                 | 61         |
| 1745       | AF221098         | Homo sapiens           | Ral guanine nucleotide exchange factor RalGPS1A  | 1224                 | 70         |
| 1746       | Y99372           | Homo sapiens           | Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.                              | 1332                 | 99         |
| 1747       | Y94294           | Homo sapiens           | Human coenzyme A-utilising   | 842                  | 100        |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES                              | DESCRIPTION  | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|--|----------------------|------------|
| 1748       | AK024436         | Homo sapiens                         | enzyme CoAEN-2.  |                      |            |
| 1749       | AE000877         | Methanobacterium thermoautotrophicum | FLJ00026 protein conserved protein   | 1619<br>231          | 100<br>36  |
| 1750       | AF101361         | Drosophila melanogaster              | Abnormal X segregation   | 193                  | 33         |
| 1751       | Y15067           | Homo sapiens                         | ZNF232   | 889                  | 100        |
| 1752       | AF251038         | Homo sapiens                         | GAP-like protein   | 822                  | 100        |
| 1753       | AC003093         | Homo sapiens                         | OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)                            | 352                  | 57         |
| 1754       | X69089           | Homo sapiens                         | 165kD protein  | 5703                 | 99         |
| 1755       | AL049795         | Homo sapiens                         | dJ622L5.3 (novel protein)  | 1039                 | 100        |
| 1756       | AL031393         | Homo sapiens                         | dJ733D15.1 (Zinc-finger protein)   | 2765                 | 100        |
| 1757       | AB040672         | Homo sapiens                         | UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase                                    | 2020                 | 99         |
| 1758       | AL022238         | Homo sapiens                         | dJ1042K10.4 (novel protein)  | 776                  | 43         |
| 1759       | AF117653         | Homo sapiens                         | double homeobox protein  | 375                  | 54         |
| 1760       | Y12065           | Homo sapiens                         | hNop56   | 2959                 | 99         |
| 1761       | AL049712         | Homo sapiens                         | dJ686C3.2 (nucleolar protein hNop56)   | 2595                 | 99         |
| 1762       | AC002394         | Homo sapiens                         | Gene product with similarity to dynein beta subunit  | 1542                 | 51         |
| 1763       | AF169017         | Homo sapiens                         | formiminotransferase cyclodeaminase  | 877                  | 100        |
| 1764       | U91541           | Homo sapiens                         | human formiminotransferase cyclodeaminase (ftcd)protein, carboxy-terminal end                | 596                  | 100        |
| 1765       | AB013365         | Bacillus halodurans                  | YlqF   | 350                  | 34         |
| 1766       | Y38421           | Homo sapiens                         | Human secreted protein encoded by gene No. 36.   | 145                  | 71         |
| 1767       | AC009176         | Arabidopsis thaliana                 | putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I | 216                  | 27         |
| 1768       | AK000647         | Homo sapiens                         | unnamed protein product  | 737                  | 99         |
| 1769       | AJ238982         | Homo sapiens                         | VNN3 protein   | 2665                 | 99         |
| 1770       | U73522           | Homo sapiens                         | AMSH   | 1214                 | 56         |
| 1771       | U89435           | Mus musculus                         | unknown  | 829                  | 86         |
| 1772       | S70011           | Rattus sp.                           | tricarboxylate carrier   | 1604                 | 95         |
| 1773       | AL035086         | Homo sapiens                         | dJ44A20.2 (novel protein)  | 2036                 | 100        |
| 1774       | Y99426           | Homo sapiens                         | Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.                                    | 1057                 | 99         |
| 1775       | AF110330         | Homo sapiens                         | glutaminase  | 3146                 | 100        |
| 1776       | AJ269529         | Homo sapiens                         | glycerol 3-phosphate permease  | 2787                 | 100        |
| 1777       | Z81579           | Caenorhabditis elegans               | cDNA EST yk76f1.5 comes from this gene   | 232                  | 31         |
| 1778       | AY007239         | Homo sapiens                         | monooxygenase X  | 1875                 | 99         |
| 1779       | AL109608         | Schizosaccharomyces pombe            | oxysterol-binding protein family   | 644                  | 38         |
| 1780       | AF254260         | Homo sapiens                         | tuftelin 1   | 1729                 | 100        |
| 1781       | L07924           | Mus musculus                         | guanine nucleotide dissociation stimulator   | 247                  | 50         |
| 1782       | AF295773         | Homo sapiens                         | ral guanine nucleotide dissociation stimulator   | 142                  | 49         |
| 1783       | AK024475         | Homo sapiens                         | FLJ00068 protein   | 4333                 | 100        |
| 1784       | AK024475         | Homo sapiens                         | FLJ00068 protein   | 3996                 | 93         |
| 1785       | G03933           | Homo sapiens                         | Human secreted protein, SEQ ID NO: 8014.   | 570                  | 100        |
| 1786       | S82637           | Homo sapiens                         | Ig lambda-like gene/beta-  | 247                  | 100        |

TABLE 2

| SEQ<br>ID<br>NO: | ACCESSION<br>NUMBER | SPECIES | DESCRIPTION                   | SMITH-<br>WATERMAN<br>SCORE | %<br>IDENTITY |
|------------------|---------------------|---------|-------------------------------|-----------------------------|---------------|
|                  |                     |         | glucuronidase exon 11 homolog |                             |               |

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TABLE 3

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*  |
|------------|---------------|---|---|
| 2          | BL00240       | Receptor tyrosine kinase class III proteins.          | BL00240B 24.70 8.250e-12 157-181  |
| 3          | PR00109       | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE            | PR00109D 17.04 8.085e-13 358-381  |
| 4          | BL00028       | Zinc finger, C2H2 type, domain proteins.              | BL00028 16.07 9.400e-10 1129-1146 BL00028 16.07 1.257e-09 820-837   |
| 5          | BL00023       | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390   |
| 6          | BL00023       | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390   |
| 7          | BL00023       | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390   |
| 8          | BL00023       | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390   |
| 9          | BL01160       | Kinesin light chain repeat proteins.                  | BL01160B 19.54 5.119e-09 863-917  |
| 10         | PR00464       | E-CLASS P450 GROUP II SIGNATURE                       | PR00464D 17.40 6.182e-12 294-312 PR00464G 12.41 4.231e-11 377-393   |
| 11         | PR00734       | GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE                 | PR00734I 11.46 4.296e-09 502-520  |
| 12         | PF00023       | Ank repeat proteins.                                  | PF00023B 14.20 6.500e-10 89-99 PF00023B 14.20 2.636e-09 56-66   |
| 14         | DM00031       | IMMUNOGLOBULIN V REGION.                              | DM00031B 15.41 3.848e-09 79-113   |
| 15         | PR00208       | GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE        | PR00208A 12.59 9.868e-10 517-535 PR00208A 12.59 2.233e-09 520-538   |
| 17         | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                      | PD00066 13.92 8.200e-14 282-295 PD00066 13.92 9.400e-14 477-490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e-13 254-267 PD00066 13.92 1.429e-12 393-406 PD00066 13.92 6.571e-12 421-434 |
| 18         | BL00845       | CAP-Gly domain proteins.                              | BL00845 16.43 2.200e-25 55-80   |
| 20         | BL00487       | IMP dehydrogenase / GMP reductase proteins.           | BL00487E 16.12 5.737e-26 154-199 BL00487F 18.79 8.984e-22 235-276 BL00487G 26.82 4.082e-12 287-329  |
| 21         | BL00487       | IMP dehydrogenase / GMP reductase proteins.           | BL00487E 16.12 5.737e-26 154-199 BL00487F 18.79 8.984e-22 235-276 BL00487G 26.82 4.082e-12 348-390  |
| 22         | BL00107       | Protein kinases ATP-binding region proteins.          | BL00107A 18.39 3.250e-26 302-333  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
| 23         | BL00107       | Protein kinases ATP-binding region proteins.               | BL00107A 18.39 3.250e-26 302-333  |
| 25         | BL00115       | Eukaryotic RNA polymerase II heptapeptide repeat proteins. | BL00115T 8.45 7.273e-29 1208-1242 BL00115Q 18.08 2.776e-21 953-983 BL00115Y 11.86 8.000e-17 1604-1650 BL00115M 19.19 8.130e-16 731-774 BL00115H 14.34 9.392e-16 463-496 BL00115A 15.44 7.414e-15 43-82 BL00115R 6.50 6.128e-14 983-1010 BL00115J 16.71 9.289e-14 591-617 BL00115I 8.33 4.336e-13 535-590 BL00115L 12.25 5.939e-13 662-694 BL00115G 11.65 6.011e-13 435-463 BL00115K 15.03 3.417e-10 617-659 BL00115O 16.76 5.805e-10 863-913 BL00115P 11.54 7.538e-10 913-953 BL00115S 18.24 7.968e-10 1010-1052 BL00115U 10.34 4.475e-09 1242-1265 |
| 26         | BL00420       | Speract receptor repeat proteins domain proteins.          | BL00420A 20.42 4.109e-11 81-110 BL00420A 20.42 8.820e-10 84-113   |
| 27         | BL00050       | Ribosomal protein L23 proteins.                            | BL00050A 23.71 9.250e-27 94-127 BL00050B 14.81 8.125e-12 133-147  |
| 28         | PR00925       | NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE      | PR00925B 3.73 3.089e-10 41-54   |
| 29         | PF00756       | Putative esterase.   | PF00756C 14.12 1.108e-09 486-516  |
| 32         | BL00557       | FMN-dependent alpha-hydroxy acid dehydrogenases proteins.  | BL00557D 17.76 5.065e-37 274-316 BL00557A 35.08 8.909e-29 24-73 BL00557C 15.59 1.000e-28 227-257 BL00557B 21.27 8.898e-22 130-169   |
| 34         | PR00629       | SHC PHOSPHOTYROSINE INTERACTION DOMAIN SIGNATURE           | PR00629E 9.90 5.886e-35 299-328 PR00629F 10.95 8.364e-32 334-361 PR00629B 13.66 3.786e-27 224-247 PR00629A 13.45 8.364e-21 206-222 PR00629C 3.80 4.000e-12 249-261 PR00629D 12.45 3.739e-11 276-286   |
| 35         | PD01270       | RECEPTOR FC IMMUNOGLOBULIN AFFIN.                          | PD01270A 17.22 1.000e-40 39-79 PD01270B 22.18 2.875e-38 94-131 PD01270D 24.66 3.700e-34 171-207 PD01270C 19.54 3.455e-30 137-166  |
| 36         | PD01270       | RECEPTOR FC IMMUNOGLOBULIN AFFIN.                          | PD01270A 17.22 1.000e-40 39-79 PD01270B 22.18 2.875e-38 94-131  |



| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*   |
|------------|---------------|---|--|
|            |               |   | PD01270D 24.66 3.700e-34 171-207 PD01270C 19.54 3.455e-30 137-166  |
| 37         | BL00412       | Neuromodulin (GAP-43) proteins.                           | BL00412C 10.28 9.241e-10 264-298   |
| 38         | BL00412       | Neuromodulin (GAP-43) proteins.                           | BL00412C 10.28 9.241e-10 264-298   |
| 39         | BL00412       | Neuromodulin (GAP-43) proteins.                           | BL00412C 10.28 9.241e-10 264-298   |
| 40         | PR00380       | KINESIN HEAVY CHAIN SIGNATURE                             | PR00380B 12.64 7.366e-14 342-360 PR00380C 13.18 6.927e-13 375-394 PR00380D 9.93 2.180e-12 429-451 PR00380A 14.18 5.154e-12 143-165   |
| 44         | BL00345       | Ets-domain proteins.                                      | BL00345B 21.28 1.000e-40 239-290 BL00345A 13.96 2.452e-14 204-223  |
| 45         | BL00345       | Ets-domain proteins.                                      | BL00345B 21.28 1.000e-40 215-266 BL00345A 13.96 2.452e-14 180-199  |
| 46         | DM01551       | kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.                    | DM01551A 15.63 3.538e-26 172-202 DM01551C 14.62 3.571e-17 232-252 DM01551B 8.84 4.750e-11 214-226  |
| 47         | PR00876       | NEMATODE METALLOTHIONEIN SIGNATURE                        | PR00876B 7.66 9.328e-11 246-260  |
| 48         | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.         | PD01066 19.43 4.231e-33 6-45   |
| 50         | BL00972       | Ubiquitin carboxyl-terminal hydrolases family 2 proteins. | BL00972D 22.55 7.750e-19 994-1019 BL00972A 11.93 7.120e-18 216-234 BL00972E 20.72 9.471e-14 1020-1042 BL00972C 16.48 7.000e-13 360-375 BL00972B 9.45 8.269e-10 302-312                         |
| 51         | BL00972       | Ubiquitin carboxyl-terminal hydrolases family 2 proteins. | BL00972D 22.55 7.750e-19 990-1015 BL00972A 11.93 7.120e-18 216-234 BL00972E 20.72 9.471e-14 1016-1038 BL00972C 16.48 7.000e-13 360-375 BL00972B 9.45 8.269e-10 302-312                         |
| 52         | BL01115       | GTP-binding nuclear protein ran proteins.                 | BL01115A 10.22 3.063e-14 10-54   |
| 53         | PR00988       | URIDINE KINASE SIGNATURE                                  | PR00988A 6.39 8.500e-17 20-38 PR00988F 12.23 7.828e-15 196-210 PR00988C 13.64 6.108e-14 104-120 PR00988E 8.27 3.872e-11 174-186 PR00988D 5.95 6.878e-10 160-171 PR00988B 11.60 2.915e-09 57-69 |
| 55         | PR00762       | CHLORIDE CHANNEL SIGNATURE                                | PR00762C 9.29 4.682e-21 294-314 PR00762D 11.29 4.103e-19 509-530 PR00762A 14.22 9.333e-18 199-217  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               |  | PR00762F 15.12 3.100e-16 563-583 PR00762B 12.12 6.063e-16 230-250 PR00762E 12.07 2.286e-15 545-562 PR00762G 14.13 6.276e-13 601-616 |
| 56         | BL00216       | Sugar transport proteins.                              | BL00216B 27.64 8.800e-10 153-203  |
| 58         | PF00791       | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 2.049e-10 1080-1135  |
| 59         | PF00791       | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 2.049e-10 1062-1117  |
| 61         | PD01929       | KINASE TYPE RESISTANCE ANTIBIOTIC TRANSFERASE AM.      | PD01929E 10.76 9.018e-09 206-221  |
| 68         | PR00360       | C2 DOMAIN SIGNATURE                                    | PR00360A 14.59 7.395e-09 680-693  |
| 69         | PR00360       | C2 DOMAIN SIGNATURE                                    | PR00360A 14.59 7.395e-09 670-683  |
| 70         | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.          | PF00651 15.00 8.714e-10 51-64   |
| 72         | DM00179       | w KINASE ALPHA ADHESION T-CELL.                        | DM00179 13.97 5.304e-09 108-118   |
| 73         | BL00239       | Receptor tyrosine kinase class II proteins.            | BL00239B 25.15 7.075e-12 118-166  |
| 74         | BL00790       | Receptor tyrosine kinase class V proteins.             | BL00790N 13.25 6.116e-10 93-120   |
| 76         | DM00471       | 0 PROKARYOTIC DNA TOPOISOMERASE I.                     | DM00471A 11.73 9.357e-13 53-66 DM00471B 8.45 4.857e-12 70-81  |
| 80         | PD02876       | DECARBOXYLASE PHOSPHATIDYLSERINE.                      | PD02876C 8.80 2.723e-13 223-236 PD02876D 12.13 2.588e-12 334-351  |
| 81         | PD02876       | DECARBOXYLASE PHOSPHATIDYLSERINE.                      | PD02876C 8.80 2.723e-13 282-295 PD02876D 12.13 2.588e-12 393-410  |
| 83         | BL00708       | Prolyl endopeptidase family serine proteins.           | BL00708B 24.91 7.197e-12 570-601  |
| 84         | PR00014       | FIBRONECTIN TYPE III REPEAT SIGNATURE                  | PR00014C 15.44 8.043e-09 985-1004   |
| 86         | PR00678       | PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE            | PR00678H 9.13 1.379e-09 246-269   |
| 89         | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                  | PR00320C 13.01 8.200e-09 264-279 PR00320B 12.19 8.650e-09 264-279   |
| 93         | BL00455       | Putative AMP-binding domain proteins.                  | BL00455 13.31 2.588e-14 316-332   |
| 95         | BL00107       | Protein kinases ATP-binding region proteins.           | BL00107A 18.39 4.000e-10 123-154  |
| 96         | BL00107       | Protein kinases ATP-binding region proteins.           | BL00107A 18.39 4.000e-10 212-243  |
| 97         | PR00081       | GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE         | PR00081B 10.38 6.318e-13 134-146 PR00081A 10.53 2.500e-12 54-72   |
| 98         | PR00380       | KINESIN HEAVY CHAIN SIGNATURE                          | PR00380A 14.18 5.500e-24 401-423 PR00380D 9.93 7.188e-20 613-635 PR00380B 12.64 7.517e-16 529-547 PR00380C 13.18 2.756e-13 560-579  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
| 102        | PR00300       | ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE | PR00300A 9.56 7.545e-14 289-308   |
| 104        | BL00479       | Phorbol esters / diacylglycerol binding domain proteins. | BL00479B 12.57 6.786e-18 298-314 BL00479A 19.86 4.913e-16 155-178 BL00479A 19.86 4.300e-13 272-295 BL00479B 12.57 6.294e-12 181-197 |
| 106        | BL01019       | ADP-ribosylation factors family proteins.                | BL01019A 13.20 8.013e-12 43-83  |
| 107        | DM01970       | 0 kw ZK632.12 YDR313C ENDOSOMAL III.                     | DM01970B 8.60 5.000e-16 403-416   |
| 108        | BL00191       | Cytochrome b5 family, heme-binding domain proteins.      | BL00191K 17.38 4.951e-27 238-282 BL00191J 11.37 6.447e-17 182-204   |
| 109        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.        | PD01066 19.43 4.938e-37 8-47  |
| 110        | BL01138       | Scorpion short toxins proteins.                          | BL01138A 10.96 8.297e-10 38-50  |
| 113        | BL00107       | Protein kinases ATP-binding region proteins.             | BL00107A 18.39 5.800e-23 156-187 BL00107B 13.31 9.100e-14 225-241   |
| 117        | BL00214       | Cytosolic fatty-acid binding proteins.                   | BL00214B 26.51 1.000e-17 46-91 BL00214A 21.17 7.052e-11 5-31  |
| 118        | BL00107       | Protein kinases ATP-binding region proteins.             | BL00107A 18.39 8.560e-13 36-67  |
| 119        | PR00529       | GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE       | PR00529C 11.03 7.506e-10 158-177  |
| 120        | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                    | PR00320C 13.01 9.400e-09 80-95  |
| 121        | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                    | PR00320C 13.01 9.400e-09 80-95  |
| 127        | BL00215       | Mitochondrial energy transfer proteins.                  | BL00215A 15.82 7.158e-13 216-241  |
| 128        | BL01032       | Protein phosphatase 2C proteins.                         | BL01032C 6.14 3.195e-12 147-157 BL01032H 11.25 5.680e-11 318-331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902e-09 379-389   |
| 129        | BL01310       | ATP1G1 / PLM / MAT8 family proteins.                     | BL01310 14.74 6.694e-26 28-64   |
| 130        | PR00990       | RIBOKINASE SIGNATURE                                     | PR00990B 12.32 9.534e-15 47-67 PR00990A 16.23 5.500e-14 20-42 PR00990C 12.62 2.412e-09 119-133                                      |
| 133        | BL00880       | Acyl-CoA-binding protein.                                | BL00880 17.52 5.575e-26 72-122  |
| 134        | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.            | BL00030A 14.39 9.308e-14 18-37  |
| 135        | PR00215       | NEUROMODULIN SIGNATURE                                   | PR00215C 13.98 6.779e-10 475-496  |
| 136        | BL01310       | ATP1G1 / PLM / MAT8 family proteins.                     | BL01310 14.74 2.432e-29 71-107  |
| 140        | BL00028       | Zinc finger, C2H2 type, domain proteins.                 | BL00028 16.07 7.882e-14 214-231 BL00028 16.07 9.471e-14 102-119 BL00028 16.07 2.800e-13 18-35                                       |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*  |
|------------|---------------|---|---|
|            |               |   | BL00028 16.07 5.500e-13 74-91 BL00028 16.07 9.100e-13 186-203 BL00028 16.07 8.043e-12 46-63 BL00028 16.07 8.435e-12 130-147 BL00028 16.07 9.217e-12 270-287 BL00028 16.07 6.192e-11 242-259 BL00028 16.07 4.000e-10 158-175 |
| 141        | BL00501       | Signal peptidases I serine proteins.                    | BL00501D 16.69 9.538e-14 113-133 BL00501C 9.61 8.688e-10 89-101   |
| 143        | BL01020       | SARI family proteins.                                   | BL01020C 15.35 7.722e-20 79-130   |
| 146        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.       | PD01066 19.43 6.400e-25 335-374   |
| 149        | BL00126       | 3'5'-cyclic nucleotide phosphodiesterases proteins.     | BL00126C 22.07 1.450e-25 509-550 BL00126E 35.22 3.951e-16 654-709 BL00126D 25.50 1.360e-15 565-604 BL00126B 15.20 8.200e-11 483-495 BL00126A 27.56 8.269e-11 442-479  |
| 151        | BL00632       | Ribosomal protein S4 proteins.                          | BL00632 23.79 5.271e-20 106-149   |
| 154        | BL00559       | Eukaryotic molybdopterin oxidoreductases proteins.      | BL00559I 13.63 5.304e-19 29-58 BL00559K 13.17 2.957e-18 172-199 BL00559J 19.63 8.385e-13 99-151 BL00559L 13.60 5.814e-12 241-259  |
| 155        | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                  | PR00449A 13.20 1.692e-13 13-35  |
| 157        | BL00406       | Actins proteins.  | BL00406D 12.58 2.547e-18 275-330 BL00406A 9.95 5.776e-16 15-50 BL00406B 5.47 7.429e-12 69-124 BL00406C 6.75 9.682e-12 128-183   |
| 160        | BL00132       | Zinc carboxypeptidases, zinc-binding region 1 proteins. | BL00132A 26.07 7.000e-14 22-63 BL00132C 21.35 3.466e-12 104-145   |
| 165        | PR00109       | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE              | PR00109B 12.27 9.043e-13 139-158  |
| 168        | BL00362       | Ribosomal protein S15 proteins.                         | BL00362 24.67 9.700e-15 129-172   |
| 169        | BL00039       | DEAD-box subfamily ATP-dependent helicases proteins.    | BL00039D 21.67 1.000e-35 640-686 BL00039A 18.44 1.964e-13 212-251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e-12 465-489   |
| 175        | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                  | PR00449A 13.20 3.721e-12 14-36  |
| 178        | BL01310       | ATP1G1 / PLM / MAT8 family proteins.                    | BL01310 14.74 2.432e-29 133-169   |
| 179        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-                  | PD01066 19.43 9.455e-36 6-45  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | BINDING NU.  |  |
| 180        | PR00007       | COMPLEMENT C1Q DOMAIN SIGNATURE                                | PR00007B 14.16 7.429e-20 160-180 PR00007A 19.33 4.938e-19 133-160 PR00007C 15.60 1.225e-15 206-228 PR00007D 9.64 6.885e-11 238-249   |
| 181        | BL00027       | 'Homeobox' domain proteins.                                    | BL00027 25.43 9.526e-24 280-323  |
| 182        | BL00027       | 'Homeobox' domain proteins.                                    | BL00027 26.43 9.526e-24 263-306  |
| 183        | BL00027       | 'Homeobox' domain proteins.                                    | BL00027 26.43 9.526e-24 280-323  |
| 184        | BL00027       | 'Homeobox' domain proteins.                                    | BL00027 26.43 9.526e-24 263-306  |
| 188        | PR00929       | AT-HOOK-LIKE DOMAIN SIGNATURE                                  | PR00929C 5.26 3.328e-09 460-471  |
| 189        | PR00929       | AT-HOOK-LIKE DOMAIN SIGNATURE                                  | PR00929C 5.26 3.328e-09 440-451  |
| 190        | BL00383       | Tyrosine specific protein phosphatases proteins.               | BL00383F 15.51 7.188e-17 666-682 BL00383A 13.34 8.714e-17 162-177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e-14 628-639 BL00383F 15.51 1.720e-13 371-387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e-13 295-308 BL00383B 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e-09 509-520 BL00383D 11.92 4.000e-09 589-602 BL00383B 7.61 8.000e-09 479-488 |
| 191        | PR00450       | RECOVERIN FAMILY SIGNATURE                                     | PR00450C 12.22 7.911e-15 83-105 PR00450C 12.22 6.286e-13 47-69   |
| 193        | PF00564       | Octicosapeptide repeat proteins.                               | PF00564B 24.74 6.164e-16 227-278   |
| 194        | PR00503       | BROMODOMAIN SIGNATURE  | PR00503D 20.81 9.156e-15 204-224 PR00503B 9.96 9.571e-13 170-187   |
| 195        | BL00901       | Cysteine synthase/cystathionine beta-synthase P-phosphate att. | BL00901C 20.63 3.429e-18 67-117  |
| 197        | BL00636       | Nt-dnaJ domain proteins.                                       | BL00636A 8.07 6.211e-17 40-57 BL00636B 15.11 2.000e-13 67-88   |
| 198        | PR00690       | ADHESIN FAMILY SIGNATURE                                       | PR00690A 10.85 9.866e-09 463-482   |
| 199        | BL01131       | Ribosomal RNA adenine dimethylases proteins.                   | BL01131A 26.62 2.343e-12 84-130  |
| 201        | PR00910       | LUTEOVIRUS ORF6 PROTEIN SIGNATURE                              | PR00910A 2.51 8.352e-12 509-522  |
| 203        | DM00215       | PROLINE-RICH PROTEIN 3.  | DM00215 19.43 2.286e-10 39-72  |
| 206        | PR00261       | LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE               | PR00261A 11.02 4.462e-19 65-87 PR00261C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e-18 65-87 PR00261B 14.12 4.000e-18 143-165 PR00261A 11.02   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               |  | 4.833e-18 143-165<br>PR00261D 12.47 7.500e-18 143-165 PR00261B<br>14.12 5.065e-16 65-87<br>PR00261C 11.37 8.967e-16 143-165 PR00261F<br>11.57 4.938e-13 143-165 PR00261E 11.08<br>7.188e-13 65-87<br>PR00261F 11.57 7.188e-13 65-87 PR00261B<br>11.08 1.643e-11 143-165 |
| 209        | PF00791       | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 6.143e-13 118-173 PF00791C<br>20.98 7.680e-10 132-171  |
| 211        | PR00007       | COMPLEMENT C1Q DOMAIN SIGNATURE                        | PR00007A 19.33 5.781e-19 131-158 PR00007B<br>14.16 4.115e-18 158-178 PR00007C 15.60<br>1.675e-15 201-223<br>PR00007D 9.64 7.231e-11 233-244   |
| 212        | BL00183       | Ubiquitin-conjugating enzymes proteins.                | BL00183 28.97 1.545e-30 43-91   |
| 213        | BL00183       | Ubiquitin-conjugating enzymes proteins.                | BL00183 28.97 1.545e-30 43-91   |
| 215        | BL00039       | DEAD-box subfamily ATP-dependent helicases proteins.   | BL00039D 21.67 1.900e-29 568-614 BL00039A<br>18.44 1.871e-23 21-60<br>BL00039C 15.63 1.720e-11 364-388 BL00039B<br>19.19 4.064e-11 277-303  |
| 217        | BL00100       | Chloramphenicol acetyltransferase proteins.            | BL00100D 17.22 8.484e-09 68-106   |
| 219        | PR00213       | MYELIN PO PROTEIN SIGNATURE                            | PR00213C 15.94 3.969e-11 199-227  |
| 222        | BL00678       | Trp-Asp (WD) repeat proteins proteins.                 | BL00678 9.67 1.947e-09 144-155  |
| 224        | PR00875       | MOLLUSC METALLOTHIONEIN SIGNATURE                      | PR00875A 5.83 1.000e-09 901-913   |
| 225        | BL00636       | Nt-dnaJ domain proteins.                               | BL00636B 15.11 8.200e-19 18-39  |
| 226        | BL00636       | Nt-dnaJ domain proteins.                               | BL00636A 8.07 1.000e-21 21-38 BL00636B<br>15.11 8.200e-19 45-66   |
| 229        | PR00301       | 70 KD HEAT SHOCK PROTEIN SIGNATURE                     | PR00301F 13.98 7.563e-13 329-346 PR00301G<br>13.78 4.300e-12 361-382  |
| 230        | BL00460       | Glutathione peroxidases selenocysteine proteins.       | BL00460A 28.67 8.773e-20 35-70 BL00460B<br>9.73 7.429e-16 78-96<br>BL00460C 14.35 2.831e-12 111-134 BL00460D<br>16.89 8.773e-11 140-160   |
| 231        | PR00647       | SENR ORPHAN RECEPTOR SIGNATURE                         | PR00647B 10.19 8.522e-09 273-287  |
| 233        | BL00292       | Cyclins proteins.                                      | BL00292B 20.31 7.429e-27 244-275 BL00292A<br>22.87 7.750e-27 201-235  |
| 234        | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                 | PR00449A 13.20 6.308e-13 7-29 PR00449C  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               |  | 17.27 4.462e-11 47-70<br>PR00449D 10.79 7.120e-11 109-123  |
| 235        | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                                  | PR00019B 11.36 7.300e-10 251-265 PR00019B 11.36 5.320e-09 119-133 PR00019B 11.36 1.000e-08 229-243   |
| 236        | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                                  | PR00019B 11.36 7.300e-10 245-259 PR00019B 11.36 5.320e-09 113-127 PR00019B 11.36 1.000e-08 223-237   |
| 237        | PD00289       | PROTEIN SH3 DOMAIN REPEAT PRESNA.                              | PD00289 9.97 8.448e-09 67-81   |
| 240        | PR00011       | TYPE III EGF-LIKE SIGNATURE                                    | PR00011D 14.03 3.492e-10 616-635   |
| 241        | PR00011       | TYPE III EGF-LIKE SIGNATURE                                    | PR00011D 14.03 3.492e-10 616-635   |
| 244        | BL00903       | Cytidine and deoxycytidylate deaminases zinc-binding region s. | BL00903 12.93 8.941e-12 54-64  |
| 245        | DM00179       | w KINASE ALPHA ADHESION T-CELL.                                | DM00179 13.97 8.043e-09 124-134  |
| 248        | BL00246       | Wnt-1 family proteins.   | BL00246D 23.97 1.000e-40 186-239 BL00246E 20.32 1.000e-40 305-351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e-24 70-90 BL00246C 15.56 4.857e-22 150-175 |
| 250        | PR00927       | ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE                    | PR00927E 14.93 5.114e-10 253-275   |
| 254        | BL00674       | AAA-protein family proteins.                                   | BL00674B 4.46 1.000e-09 223-245  |
| 255        | PD01796       | PROTEIN TRANSMEMBRANE COBALT ZINC CADMIUM.                     | PD01796 15.01 6.045e-09 61-88  |
| 255        | BL50002       | Src homology 3 (SH3) domain proteins profile.                  | BL50002B 15.18 2.800e-10 421-435   |
| 258        | PR00094       | ADENYLATE KINASE SIGNATURE                                     | PR00094C 12.94 2.200e-18 87-104 PR00094D 12.52 2.731e-14 161-177 PR00094A 10.31 5.530e-14 11-25 PR00094B 11.01 4.115e-13 39-54 PR00094E 11.25 7.333e-13 178-193    |
| 259        | BL00892       | HIT family proteins.   | BL00892A 18.17 5.500e-13 60-91   |
| 262        | BL00388       | Proteasome A-type subunits proteins.                           | BL00388A 23.14 1.000e-40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e-21 153-184 BL00388C 18.79 8.147e-16 126-148                                    |
| 264        | BL00903       | Cytidine and deoxycytidylate deaminases zinc-binding region s. | BL00903 12.93 5.821e-09 91-101   |
| 267        | BL00107       | Protein kinases ATP-binding region proteins.                   | BL00107B 13.31 1.529e-09 241-257   |
| 270        | BL00226       | Intermediate filaments proteins.                               | BL00226D 19.10 1.000e-37 362-409 BL00226B  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               |  | 23.86 8.043e-35 196-244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e-15 96-111  |
| 271        | PD02952       | KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI. | PD02952C 15.76 9.731e-16 235-265 PD02952B 15.57 5.625e-09 215-229   |
| 272        | PD02929       | ADHESION GLYCOPROTEIN PRECURSOR I.                 | PD02929A 28.27 1.000e-40 106-160 PD02929B 18.36 8.800e-17 179-199   |
| 274        | BL01027       | Glycosyl hydrolases family 39 proteins.            | BL01027B 15.34 3.486e-09 213-250  |
| 275        | PR00424       | ADENOSINE RECEPTOR SIGNATURE                       | PR00424D 14.32 6.451e-11 39-59  |
| 277        | BL00052       | Ribosomal protein S7 proteins.                     | BL00052A 27.85 6.000e-13 137-184 BL00052B 15.17 5.143e-12 208-235   |
| 279        | BL00790       | Receptor tyrosine kinase class V proteins.         | BL00790N 13.25 5.659e-13 267-294  |
| 280        | PR00319       | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE              | PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e-21 51-68 PR00319B 11.47 8.200e-19 70-85  |
| 281        | PR00319       | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE              | PR00319D 11.64 6.625e-23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e-21 38-55 PR00319B 11.47 8.200e-19 57-72  |
| 287        | PF00929       | Exonuclease.                                       | PF00929D 16.17 7.366e-09 149-163  |
| 291        | BL00326       | Tropomyosins proteins.                             | BL00326A 14.01 2.360e-09 93-127   |
| 292        | BL00326       | Tropomyosins proteins.                             | BL00326A 14.01 2.360e-09 93-127   |
| 294        | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                   | PD00066 13.92 8.714e-12 203-216   |
| 295        | BL00028       | Zinc finger, C2H2 type, domain proteins.           | BL00028 16.07 5.500e-15 322-339 BL00028 16.07 9.471e-14 433-450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e-13 760-777 BL00028 16.07 9.550e-13 788-805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e-12 461-478 BL00028 16.07 8.435e-12 844-861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e-11 211-228 BL00028 16.07 5.154e-11 732-749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e-11 816-833 BL00028 16.07 7.231e-11 676-693 BL00028 16.07 9.654e-11 564-581 |



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|------------|---------------|--|---|
|            |               |  | BL00028 16.07 4.086e-09 517-534 BL00028 16.07 7.429e-09 489-506   |
| 296        | BL00215       | Mitochondrial energy transfer proteins.                        | BL00215A 15.82 8.333e-16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e-11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-10 205-230  |
| 302        | PF00953       | Glycosyl transferase.  | PF00953C 19.70 8.773e-34 236-269 PF00953A 19.68 5.000e-25 102-129 PF00953B 6.17 1.000e-13 182-194   |
| 304        | PF00152       | tRNA synthetases class II.                                     | PF00152D 21.30 8.364e-28 422-461 PF00152C 28.03 9.250e-21 220-257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e-11 44-67   |
| 305        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.              | PD01066 19.43 8.250e-35 37-76   |
| 305        | PD02784       | PROTEIN NUCLEAR RIBONUCLEOPROTEIN.                             | PD02784B 26.46 5.840e-09 92-135   |
| 307        | PR00454       | ETS DOMAIN SIGNATURE   | PR00454C 11.24 7.808e-09 1167-1186  |
| 308        | PR00237       | RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE                      | PR00237E 13.03 5.091e-13 188-212 PR00237G 19.63 7.207e-13 268-295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e-10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237F 13.57 5.364e-10 230-255 PR00237B 13.50 9.438e-10 57-79 |
| 309        | BL00522       | DNA polymerase family X proteins.                              | BL00522C 11.90 7.577e-24 315-339 BL00522F 14.90 1.310e-15 470-494 BL00522A 25.52 1.265e-14 179-226 BL00522E 19.63 8.615e-14 430-460 BL00522B 27.30 9.625e-12 267-313  |
| 310        | BL00326       | Tropomyosins proteins.   | BL00326D 8.76 5.235e-10 856-897   |
| 312        | BL00290       | Immunoglobulins and major histocompatibility complex proteins. | BL00290A 20.89 4.706e-14 151-174 BL00290B 13.17 9.000e-12 211-229   |
| 313        | BL00345       | Ets-domain proteins.   | BL00345B 21.28 1.000e-40 34-85 BL00345A 13.96 9.217e-16 1-20  |
| 315        | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.                  | PF00651 15.00 5.091e-15 63-76   |
| 317        | BL01020       | SARI family proteins.  | BL01020C 15.35 3.198e-17 79-130   |
| 318        | BL00216       | Sugar transport proteins.                                      | BL00216B 27.64 4.696e-11 164-214  |
| 320        | PR00109       | TYROSINE KINASE CATALYTIC DOMAIN                               | PR00109B 12.27 4.814e-10 216-235  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | SIGNATURE  |  |
| 321        | BL00027       | 'Homeobox' domain proteins.                              | BL00027 26.43 5.688e-10 329-372  |
| 322        | PR00109       | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE               | PR00109B 12.27 8.765e-12 558-577   |
| 324        | BL01241       | Link domain proteins.                                    | BL01241 35.81 8.313e-30 183-236 BL01241 35.81 3.222e-13 282-335  |
| 326        | BL00412       | Neuromodulin (GAP-43) proteins.                          | BL00412D 16.54 4.000e-12 515-565 BL00412D 16.54 5.705e-11 516-567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e-09 514-565 BL00412D 16.54 1.918e-09 513-564 BL00412D 16.54 2.102e-09 520-571  |
| 328        | BL00232       | Cadherins extracellular repeat proteins domain proteins. | BL00232B 32.79 9.557e-20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e-18 370-418 BL00232B 32.79 5.500e-16 258-306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e-12 256-274 BL00232C 10.65 4.326e-11 368-386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e-11 39-57 |
| 330        | PR00454       | ETS DOMAIN SIGNATURE                                     | PR00454C 11.24 7.808e-09 1167-1186   |
| 331        | BL00598       | Chromo domain proteins.                                  | BL00598 14.45 8.393e-18 27-49  |
| 333        | BL01016       | Glycoprotease family proteins.                           | BL01016C 22.84 3.925e-32 70-115 BL01016E 14.88 5.286e-19 149-177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e-11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e-10 4-19 BL01016F 13.34 1.563e-09 200-212 BL01016B 8.93 8.855e-09 38-50  |
| 339        | BL01115       | GTP-binding nuclear protein ran proteins.                | BL01115A 10.22 5.500e-11 17-61   |
| 340        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.        | PD01066 19.43 1.231e-33 10-49  |
| 341        | BL01160       | Kinesin light chain repeat proteins.                     | BL01160B 19.54 5.042e-09 55-109  |
| 342        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.        | PD01066 19.43 2.400e-30 16-55  |
| 343        | DM00031       | IMMUNOGLOBULIN V REGION.                                 | DM00031A 16.80 1.000e-40 20-68   |
| 346        | PR00109       | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE               | PR00109B 12.27 4.764e-11 135-154   |
| 347        | PR00109       | TYROSINE KINASE  | PR00109B 12.27 4.764e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | CATALYTIC DOMAIN SIGNATURE                                 | 11 135-154   |
| 351        | BL01187       | Calcium-binding EGF-like domain proteins pattern proteins. | BL01187B 12.04 1.783e-13 100-116 BL01187B 12.04 8.435e-13 276-292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e-10 54-70 BL01187B 12.04 5.725e-09 231-247 BL01187A 9.98 7.000e-09 255-267 |
| 352        | PD00078       | REPEAT PROTEIN ANK NUCLEAR ANKYR.                          | PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181  |
| 354        | BL00380       | Rhodanese proteins.  | BL00380F 9.76 6.694e-11 542-553  |
| 355        | PF00628       | PHD-finger.  | PF00628 15.84 1.000e-11 116-131  |
| 356        | PR00587       | SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE                     | PR00587A 8.06 9.700e-09 17-37  |
| 359        | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                           | PD00066 13.92 4.462e-15 261-274 PD00066 13.92 6.500e-13 233-246 PD00066 13.92 4.300e-09 289-302  |
| 361        | PF00791       | Domain present in ZO-1 and Unc5-like netrin receptors.     | PF00791B 28.49 9.604e-13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e-09 71-126 PF00791B 28.49 7.440e-09 184-239  |
| 362        | PF00791       | Domain present in ZO-1 and Unc5-like netrin receptors.     | PF00791B 28.49 2.273e-11 279-334   |
| 363        | PR00450       | RECOVERIN FAMILY SIGNATURE                                 | PR00450C 12.22 5.080e-10 73-95 PR00450C 12.22 3.278e-09 109-131  |
| 364        | PF00242       | DNA polymerase (viral) N-terminal domain proteins.         | PF00242Q 13.51 2.328e-09 22-68   |
| 365        | PF00242       | DNA polymerase (viral) N-terminal domain proteins.         | PF00242Q 13.51 2.328e-09 22-68   |
| 366        | BL01160       | Kinesin light chain repeat proteins.                       | BL01160B 19.54 6.644e-09 1038-1092   |
| 367        | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                              | PR00019B 11.36 1.360e-09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e-09 370-384  |
| 368        | PR00011       | TYPE III EGF-LIKE SIGNATURE                                | PR00011D 14.03 9.000e-15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e-14 30-49 PR00011C 24.25 5.143e-09 6-35   |
| 369        | BL01032       | Protein phosphatase 2C proteins.                           | BL01032H 11.25 4.150e-09 417-430   |
| 372        | BL00478       | LIM domain proteins.                                       | BL00478B 14.79 7.750e-12 410-425   |
| 373        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.          | PD01066 19.43 9.757e-34 26-65  |
| 376        | PR00170       | SODIUM CHANNEL SIGNATURE                                   | PR00170E 6.48 2.739e-  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               |  | 10 88-118   |
| 380        | BL00107       | Protein kinases ATP-binding region proteins.                   | BL00107A 18.39 1.000e-23 276-307 BL00107B 13.31 1.692e-12 342-358   |
| 381        | BL00455       | Putative AMP-binding domain proteins.                          | BL00455 13.31 5.714e-12 50-66   |
| 382        | PR00624       | HISTONE H5 SIGNATURE   | PR00624G 4.08 4.900e-09 524-544   |
| 384        | PD00078       | REPEAT PROTEIN ANK NUCLEAR ANKYR.                              | PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181   |
| 385        | PR00511       | TEKTIN SIGNATURE   | PR00511D 7.11 5.371e-09 67-80   |
| 386        | PD02870       | RECEPTOR INTERLEUKIN-1 PRECURSOR.                              | PD02870B 18.83 6.000e-10 97-130   |
| 388        | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                               | PD00066 13.92 5.000e-13 516-529   |
| 389        | BL00290       | Immunoglobulins and major histocompatibility complex proteins. | BL00290A 20.89 7.657e-09 151-174  |
| 390        | BL00215       | Mitochondrial energy transfer proteins.                        | BL00215A 15.82 5.200e-15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e-11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e-09 272-285 BL00215B 10.44 8.500e-09 165-178 |
| 394        | BL00674       | AAA-protein family proteins.                                   | BL00674B 4.46 2.723e-16 299-321   |
| 397        | PR00048       | C2H2-TYPE ZINC FINGER SIGNATURE                                | PR00048A 10.52 8.579e-11 141-155  |
| 398        | PR00761       | BINDIN PRECURSOR SIGNATURE                                     | PR00761B 9.93 6.764e-09 55-74   |
| 399        | BL00240       | Receptor tyrosine kinase class III proteins.                   | BL00240B 24.70 7.907e-10 118-142  |
| 401        | PF00676       | Dehydrogenase E1 component.                                    | PF00676B 24.71 8.071e-18 331-369 PF00676D 14.40 3.854e-15 486-506 PF00676C 16.88 9.182e-14 454-478  |
| 402        | BL00514       | Fibrinogen beta and gamma chains C-terminal domain proteins.   | BL00514C 17.41 4.673e-28 4432-4469 BL00514G 15.98 6.092e-14 4555-4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e-10 4519-4534 BL00514H 14.95 4.955e-10 4584-4609                    |
| 403        | PF00992       | Troponin.  | PF00992A 16.67 5.974e-09 105-140  |
| 404        | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                                  | PR00019B 11.36 1.450e-10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e-09 50-64 PR00019B 11.36 1.000e-09 96-110  |
| 405        | BL00232       | Cadherins extracellular repeat proteins domain proteins.       | BL00232B 32.79 9.557e-20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e-18 358-406 BL00232B 32.79 5.500e-16 246-  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               |  | 294 BL00232B 32.79<br>9.384e-15 463-511<br>BL00232C 10.65 2.537e-<br>12 244-262 BL00232C<br>10.65 4.326e-11 356-<br>374 BL00232C 10.65<br>7.261e-11 461-479<br>BL00232C 10.65 7.457e-<br>11 27-45  |
| 407        | PF00426       | Outer Capsid protein VP4<br>(Hemagglutinin).                         | PF00426S 15.67 5.634e-<br>09 902-940   |
| 409        | BL01160       | Kinesin light chain<br>repeat proteins.                              | BL01160B 19.54 9.695e-<br>09 126-180   |
| 410        | BL00741       | Guanine-nucleotide<br>dissociation stimulators<br>CDC24 family sign. | BL00741B 14.27 2.731e-<br>09 252-275   |
| 411        | PF00646       | F-box domain proteins.   | PF00646A 14.37 6.344e-<br>09 86-100  |
| 412        | BL00603       | Thymidine kinase<br>cellular-type proteins.                          | BL00603B 11.39 8.500e-<br>09 542-557   |
| 415        | BL00866       | Carbamoyl-phosphate<br>synthase subdomain<br>proteins.               | BL00866B 36.29 3.571e-<br>31 245-291 BL00866C<br>23.26 9.000e-25 331-<br>366   |
| 418        | PR00239       | MOLLUSCAN RHODOPSIN C-<br>TERMINAL TAIL SIGNATURE                    | PR00239E 1.58 6.114e-<br>09 590-602  |
| 421        | PF00791       | Domain present in ZO-1<br>and Unc5-like netrin<br>receptors.         | PF00791B 28.49 7.955e-<br>14 23-78 PF00791B<br>28.49 3.653e-12 273-<br>328 PF00791B 28.49<br>4.273e-11 156-211<br>PF00791B 28.49 7.818e-<br>11 89-144 PF00791B<br>28.49 1.524e-10 56-111<br>PF00791C 20.98 3.559e-<br>09 37-76 PF00791C<br>20.98 5.235e-09 170-<br>209 PF00791C 20.98<br>5.235e-09 381-420<br>PF00791B 28.49 6.202e-<br>09 189-244 PF00791B<br>28.49 7.028e-09 435-<br>490 PF00791B 28.49<br>8.679e-09 367-422 |
| 424        | DM00892       | 3 RETROVIRAL PROTEINASE.   | DM00892C 23.55 7.207e-<br>28 1645-1679   |
| 425        | PR00109       | TYROSINE KINASE<br>CATALYTIC DOMAIN<br>SIGNATURE                     | PR00109D 17.04 5.881e-<br>10 228-251   |
| 429        | BL00518       | Zinc finger, C3HC4 type<br>(RING finger), proteins.                  | BL00518 12.23 4.600e-<br>11 31-40  |
| 431        | BL00039       | DEAD-box subfamily ATP-<br>dependent helicases<br>proteins.          | BL00039D 21.67 1.844e-<br>34 490-536 BL00039A<br>18.44 5.615e-19 205-<br>244 BL00039B 19.19<br>8.920e-16 251-277<br>BL00039C 15.63 5.781e-<br>15 333-357   |
| 432        | PR00452       | SH3 DOMAIN SIGNATURE   | PR00452B 11.65 7.652e-<br>12 169-185   |
| 433        | PR00828       | FORMIN SIGNATURE   | PR00828B 5.23 8.218e-<br>10 382-405  |
| 436        | BL00415       | Synapsins proteins.  | BL00415N 4.29 8.643e-<br>11 195-239 BL00415N<br>4.29 3.036e-09 809-853   |
| 443        | PR00834       | HTRA/DEGP PROTEASE<br>FAMILY SIGNATURE                               | PR00834F 10.91 6.040e-<br>11 221-234   |
| 446        | PF01140       | Matrix protein (MA),   | PF01140D 15.54 9.663e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION                                       | RESULTS*  |
|------------|---------------|---|---|
|            |               | p15.  | 10 183-218 PF01140D<br>15.54 3.093e-09 246-281  |
| 449        | PR00568       | DOPAMINE D3 RECEPTOR SIGNATURE                    | PR00568G 13.95 5.551e-09 39-53  |
| 451        | PF00084       | Sushi domain proteins (SCR repeat proteins.       | PF00084B 9.45 3.813e-10 47-59   |
| 452        | BL00790       | Receptor tyrosine kinase class V proteins.        | BL00790I 20.01 2.821e-09 618-649  |
| 456        | PR00380       | KINESIN HEAVY CHAIN SIGNATURE                     | PR00380A 14.18 1.000e-25 77-99 PR00380D<br>9.93 1.000e-21 281-303<br>PR00380C 13.18 8.286e-17 230-249 PR00380B<br>12.64 4.724e-16 194-212   |
| 457        | PR00253       | GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE | PR00253A 9.15 9.143e-24 246-267 PR00253B<br>13.47 2.000e-23 272-294 PR00253C 13.85<br>7.000e-23 306-328<br>PR00253D 16.68 5.950e-21 452-473 |
| 467        | PR00849       | GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE            | PR00849D 9.77 9.236e-09 910-937   |
| 471        | BL00678       | Trp-Asp (WD) repeat proteins proteins.            | BL00678 9.67 8.200e-12 33-44  |
| 472        | BL00226       | Intermediate filaments proteins.                  | BL00226B 23.86 3.721e-09 282-330  |
| 473        | BL00344       | GATA-type zinc finger domain proteins.            | BL00344 17.99 7.000e-12 814-852   |
| 474        | BL00481       | Thiol-activated cytolytic proteins.               | BL00481E 13.07 8.909e-09 173-199  |
| 479        | PR00319       | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE             | PR00319B 11.47 2.571e-09 393-408  |
| 480        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 1.900e-38 8-47  |
| 481        | PR00405       | HIV REV INTERACTING PROTEIN SIGNATURE             | PR00405C 19.41 1.000e-19 451-473 PR00405B<br>11.83 4.333e-18 430-448 PR00405A 17.71<br>4.971e-18 411-431                                    |
| 482        | PR00049       | WILM'S TUMOUR PROTEIN SIGNATURE                   | PR00049D 0.00 9.286e-10 959-974 PR00049D<br>0.00 9.857e-10 958-973<br>PR00049D 0.00 1.305e-09 937-952 PR00049D<br>0.00 8.322e-09 939-954    |
| 486        | PR00007       | COMPLEMENT C1Q DOMAIN SIGNATURE                   | PR00007B 14.16 8.615e-23 653-673 PR00007A<br>19.33 6.192e-22 626-653 PR00007C 15.60<br>5.846e-19 698-720<br>PR00007D 9.64 3.647e-13 732-743 |
| 487        | PD00567       | PROTEIN RNA-BINDING RNA REPEAT HYD.               | PD00567B 18.23 2.853e-09 200-214  |
| 488        | PR00988       | URIDINE KINASE SIGNATURE                          | PR00988A 6.39 4.569e-12 3-21  |
| 489        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 4.882e-27 30-69 PD01066<br>19.43 3.430e-10 71-110   |
| 490        | PR00049       | WILM'S TUMOUR PROTEIN SIGNATURE                   | PR00049D 0.00 7.864e-09 663-678   |
| 492        | BL01128       | Shikimate kinase proteins.                        | BL01128A 18.84 6.464e-17 58-92  |
| 497        | PF00429       | ENV polyprotein (coat                             | PF00429 31.08 7.171e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*   |
|------------|---------------|---|--|
|            |               | polyprotein).   | 15 21-71   |
| 498        | BL00120       | Lipases, serine proteins.                                 | BL00120B 11.37 7.923e-09 185-200   |
| 500        | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.             | BL00030A 14.39 7.353e-11 299-318   |
| 501        | BL01159       | WW/rsp5/WWP domain proteins.                              | BL01159 13.85 8.579e-12 131-146  |
| 505        | BL00021       | Kringle domain proteins.                                  | BL00021B 13.33 3.739e-17 492-510   |
| 508        | PR00120       | H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE             | PR00120C 9.90 5.800e-19 705-722  |
| 509        | DM01417       | 6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.                 | DM01417E 20.62 2.938e-16 362-395 DM01417D 11.08 3.800e-13 322-338  |
| 510        | PF00534       | Glycosyl transferases group 1.                            | PF00534B 14.47 6.625e-09 346-370   |
| 511        | PF00534       | Glycosyl transferases group 1.                            | PF00534B 14.47 6.625e-09 293-317   |
| 512        | PF00534       | Glycosyl transferases group 1.                            | PF00534B 14.47 6.625e-09 366-390   |
| 513        | PD01841       | PHOSPHORYLASE KINASE ALPHA MUSCL.                         | PD01841A 21.71 1.000e-40 110-160 PD01841B 14.35 1.000e-40 181-222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e-40 333-382 PD01841G 24.26 1.000e-40 386-440 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e-37 762-804 PD01841E 18.60 3.750e-36 295-333 PD01841J 14.94 6.023e-35 851-888 PD01841H 21.30 2.909e-33 490-527 PD01841K 14.81 7.088e-33 924-954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e-21 1054-1073 PD01841I 23.00 2.667e-13 549-591 |
| 514        | PR00153       | CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE | PR00153C 11.01 7.188e-13 95-111 PR00153E 9.10 4.150e-12 122-138  |
| 515        | BL00740       | MAM domain proteins.                                      | BL00740A 13.87 7.188e-12 410-423   |
| 516        | DM00892       | 3 RETROVIRAL PROTEINASE.                                  | DM00892C 23.55 6.087e-12 1018-1052   |
| 517        | BL00242       | Integrins alpha chain proteins.                           | BL00242C 16.86 8.320e-09 12-42   |
| 523        | DM00031       | IMMUNOGLOBULIN V REGION.                                  | DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 1.000e-25 84-118   |
| 525        | BL00319       | Amyloidogenic glycoprotein extracellular domain proteins. | BL00319C 17.12 8.375e-10 61-95   |
| 526        | PF00789       | Domain present in ubiquitin-regulatory proteins.          | PF00789B 19.70 3.308e-12 322-343 PF00789C 20.98 5.269e-09 367-392  |
| 528        | BL01162       | Quinone oxidoreductase / zeta-crystallin proteins.        | BL01162C 22.80 1.500e-16 120-164   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION                                      | RESULTS*  |
|------------|---------------|--|---|
| 529        | PR00910       | LUTEOVIRUS ORF6 PROTEIN SIGNATURE                | PR00910A 2.51 3.893e-09 60-73   |
| 532        | BL00215       | Mitochondrial energy transfer proteins.          | BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 123-148   |
| 533        | BL00215       | Mitochondrial energy transfer proteins.          | BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 97-122  |
| 534        | BL00098       | Thiolases acyl-enzyme intermediate proteins.     | BL00098C 21.65 2.800e-38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e-35 245-288 BL00098E 22.12 1.000e-34 314-352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e-11 38-50                              |
| 535        | PR00370       | FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE  | PR00370E 11.96 7.429e-22 321-340 PR00370D 16.33 6.143e-21 185-204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e-21 27-46 PR00370C 12.72 3.500e-20 140-157 PR00370A 3.35 6.442e-17 4-20                                 |
| 536        | BL00028       | Zinc finger, C2H2 type, domain proteins.         | BL00028 16.07 7.429e-16 285-302 BL00028 16.07 6.294e-14 341-358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e-11 397-414 BL00028 16.07 4.452e-11 453-470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e-10 313-330 |
| 537        | BL00762       | WHEP-TRS domain proteins.                        | BL00762A 23.43 9.419e-15 844-881  |
| 538        | BL00762       | WHEP-TRS domain proteins.                        | BL00762A 23.43 9.419e-15 819-856  |
| 539        | BL00762       | WHEP-TRS domain proteins.                        | BL00762A 23.43 9.419e-15 822-859  |
| 540        | PR00985       | LEUCYL-TRNA SYNTHETASE SIGNATURE                 | PR00985A 12.10 9.000e-10 357-375  |
| 541        | PD02102       | SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. | PD02102A 16.74 1.000e-40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e-30 179-218 PD02102C 26.34 8.929e-26 100-146   |
| 543        | BL00028       | Zinc finger, C2H2 type, domain proteins.         | BL00028 16.07 1.000e-10 48-65 BL00028 16.07 6.400e-10 193-210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e-09 78-95   |
| 545        | BL00250       | TGF-beta family proteins.                        | BL00250A 21.24 8.000e-31 293-329 BL00250B 27.37 5.286e-24 354-390   |
| 547        | PR00319       | BETA G-PROTEIN                                   | PR00319B 11.47 2.714e-  |



| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | (TRANSDUCIN) SIGNATURE   | 09 186-201 PR00319A<br>15.27 7.344e-09 210-227   |
| 548        | BL01204       | NF-kappa-B/Rel/dorsal domain proteins.                         | BL01204A 17.74 1.000e-40 8-56 BL01204D<br>16.42 1.000e-40 177-221 BL01204E 13.83<br>7.652e-30 225-250<br>BL01204C 13.93 8.714e-22 141-150 BL01204B<br>15.41 4.333e-16 102-116    |
| 549        | PR00326       | GTP1/ORG GTP-BINDING PROTEIN FAMILY SIGNATURE                  | PR00326A 8.75 8.364e-15 255-276  |
| 551        | PF00632       | HECT-domain (ubiquitin-transferase).                           | PF00632C 20.66 3.302e-23 1569-1601 PF00632B<br>18.45 3.700e-21 1515-1543   |
| 554        | BL00290       | Immunoglobulins and major histocompatibility complex proteins. | BL00290B 13.17 1.600e-14 187-205 BL00290A<br>20.89 2.059e-14 130-153   |
| 557        | DM00215       | PROLINE-RICH PROTEIN 3.  | DM00215 19.43 6.339e-09 846-879  |
| 559        | DM01111       | 4 kw PHOSPHATASE TRANSFORMING 61K PDF1.                        | DM01111L 11.93 3.762e-09 7-35  |
| 562        | PF00658       | Poly-adenylate binding protein, unique domain proteins.        | PF00658C 16.33 9.455e-32 118-155   |
| 564        | BL00141       | Eukaryotic and viral aspartyl proteases proteins.              | BL00141A 12.10 4.150e-10 472-488   |
| 566        | PF00855       | PWWP domain proteins.  | PF00855 13.75 5.667e-15 272-289  |
| 567        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.              | PD01066 19.43 4.977e-13 229-268  |
| 569        | BL00107       | Protein kinases ATP-binding region proteins.                   | BL00107A 18.39 7.000e-19 118-149 BL00107B<br>13.31 5.500e-15 183-199   |
| 570        | BL00107       | Protein kinases ATP-binding region proteins.                   | BL00107A 18.39 7.000e-19 118-149 BL00107B<br>13.31 5.500e-15 183-199   |
| 572        | PR00193       | MYOSIN HEAVY CHAIN SIGNATURE                                   | PR00193D 14.36 1.857e-34 454-483 PR00193C<br>12.60 2.636e-31 223-251 PR00193B 11.69<br>7.750e-29 171-197<br>PR00193A 15.41 2.588e-22 115-135 PR00193E<br>19.47 6.559e-19 508-537 |
| 573        | PR00193       | MYOSIN HEAVY CHAIN SIGNATURE                                   | PR00193D 14.36 1.857e-34 470-499 PR00193C<br>12.60 2.636e-31 239-267 PR00193B 11.69<br>7.750e-29 171-197<br>PR00193A 15.41 2.588e-22 115-135 PR00193E<br>19.47 6.559e-19 524-553 |
| 575        | BL00752       | XPA protein.   | BL00752B 19.17 9.703e-10 885-929   |
| 576        | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.                  | BL00030A 14.39 7.000e-09 276-295   |
| 577        | BL00116       | DNA polymerase family B  | BL00116A 12.81 5.737e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | proteins.  | 13 864-877 BL00116B<br>11.82 1.529e-12 952-965   |
| 578        | BL00195       | Glutaredoxin proteins.                                   | BL00195B 15.31 7.158e-09 121-141   |
| 579        | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                            | PR00019B 11.36 9.000e-11 217-231 PR00019B<br>11.36 1.360e-09 386-400 PR00019A 11.19<br>3.333e-09 389-403<br>PR00019B 11.36 8.920e-09 363-377   |
| 580        | PR00253       | GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE        | PR00253A 9.15 2.125e-25 275-296 PR00253B<br>13.47 7.923e-24 301-323 PR00253D 16.68<br>5.846e-23 444-465<br>PR00253C 13.85 2.241e-20 335-357  |
| 583        | PR00343       | SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE | PR00343C 16.85 2.286e-11 1233-1252 PR00343C<br>16.85 5.500e-11 333-352 PR00343C 16.85<br>5.500e-11 783-802<br>PR00343C 16.85 4.246e-10 1491-1510 PR00343C<br>16.85 8.230e-10 1686-1705         |
| 584        | DM01537       | kw SKI2W SKI2 NUCLEOLAR HELICASE.                        | DM01537B 21.63 1.878e-37 79-126 DM01537B<br>21.63 9.491e-30 916-963 DM01537A 15.14<br>3.186e-11 784-804  |
| 586        | PFC0013       | KH domain proteins family of RNA binding proteins.       | PF00013 5.78 1.450e-09 124-136   |
| 587        | DM00892       | 3 RETROVIRAL PROTEINASE.                                 | DM00892C 23.55 4.409e-13 262-296   |
| 589        | BL00478       | LIM domain proteins.                                     | BL00478B 14.79 1.643e-13 261-276 BL00478B<br>14.79 7.709e-09 321-336   |
| 590        | PF00855       | PWWP domain proteins.                                    | PF00855 13.75 8.000e-15 931-948  |
| 591        | PF00855       | PWWP domain proteins.                                    | PF00855 13.75 8.000e-15 1062-1079  |
| 593        | PF00628       | PHD-finger.  | PF00628 15.84 3.455e-12 424-439  |
| 594        | PR00205       | CADHERIN SIGNATURE                                       | PR00205B 11.39 2.241e-16 558-576 PR00205A<br>14.73 9.308e-13 542-558 PR00205C 13.65<br>5.304e-12 594-609<br>PR00205B 11.39 4.273e-10 336-354   |
| 595        | BL00107       | Protein kinases ATP-binding region proteins.             | BL00107A 18.39 4.789e-18 307-338   |
| 598        | PD01675       | GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.                 | PD01675C 19.89 2.330e-10 55-89   |
| 600        | BL00242       | Integrins alpha chain proteins.                          | BL00242E 9.03 9.591e-27 985-1014 BL00242C<br>16.86 4.115e-26 286-316 BL00242D 13.57<br>4.150e-25 357-382<br>BL00242B 8.13 7.353e-12 189-199 BL00242D<br>13.57 3.455e-11 421-446 BL00242A 13.80 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               |  | 5.000e-11 61-73<br>BL00242D 13.57 4.986e-10 291-316  |
| 601        | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                    | PR00320A 16.74 5.610e-09 198-213   |
| 602        | PR00278       | PANCREATIC HORMONE SIGNATURE                             | PR00278A 12.43 4.569e-10 331-348   |
| 603        | BL00479       | Phorbol esters / diacylglycerol binding domain proteins. | BL00479C 12.01 3.250e-12 170-183   |
| 604        | BL00315       | Dehydrins proteins.                                      | BL00315A 9.35 1.672e-09 424-452  |
| 605        | BL00415       | Synapsins proteins.                                      | BL00415N 4.29 9.794e-10 295-339  |
| 606        | PR00926       | MITOCHONDRIAL CARRIER PROTEIN SIGNATURE                  | PR00926F 17.75 1.000e-13 335-358   |
| 608        | PF00855       | PWWP domain proteins.                                    | PF00855 13.75 5.167e-15 265-282  |
| 609        | PF00855       | PWWP domain proteins.                                    | PF00855 13.75 5.167e-15 211-228  |
| 612        | DM01206       | CORONAVIRUS NUCLEOCAPSID PROTEIN.                        | DM01206B 10.69 7.411e-10 877-897 DM01206B 10.69 8.027e-10 861-881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10.69 1.456e-09 859-879 DM01206B 10.69 1.797e-09 879-899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e-09 898-918 DM01206B 10.69 7.949e-09 871-891 DM01206B 10.69 8.291e-09 767-787 |
| 615        | PD02699       | PROTEIN DNA-BINDING BINDING DNA.                         | PD02699A 8.91 2.023e-28 129-158 PD02699C 24.84 1.000e-27 317-364 PD02699B 18.28 1.000e-17 158-182  |
| 616        | PR00380       | KINESIN HEAVY CHAIN SIGNATURE                            | PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455   |
| 617        | PR00380       | KINESIN HEAVY CHAIN SIGNATURE                            | PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455   |
| 618        | DM01206       | CORONAVIRUS NUCLEOCAPSID PROTEIN.                        | DM01206B 10.69 5.143e-12 531-551 DM01206B 10.69 2.603e-10 535-555  |
| 621        | PR00700       | PROTEIN TYROSINE PHOSPHATASE SIGNATURE                   | PR00700B 16.80 3.160e-21 561-582   |
| 622        | BL00239       | Receptor tyrosine kinase class II proteins.              | BL00239F 28.15 3.222e-10 647-692 BL00239C 18.75 8.304e-10 543-566  |
| 623        | PR00407       | EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE                | PR00407K 9.94 8.448e-09 326-339  |
| 624        | BL00641       | Respiratory-chain NADH dehydrogenase 75 Kd               | BL00641C 21.10 1.000e-40 157-202 BL00641E  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION                                       | RESULTS*   |
|------------|---------------|---|--|
|            |               | subunit proteins.                                 | 24.37 1.000e-40 255-308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e-37 48-80 BL00641B 12.62 5.846e-34 113-139 BL00641D 13.23 9.308e-29 216-240  |
| 627        | PR00103       | CAMP-DEPENDENT PROTEIN KINASE SIGNATURE           | PR00103E 17.80 2.500e-18 367-380 PR00103B 13.39 2.080e-14 297-312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e-12 346-358 PR00103C 15.68 1.000e-11 334-344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e-10 160-175 |
| 630        | PR00081       | GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE    | PR00081A 10.53 6.211e-16 4-22  |
| 631        | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.     | PF00651 15.00 8.500e-14 37-50  |
| 632        | DM01206       | CORONAVIRUS NUCLEOCAPSID PROTEIN.                 | DM01206B 10.69 2.233e-10 1324-1344 DM01206B 10.69 4.822e-10 1276-1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e-10 1280-1300 DM01206B 10.69 4.532e-09 1320-1340 DM01206B 10.69 7.266e-09 1326-1346                    |
| 635        | BL00107       | Protein kinases ATP-binding region proteins.      | BL00107A 18.39 7.600e-23 145-176 BL00107B 13.31 2.636e-13 211-227  |
| 636        | BL00657       | Fork head domain proteins.                        | BL00657A 19.39 1.545e-30 101-143 BL00657B 22.27 7.750e-26 149-192  |
| 637        | BL00107       | Protein kinases ATP-binding region proteins.      | BL00107B 13.31 1.000e-10 607-623   |
| 643        | BL00018       | EF-hand calcium-binding domain proteins.          | BL00018 7.41 4.913e-09 199-212   |
| 647        | PF00628       | PHD-finger.                                       | PF00628 15.84 2.350e-13 385-400 PF00628 15.84 3.455e-12 464-479  |
| 648        | BL01129       | Hypothetical yabO/yceC/sfhB family proteins.      | BL01129E 13.25 4.000e-25 332-357 BL01129C 25.56 8.200e-23 236-279 BL01129B 12.51 6.118e-13 191-212   |
| 649        | BL01228       | Hypothetical cof family proteins.                 | BL01228D 17.44 3.908e-10 455-480   |
| 650        | BL00027       | 'Homeobox' domain proteins.                       | BL00027 26.43 6.681e-13 771-814  |
| 651        | BL50002       | Src homology 3 (SH3) domain proteins profile.     | BL50002A 14.19 1.750e-12 1026-1045   |
| 653        | PR00253       | GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE | PR00253A 9.15 4.000e-24 253-274 PR00253C 13.85 8.800e-24 313-335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               |  | 20 422-443  |
| 654        | PD01719       | PRECURSOR GLYCOPROTEIN SIGNAL RE.                    | PD01719A 12.89 4.452e-11 969-997 PD01719A 12.89 3.961e-10 128-156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e-09 1220-1248   |
| 657        | BL00354       | HMG-I and HMG-Y DNA-binding domain proteins (Ahook). | BL00354C 6.61 8.397e-09 563-578   |
| 658        | BL00354       | HMG-I and HMG-Y DNA-binding domain proteins (Ahook). | BL00354C 6.61 8.397e-09 580-595   |
| 659        | DM00215       | PROLINE-RICH PROTEIN 3.                              | DM00215 19.43 2.174e-13 539-572 DM00215 19.43 4.750e-12 549-582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e-10 548-581 DM00215 19.43 4.054e-10 550-583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e-10 544-577 |
| 660        | PR00688       | XYLOSE ISOMERASE SIGNATURE                           | PR00688I 13.78 9.518e-09 224-236  |
| 661        | BL00027       | 'Homeobox' domain proteins.                          | BL00027 26.43 5.950e-23 249-292   |
| 662        | PR00360       | C2 DOMAIN SIGNATURE                                  | PR00360B 13.61 7.158e-10 596-610  |
| 663        | PR00360       | C2 DOMAIN SIGNATURE                                  | PR00360B 13.61 7.158e-10 596-610  |
| 664        | PR00360       | C2 DOMAIN SIGNATURE                                  | PR00360B 13.61 7.158e-10 596-610  |
| 665        | PR00819       | CBXX/CFQX SUPERFAMILY SIGNATURE                      | PR00819B 10.83 8.988e-10 704-720  |
| 667        | BL50040       | Elongation factor 1 gamma chain profile.             | BL50040C 22.62 2.143e-16 135-178  |
| 668        | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                        | PR00019B 11.36 1.360e-09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e-09 163-177   |
| 670        | BL00018       | EF-hand calcium-binding domain proteins.             | BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730   |
| 672        | PD00131       | ATP-BINDING TRANSPORT TRANSMEMBR.                    | PD00131B 34.97 1.000e-34 356-410 PD00131C 19.59 1.346e-26 504-542   |
| 673        | PR00667       | RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE    | PR00667G 15.33 7.557e-10 106-123  |
| 674        | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                | PR00320A 16.74 4.857e-13 593-608 PR00320B 12.19 4.115e-12 635-650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e-10 635-650 PR00320C 13.01 6.400e-10 593-608 PR00320B 12.19 3.250e-09 593-608                           |
| 675        | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                | PR00320A 16.74 4.857e-13 572-587 PR00320B 12.19 4.115e-12 614-  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               |  | 629 PR00320C 13.01<br>8.435e-11 696-711<br>PR00320C 13.01 2.800e-<br>10 614-629 PR00320C<br>13.01 6.400e-10 572-<br>587 PR00320B 12.19<br>3.250e-09 572-587  |
| 676        | PR00019       | LEUCINE-RICH REPEAT<br>SIGNATURE                                     | PR00019A 11.15 9.667e-<br>09 249-263   |
| 679        | PF00642       | Zinc finger C-x8-C-x5-C-<br>x3-H type (and similar).                 | PF00642 11.59 3.700e-<br>16 225-236 PF00642<br>11.59 7.900e-12 187-<br>198   |
| 680        | PR00308       | TYPE I ANTIFREEZE<br>PROTEIN SIGNATURE                               | PR00308C 3.83 8.754e-<br>10 286-296  |
| 681        | BL00019       | Actinin-type actin-<br>binding domain proteins.                      | BL00019D 15.33 4.200e-<br>19 227-257   |
| 682        | PR00700       | PROTEIN TYROSINE<br>PHOSPHATASE SIGNATURE                            | PR00700D 12.47 4.000e-<br>09 99-118  |
| 687        | PR00049       | WILM'S TUMOUR PROTEIN<br>SIGNATURE                                   | PR00049D 0.00 8.500e-<br>10 538-553  |
| 689        | BL01024       | Protein phosphatase 2A<br>regulatory subunit PR55<br>proteins.       | BL01024A 10.26 1.000e-<br>40 22-69 BL01024B<br>8.91 1.000e-40 86-127<br>BL01024C 7.80 1.000e-<br>40 146-185 BL01024D<br>13.22 1.000e-40 185-<br>222 BL01024E 11.96<br>1.000e-40 222-266<br>BL01024F 9.42 1.000e-<br>40 266-317 BL01024G<br>11.09 1.000e-40 317-<br>349 BL01024H 13.88<br>1.000e-40 389-442 |
| 691        | BL00027       | 'Homeobox' domain<br>proteins.                                       | BL00027 26.43 8.071e-<br>31 152-195  |
| 692        | BL00211       | ABC transporters family<br>proteins.                                 | BL00211A 12.23 5.050e-<br>09 45-57   |
| 693        | BL00211       | ABC transporters family<br>proteins.                                 | BL00211A 12.23 5.050e-<br>09 45-57   |
| 694        | BL00211       | ABC transporters family<br>proteins.                                 | BL00211A 12.23 5.050e-<br>09 58-70   |
| 696        | BL00680       | Methionine<br>aminopeptidase subfamily<br>1 proteins.                | BL00680 14.37 5.304e-<br>17 173-195  |
| 697        | BL00741       | Guanine-nucleotide<br>dissociation stimulators<br>CDC24 family sign. | BL00741B 14.27 3.418e-<br>11 242-265   |
| 698        | DM01930       | 2 kw FINGER SMCX SMCY<br>YDR096W.                                    | DM01930E 15.41 1.367e-<br>37 170-215 DM01930F<br>14.16 8.232e-28 267-<br>303 DM01930B 19.86<br>9.163e-10 37-71   |
| 700        | PR00869       | DNA-POLYMERASE FAMILY X<br>SIGNATURE                                 | PR00869A 12.80 1.281e-<br>16 245-263   |
| 701        | PR00048       | C2H2-TYPE ZINC FINGER<br>SIGNATURE                                   | PR00048A 10.52 2.174e-<br>10 77-91 PR00048A<br>10.52 6.870e-10 133-<br>147 PR00048A 10.52<br>8.826e-10 105-119<br>PR00048A 10.52 5.320e-<br>09 161-175   |
| 702        | BL00523       | Sulfatases proteins.   | BL00523E 19.27 2.565e-<br>25 326-356 BL00523A<br>13.36 5.050e-16 38-55<br>BL00523B 8.64 5.909e-<br>15 86-98 BL00523C<br>12.64 5.500e-13 137-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*   |
|------------|---------------|---|--|
|            |               |   | 148 BL00523D 9.89<br>1.844e-11 290-302<br>BL00523G 9.46 5.500e-<br>10 513-523 BL00523F<br>10.85 6.351e-09 413-<br>424  |
| 703        | PR00048       | C2H2-TYPE ZINC FINGER<br>SIGNATURE                          | PR00048A 10.52 8.412e-<br>12 376-390 PR00048B<br>6.02 1.000e-10 334-344<br>PR00048B 6.02 1.474e-<br>09 364-374   |
| 707        | PD00787       | SYNTHASE BIOSYNTHESIS<br>TRANSFERASE                        | PD00787A 14.84 8.941e-<br>14 66-82   |
| 708        | PR00761       | BINDIN PRECURSOR<br>SIGNATURE                               | PR00761E 14.32 8.500e-<br>10 822-841   |
| 712        | DM01354       | kw TRANSCRIPTASE REVERSE<br>II ORF2.                        | DM01354Y 10.69 4.977e-<br>38 425-465 DM01354X<br>13.86 7.300e-34 376-<br>415 DM01354V 12.97<br>4.923e-17 311-358<br>DM01354W 12.64 5.596e-<br>10 356-376   |
| 713        | BL00039       | DEAD-box subfamily ATP-<br>dependent helicases<br>proteins. | BL00039D 21.67 7.545e-<br>27 450-496 BL00039A<br>18.44 2.537e-18 147-<br>186 BL00039C 15.63<br>2.216e-14 280-304<br>BL00039B 19.19 1.947e-<br>13 194-220   |
| 715        | BL00383       | Tyrosine specific<br>protein phosphatases<br>proteins.      | BL00383E 10.35 4.981e-<br>10 150-161   |
| 717        | PF00777       | Sialyltransferase<br>family.                                | PF00777C 18.60 4.035e-<br>21 106-161   |
| 718        | DM00031       | IMMUNOGLOBULIN V REGION.                                    | DM00031A 16.80 3.750e-<br>39 20-68 DM00031B<br>15.41 2.688e-28 84-118<br>DM00031C 12.79 1.300e-<br>12 131-142  |
| 719        | BL00243       | Integrins beta chain<br>cysteine-rich domain<br>proteins.   | BL00243B 17.54 1.000e-<br>40 131-172 BL00243C<br>16.42 1.000e-40 172-<br>208 BL00243D 24.07<br>1.000e-40 222-274<br>BL00243F 22.63 1.000e-<br>40 314-358 BL00243I<br>31.77 6.571e-39 607-<br>650 BL00243E 16.70<br>3.077e-35 274-304<br>BL00243G 21.38 3.625e-<br>34 358-400 BL00243H<br>17.53 5.235e-29 567-<br>593 BL00243A 17.61<br>3.250e-21 63-84<br>BL00243H 17.53 7.167e-<br>16 477-503 BL00243H<br>17.53 2.304e-11 524-<br>550 BL00243H 17.53<br>5.304e-11 606-632<br>BL00243I 31.77 1.380e-<br>09 610-653 |
| 720        | PR00217       | 43 KD POSTSYNAPTIC<br>PROTEIN SIGNATURE                     | PR00217C 10.91 8.022e-<br>09 20-36   |
| 722        | PR00704       | CALPAIN CYSTEINE<br>PROTEASE (C2) FAMILY<br>SIGNATURE       | PR00704D 11.05 5.909e-<br>34 135-161 PR00704F<br>13.61 7.000e-26 190-<br>218 PR00704E 12.55<br>8.071e-26 165-189   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               |  | PR00704B 17.94 2.241e-23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e-18 99-116   |
| 725        | PR00194       | TROPOMYOSIN SIGNATURE                                | PR00194A 7.86 7.652e-09 169-187   |
| 726        | PR00194       | TROPOMYOSIN SIGNATURE                                | PR00194A 7.86 7.652e-09 169-187   |
| 727        | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                | PR00320C 13.01 2.125e-13 277-292 PR00320A 16.74 1.310e-11 277-292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e-11 323-338 PR00320B 12.19 4.343e-10 323-338 PR00320B 12.19 6.914e-10 277-292 |
| 731        | PR00195       | DYNAMIN SIGNATURE                                    | PR00195A 11.94 8.627e-16 288-307 PR00195E 9.82 3.912e-11 457-474  |
| 733        | PF00642       | Zinc finger C-x8-C-x5-C-x3-H type (and similar).     | PF00642 11.59 9.082e-10 787-798   |
| 738        | BL00039       | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039A 18.44 2.565e-28 26-65 BL00039D 21.67 2.105e-20 338-384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e-11 73-99   |
| 739        | BL01289       | TSC-22 / dip / bun family proteins.                  | BL01289A 12.18 8.909e-31 326-353 BL01289B 10.45 9.571e-17 353-383   |
| 742        | BL01019       | ADP-ribosylation factors family proteins.            | BL01019A 13.20 7.078e-12 41-81  |
| 743        | BL00965       | Phosphomannose isomerase type I proteins.            | BL00965C 23.78 1.000e-40 256-305 BL00965B 17.77 1.600e-25 126-153 BL00965A 10.57 6.400e-19 94-113   |
| 747        | BL00021       | Kringle domain proteins.                             | BL00021D 24.56 4.563e-25 231-273 BL00021B 13.33 5.345e-21 60-78   |
| 748        | BL00612       | Osteonectin domain proteins.                         | BL00612B 11.35 2.034e-11 93-126   |
| 749        | PR00450       | RECOVERIN FAMILY SIGNATURE                           | PR00450C 12.22 6.880e-10 135-157  |
| 752        | BL00795       | Involucrin proteins.                                 | BL00795C 17.06 6.000e-11 384-429 BL00795C 17.06 9.444e-11 370-415   |
| 754        | BL00051       | Ribosomal protein L39e proteins.                     | BL00051 20.92 1.935e-16 4-50  |
| 755        | DM01970       | 0 kw ZK632.12 YDR313C ENDOSOMAL III.                 | DM01970B 8.60 7.723e-09 171-184   |
| 760        | BL01020       | SAR1 family proteins.                                | BL01020C 15.35 9.020e-12 99-150   |
| 762        | BL00046       | Histone H2A proteins.                                | BL00046 12.95 1.000e-40 33-88   |
| 763        | PD02411       | PROTEIN TRANSCRIPTION REGULATION NUCLEAR.            | PD02411 21.89 9.137e-10 206-240   |
| 764        | BL00027       | 'Homeobox' domain proteins.                          | BL00027 26.43 8.800e-29 417-460   |
| 767        | BL01208       | VWFC domain proteins.                                | BL01208B 15.83 6.063e-10 309-324 BL01208B 15.83 8.031e-10 165-  |



| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*   |
|------------|---------------|---|--|
|            |               |   | 180 BL01208B 15.83<br>4.162e-09 85-100   |
| 770        | BL00031       | Nuclear hormones receptors DNA-binding region proteins. | BL00031A 19.55 9.571e-32 208-241 BL00031B 22.25 5.500e-27 242-274  |
| 772        | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                  | PR00449A 13.20 1.450e-18 4-26 PR00449E 13.50 3.520e-14 142-165 PR00449C 17.27 3.032e-13 44-67 PR00449D 10.79 8.579e-13 107-121 PR00449B 14.34 3.455e-11 27-44                                    |
| 773        | BL00523       | Sulfatases proteins.                                    | BL00523E 19.27 9.333e-23 299-329 BL00523A 13.36 2.200e-13 47-64 BL00523B 8.64 2.607e-13 91-103 BL00523D 9.89 7.923e-12 224-236 BL00523C 12.64 4.512e-10 141-152 BL00523F 10.85 5.821e-10 373-384 |
| 775        | BL00028       | Zinc finger, C2H2 type, domain proteins.                | BL00028 16.07 7.686e-09 568-585  |
| 776        | BL00028       | Zinc finger, C2H2 type, domain proteins.                | BL00028 16.07 7.686e-09 621-638  |
| 777        | BL00028       | Zinc finger, C2H2 type, domain proteins.                | BL00028 16.07 7.686e-09 595-612  |
| 778        | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.           | BL00030A 14.39 8.412e-11 322-341 BL00030A 14.39 7.000e-10 220-239  |
| 779        | PR00079       | GLUCOSE-6-PHOSPHATE DEHYDROGENASE SIGNATURE             | PR00079B 12.98 2.929e-26 193-222 PR00079E 16.65 4.150e-23 348-375 PR00079C 8.68 6.351e-16 246-264 PR00079D 13.51 7.070e-16 264-281 PR00079A 16.12 6.769e-13 169-183                              |
| 781        | BL00215       | Mitochondrial energy transfer proteins.                 | BL00215A 15.82 9.250e-17 10-35 BL00215A 15.82 6.000e-16 221-246 BL00215A 15.82 7.857e-12 108-133 BL00215B 10.44 9.526e-11 168-181  |
| 783        | PD00289       | PROTEIN SH3 DOMAIN REPEAT PRESNA.                       | PD00289 9.97 6.276e-09 159-173   |
| 785        | BL00690       | DRAH-box subfamily ATP-dependent helicases proteins.    | BL00690B 13.38 1.000e-12 147-165 BL00690A 6.87 5.320e-10 114-124 BL00690C 7.51 3.189e-09 218-228   |
| 786        | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                  | PR00449C 17.27 8.500e-16 50-73 PR00449A 13.20 5.235e-14 8-30 PR00449E 13.50 2.853e-11 150-173 PR00449D 10.79 1.545e-09 111-125   |
| 788        | DM01206       | CORONAVIRUS NUCLEOCAPSID PROTEIN.                       | DM01206B 10.69 8.767e-10 1-21  |
| 790        | BL00915       | Phosphatidylinositol 3- and 4-kinases proteins.         | BL00915C 22.43 9.182e-39 725-764 BL00915B  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               |  | 22.78 5.050e-33 633-671 BL00915D 27.02<br>1.529e-21 795-831<br>BL00915A 10.09 1.000e-13 395-407  |
| 791        | PR00208       | GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE                 | PR00208A 12.59 6.294e-10 120-138 PR00208A 12.59 6.294e-10 121-139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e-10 123-141 PR00208A 12.59 6.294e-10 124-142 PR00208A 12.59 6.294e-10 125-143 PR00208A 12.59 6.294e-10 126-144 PR00208A 12.59 6.294e-10 127-145 PR00208A 12.59 6.294e-10 128-146 PR00208A 12.59 6.294e-10 129-147 PR00208A 12.59 7.411e-09 130-148 PR00208A 12.59 7.658e-09 131-149 PR00208A 12.59 7.904e-09 132-150 PR00208A 12.59 8.274e-09 118-136 PR00208A 12.59 8.274e-09 119-137 |
| 795        | PR00205       | CADHERIN SIGNATURE   | PR00205B 11.39 5.034e-16 302-320 PR00205A 14.73 1.257e-11 284-300 PR00205C 13.65 1.333e-11 337-352   |
| 796        | BL00412       | Neuromodulin (GAP-43) proteins.                                | BL00412D 16.54 4.000e-12 196-247 BL00412D 16.54 5.705e-11 197-248 BL00412D 16.54 7.848e-10 199-250 BL00412D 16.54 1.827e-09 195-246 BL00412D 16.54 1.918e-09 194-245 BL00412D 16.54 2.102e-09 201-252  |
| 797        | BL00021       | Kringle domain proteins.                                       | BL00021B 13.33 6.339e-13 40-58   |
| 799        | BL01052       | Calponin family repeat proteins.                               | BL01052C 18.51 1.000e-40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e-25 52-78 BL01052D 10.26 5.737e-25 174-194  |
| 800        | BL00348       | p53 tumor antigen proteins.                                    | BL00348F 23.19 3.714e-09 197-240   |
| 801        | BL00309       | Vertebrate galactoside-binding lectin proteins.                | BL00309C 18.65 1.621e-09 62-87   |
| 802        | PR00245       | OLFACTORY RECEPTOR SIGNATURE                                   | PR00245D 10.47 5.224e-09 187-199   |
| 804        | PF00774       | Dihydropyridine sensitive L-type calcium channel (Beta subuni. | PF00774A 16.47 8.457e-10 110-156   |
| 808        | PR00667       | RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE              | PR00667C 11.71 9.875e-09 12-28   |
| 810        | PD02346       | PHOTOSYSTEM II PROTEIN PRECURSOR                               | PD02346F 12.89 4.340e-09 317-354   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*  |
|------------|---------------|---|---|
|            |               | PHOTOSYNTHESIS.   |   |
| 811        | BL00685       | CBP-A/NF-YB subunit proteins.                             | BL00685B 14.41 6.779e-14 54-95 BL00685A 11.22 4.798e-13 5-54  |
| 812        | PR00080       | ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE               | PR00080A 9.32 9.419e-10 93-105  |
| 813        | BL00357       | Histone H2B proteins.                                     | BL00357 7.74 1.988e-17 22-65  |
| 815        | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                          | PD00066 13.92 7.923e-15 158-171 PD00066 13.92 5.200e-14 46-59 PD00066 13.92 7.000e-14 18-31 PD00066 13.92 7.000e-13 130-143 PD00066 13.92 7.500e-13 214-227 PD00066 13.92 9.000e-13 102-115 PD00066 13.92 4.429e-12 186-199 PD00066 13.92 1.783e-11 74-87 |
| 816        | BL01195       | Peptidyl-tRNA hydrolase proteins.                         | BL01195C 20.12 3.348e-20 100-139  |
| 820        | BL00520       | Interleukin-10 family proteins.                           | BL00520A 6.21 6.471e-09 1-14  |
| 822        | BL00972       | Ubiquitin carboxyl-terminal hydrolases family 2 proteins. | BL00972A 11.93 8.113e-09 224-242  |
| 825        | PR00876       | NEMATODE METALLOTHIONEIN SIGNATURE                        | PR00876B 7.66 2.268e-10 101-115   |
| 829        | PD02855       | FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.                       | PD02855A 18.37 4.732e-28 88-124 PD02855B 8.36 6.478e-09 132-142   |
| 830        | PR00405       | HIV REV INTERACTING PROTEIN SIGNATURE                     | PR00405B 11.83 7.000e-21 44-62 PR00405C 19.41 1.000e-13 65-87 PR00405A 17.71 7.283e-13 25-45  |
| 831        | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                             | PR00019A 11.19 1.000e-09 47-61 PR00019B 11.36 1.720e-09 136-150 PR00019B 11.36 3.880e-09 44-58  |
| 832        | PR00011       | TYPE III EGF-LIKE SIGNATURE                               | PR00011B 13.08 3.438e-16 164-183 PR00011D 14.03 6.850e-16 164-183 PR00011A 14.06 8.364e-14 164-183 PR00011C 24.25 5.415e-12 231-260 PR00011D 14.03 9.852e-11 212-231  |
| 834        | PD00306       | PROTEIN GLYCOPROTEIN PRECURSOR RE.                        | PD00306A 10.26 7.000e-12 232-246  |
| 835        | PD00306       | PROTEIN GLYCOPROTEIN PRECURSOR RE.                        | PD00306A 10.26 4.000e-10 290-304  |
| 836        | PD00306       | PROTEIN GLYCOPROTEIN PRECURSOR RE.                        | PD00306A 10.26 7.000e-12 216-230  |
| 837        | DM00215       | PROLINE-RICH PROTEIN 3.                                   | DM00215 19.43 3.898e-09 78-111  |
| 839        | PD02784       | PROTEIN NUCLEAR RIBONUCLEOPROTEIN.                        | PD02784B 26.46 8.302e-09 73-116   |
| 840        | PR00700       | PROTEIN TYROSINE PHOSPHATASE SIGNATURE                    | PR00700B 16.80 5.091e-22 369-390 PR00700D 12.47 5.765e-21 491-510 PR00700C 13.17 4.750e-14 449-467 PR00700F 11.18 8.500e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION                                       | RESULTS*  |
|------------|---------------|---|---|
|            |               |   | 11 538-549 PR00700E<br>17.57 3.100e-10 522-538  |
| 841        | PR00109       | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE        | PR00109B 12.27 5.404e-13 134-153  |
| 844        | PD02785       | PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.        | PD02785B 14.43 1.000e-40 58-112 PD02785A<br>15.23 1.915e-28 8-57  |
| 845        | BL00826       | MARCKS family proteins.                           | BL00826C 7.63 6.738e-09 203-230   |
| 846        | BL00518       | Zinc finger, C3HC4 type (RING finger), proteins.  | BL00518 12.23 4.429e-10 15-24   |
| 849        | BL00518       | Zinc finger, C3HC4 type (RING finger), proteins.  | BL00518 12.23 1.000e-08 340-349   |
| 850        | PR00308       | TYPE I ANTIFREEZE PROTEIN SIGNATURE               | PR00308A 5.90 6.506e-09 12-27   |
| 851        | PD02411       | PROTEIN TRANSCRIPTION REGULATION NUCLEAR.         | PD02411 21.89 7.000e-16 246-280   |
| 852        | BL00420       | Speract receptor repeat proteins domain proteins. | BL00420B 22.67 1.000e-40 723-778 BL00420B<br>22.67 1.321e-38 933-988 BL00420B 22.67<br>8.457e-28 482-537<br>BL00420B 22.67 4.500e-27 587-642 BL00420B<br>22.67 9.625e-27 270-325 BL00420B 22.67<br>4.205e-26 163-218<br>BL00420B 22.67 5.731e-23 55-110 BL00420B<br>22.67 6.464e-20 377-432 BL00420B 22.67<br>2.800e-15 830-885<br>BL00420C 11.90 1.900e-13 355-366 BL00420C<br>11.90 1.900e-12 808-819 BL00420C 11.90<br>3.550e-12 248-259<br>BL00420C 11.90 2.831e-11 141-152 BL00420C<br>11.90 5.119e-11 1018-1029 BL00420C 11.90<br>7.955e-10 567-578 |
| 853        | BL00420       | Speract receptor repeat proteins domain proteins. | BL00420B 22.67 1.000e-40 756-811 BL00420B<br>22.67 1.321e-38 966-1021 BL00420B 22.67<br>8.457e-28 482-537<br>BL00420B 22.67 4.500e-27 620-675 BL00420B<br>22.67 9.625e-27 270-325 BL00420B 22.67<br>4.205e-26 163-218<br>BL00420B 22.67 5.731e-23 55-110 BL00420B<br>22.67 6.464e-20 377-432 BL00420B 22.67<br>2.800e-15 863-918<br>BL00420C 11.90 1.900e-13 355-366 BL00420C<br>11.90 1.900e-12 841-852 BL00420C 11.90<br>3.550e-12 248-259<br>BL00420C 11.90 2.831e-11 141-152 BL00420C<br>11.90 5.119e-11 1051-1062 BL00420C 11.90                     |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               |  | 7.955e-10 567-578   |
| 857        | PR00388       | 3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE | PR00388A 10.45 2.778e-09 64-83  |
| 859        | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.                | BL00030A 14.39 2.929e-13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e-10 128-147   |
| 861        | PR00988       | URIDINE KINASE SIGNATURE                                     | PR00988A 6.39 4.250e-17 23-41 PR00988C 13.64 8.714e-16 107-123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-12 176-188 PR00988D 5.95 8.250e-11 163-174 PR00988B 11.60 4.512e-10 60-72                                    |
| 863        | BL00215       | Mitochondrial energy transfer proteins.                      | BL00215B 10.44 8.071e-12 41-54  |
| 864        | PR00775       | 90 KD HEAT SHOCK PROTEIN SIGNATURE                           | PR00775E 8.06 1.000e-24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e-17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e-17 153-171 PR00775G 10.64 6.850e-15 267-286 PR00775F 12.76 6.769e-14 249-267 |
| 866        | DM01688       | 2 POLY-IG RECEPTOR.  | DM01688G 16.45 9.460e-09 89-121   |
| 867        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.            | PD01066 19.43 5.596e-29 14-53   |
| 868        | BL01287       | RNA 3'-terminal phosphate cyclase proteins.                  | BL01287A 17.95 2.688e-26 16-48  |
| 869        | DM00215       | PROLINE-RICH PROTEIN 3.                                      | DM00215 19.43 6.464e-10 304-337   |
| 872        | BL00046       | Histone H2A proteins.  | BL00046 12.95 1.000e-40 30-85   |
| 874        | BL00188       | Biotin-requiring enzymes attachment site proteins.           | BL00188 30.29 9.036e-32 665-711   |
| 876        | BL00028       | Zinc finger, C2H2 type, domain proteins.                     | BL00028 16.07 7.686e-09 298-315   |
| 877        | PD02102       | SUBUNIT F V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.             | PD02102A 16.74 4.176e-10 97-141   |
| 879        | BL01189       | Ribosomal protein S12e proteins.                             | BL01189A 14.27 1.000e-40 35-71 BL01189B 13.49 1.000e-40 71-125  |
| 882        | BL00284       | Serpins proteins.  | BL00284C 28.56 6.400e-25 62-104 BL00284B 17.99 6.182e-12 35-56  |
| 889        | BL00216       | Sugar transport proteins.                                    | BL00216B 27.64 4.375e-21 35-85  |
| 896        | PR00391       | PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE              | PR00391E 12.50 7.785e-15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e-13 191-207 PR00391A 7.83 5.390e-11 16-36  |
| 897        | PR00327       | ICE NUCLEATION PROTEIN                                       | PR00327C 6.37 5.247e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | SIGNATURE  | 09 313-328   |
| 898        | BL00039       | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 7.800e-26 386-432 BL00039A 18.44 6.674e-16 113-152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e-11 236-260  |
| 901        | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                     | PD00066 13.92 8.200e-16 254-267 PD00066 13.92 8.200e-16 282-295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e-16 366-379 PD00066 13.92 8.200e-16 394-407 PD00066 13.92 8.200e-14 338-351  |
| 902        | BL01115       | GTP-binding nuclear protein ran proteins.            | BL01115A 10.22 9.321e-11 6-50  |
| 903        | PR00806       | VINCULIN SIGNATURE                                   | PR00806B 4.28 9.160e-09 97-111   |
| 904        | PR00381       | KINESIN LIGHT CHAIN SIGNATURE                        | PR00381E 8.75 6.586e-25 335-356 PR00381B 18.17 2.667e-24 204-224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e-24 226-245 PR00381D 13.94 1.084e-22 291-309 PR00381F 9.13 1.288e-22 370-392 PR00381F 9.13 7.181e-13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e-11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e-09 333-351 PR00381C 12.48 7.120e-09 310-329 |
| 906        | PR00345       | STATHMIN FAMILY SIGNATURE                            | PR00345C 4.54 8.557e-09 525-549  |
| 907        | PR00345       | STATHMIN FAMILY SIGNATURE                            | PR00345C 4.54 8.557e-09 513-537  |
| 908        | BL00678       | Trp-Asp (WD) repeat proteins proteins.               | BL00678 9.67 9.308e-11 144-155   |
| 910        | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.    | PD01066 19.43 2.800e-30 48-87  |
| 912        | BL01104       | Ribosomal protein L13e proteins.                     | BL01104C 15.14 6.000e-09 364-392   |
| 922        | BL00678       | Trp-Asp (WD) repeat proteins proteins.               | BL00678 9.67 3.842e-09 500-511   |
| 923        | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                | PR00320C 13.01 2.500e-09 323-338 PR00320C 13.01 5.500e-09 187-202  |
| 924        | PD02181       | PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.             | PD02181D 12.85 8.609e-09 36-64   |
| 926        | BL00019       | Actinin-type actin-binding domain proteins.          | BL00019C 14.66 7.453e-25 108-144 BL00019B 13.34 6.510e-11 61-84 BL00019D 15.33 9.338e-11 205-235 BL00019A 12.56 2.373e-10 34-45  |
| 928        | BL00678       | Trp-Asp (WD) repeat                                  | BL00678 9.67 9.308e-11   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | proteins proteins.                                       | 273-284 BL00678 9.67<br>1.600e-10 314-325<br>BL00678 9.67 7.600e-10<br>360-371 BL00678 9.67<br>8.579e-09 206-217   |
| 929        | BL00518       | Zinc finger, C3HC4 type (RING finger), proteins.         | BL00518 12.23 1.857e-10 137-146  |
| 930        | BL01085       | Ribulose-phosphate 3-epimerase family proteins.          | BL01085D 16.55 4.600e-24 134-165 BL01085B<br>10.15 5.680e-22 30-52<br>BL01085E 18.87 8.676e-20 172-202 BL01085C<br>21.81 2.038e-14 66-97                                   |
| 931        | BL01085       | Ribulose-phosphate 3-epimerase family proteins.          | BL01085D 16.55 4.600e-24 152-183 BL01085B<br>10.15 5.680e-22 30-52<br>BL01085E 18.87 8.676e-20 190-220 BL01085C<br>21.81 2.038e-14 66-97                                   |
| 933        | PD00301       | PROTEIN REPEAT MUSCLE CALCIUM-BI.                        | PD00301A 10.24 6.400e-09 160-171   |
| 936        | PF00168       | C2 domain proteins.                                      | PF00168C 27.49 4.000e-12 336-362   |
| 937        | BL00415       | Synapsins proteins.                                      | BL00415N 4.29 9.519e-10 5-49   |
| 940        | PR00862       | PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE    | PR00862D 16.17 4.086e-09 63-84   |
| 945        | BL01230       | RNA methyltransferase trmA family proteins.              | BL01230B 11.62 2.373e-09 407-420   |
| 948        | BL00479       | Phorbol esters / diacylglycerol binding domain proteins. | BL00479B 12.57 7.429e-18 52-68 BL00479A<br>19.86 2.200e-13 26-49   |
| 949        | BL00678       | Trp-Asp (WD) repeat proteins.                            | BL00678 9.67 1.474e-09 100-111   |
| 954        | PD01311       | PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE.                | PD01311A 30.23 5.909e-10 66-111  |
| 955        | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.            | PF00651 15.00 3.250e-12 47-60  |
| 956        | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.            | PF00651 15.00 3.250e-12 47-60  |
| 957        | BL00379       | CDP-alcohol phosphatidyltransferases proteins.           | BL00379 24.64 1.610e-15 111-148  |
| 959        | BL01115       | GTP-binding nuclear protein ran proteins.                | BL01115A 10.22 1.884e-10 31-75   |
| 960        | BL01115       | GTP-binding nuclear protein ran proteins.                | BL01115A 10.22 3.438e-14 110-154   |
| 962        | BL00061       | Short-chain dehydrogenases/reductase s family proteins.  | BL00061B 25.79 6.586e-13 198-236   |
| 963        | PR00502       | MUTT DOMAIN SIGNATURE                                    | PR00502A 15.06 8.200e-11 210-225   |
| 966        | PR00308       | TYPE I ANTIFREEZE PROTEIN SIGNATURE                      | PR00308A 5.90 7.035e-09 55-70  |
| 967        | DM01206       | CORONAVIRUS NUCLEOCAPSID PROTEIN.                        | DM01206B 10.69 1.286e-12 104-124 DM01206B<br>10.69 5.299e-11 23-43<br>DM01206B 10.69 8.274e-10 73-93 DM01206B<br>10.69 3.962e-09 108-128 DM01206B 10.69<br>5.671e-09 38-58 |
| 969        | PF01008       | Initiation factor 2 subunit.                             | PF01008B 25.59 4.724e-31 417-460 PF01008C<br>12.25 5.333e-18 506-526 PF01008A 20.14<br>5.875e-15 369-390   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
| 970        | BL01277       | Ribonuclease PH proteins.                                    | BL01277C 10.18 7.648e-10 112-143 BL01277A 17.39 9.806e-10 40-78  |
| 975        | BL01159       | WW/rsp5/WWP domain proteins.                                 | BL01159 13.85 3.605e-12 130-145 BL01159 13.85 4.122e-10 171-186  |
| 977        | PF00791       | Domain present in ZO-1 and Unc5-like netrin receptors.       | PF00791C 20.98 2.235e-09 55-94   |
| 978        | BL01167       | Ribosomal protein L17 proteins.                              | BL01167B 20.66 8.258e-19 88-127  |
| 979        | BL00478       | LIM domain proteins.   | BL00478B 14.79 9.357e-13 33-48 BL00478B 14.79 7.250e-12 98-113   |
| 980        | PR00312       | CALSEQUESTRIN SIGNATURE                                      | PR00312E 8.32 3.423e-36 169-199 PR00312I 15.78 5.286e-35 332-361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e-35 263-291 PR00312J 13.73 5.688e-34 363-392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e-33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e-32 230-258 PR00312A 11.70 6.914e-27 35-59 |
| 981        | PF00992       | Troponin.  | PF00992A 16.67 8.816e-09 414-449   |
| 982        | PR00299       | ALPHA CRYSTALLIN SIGNATURE                                   | PR00299F 13.20 2.367e-09 127-149   |
| 983        | BL01150       | Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins. | BL01150B 17.16 1.000e-40 156-202 BL01150A 14.10 8.200e-39 100-138  |
| 986        | BL00795       | Involucrin proteins.   | BL00795C 17.06 7.211e-14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e-10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e-10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e-09 3-48   |
| 987        | BL00939       | Ribosomal protein L1e proteins.                              | BL00939F 17.27 5.393e-09 810-840   |
| 988        | PR00452       | SH3 DOMAIN SIGNATURE   | PR00452B 11.65 6.538e-11 525-541   |
| 989        | PR00452       | SH3 DOMAIN SIGNATURE   | PR00452B 11.65 6.538e-11 497-513   |
| 994        | BL00027       | 'Homeobox' domain proteins.                                  | BL00027 26.43 2.500e-25 146-189  |
| 997        | BL01304       | ubiH/COQ6 monooxygenase family proteins.                     | BL01304A 8.05 3.893e-11 65-79  |
| 998        | DM01767       | 5 TRANSMITTER DOMAIN.  | DM01767B 10.07 7.868e-09 22-39   |
| 1000       | PR00926       | MITOCHONDRIAL CARRIER PROTEIN SIGNATURE                      | PR00926C 16.07 1.750e-24 73-94 PR00926D 10.53 3.250e-23 126-145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e-  |



| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*  |
|------------|---------------|---|---|
|            |               |   | 20 174-193 PR00926B<br>16.07 2.125e-18 24-39<br>PR00926A 10.41 1.000e-<br>15 11-25 PR00926F<br>17.75 5.565e-09 120-<br>143  |
| 1005       | BL00406       | Actins proteins.  | BL00406B 5.47 1.000e-<br>40 88-143 BL00406C<br>6.75 1.000e-40 147-202<br>BL00406D 12.58 3.700e-<br>40 270-325 BL00406E<br>8.44 7.375e-38 327-377<br>BL00406A 9.95 3.348e-<br>29 11-46 |
| 1006       | BL00406       | Actins proteins.  | BL00406B 5.47 1.000e-<br>40 88-143 BL00406C<br>6.75 1.000e-40 147-202<br>BL00406E 8.44 1.000e-<br>35 248-298 BL00406A<br>9.95 3.348e-29 11-46   |
| 1007       | PR00304       | TAILLESS COMPLEX<br>POLYPEPTIDE 1<br>(CHAPERONE) SIGNATURE        | PR00304D 11.04 8.714e-<br>22 384-407 PR00304C<br>8.69 4.667e-20 98-118<br>PR00304B 11.60 7.577e-<br>19 68-87 PR00304A<br>9.20 3.382e-16 46-63<br>PR00304E 7.79 6.870e-<br>13 418-431  |
| 1009       | PD01066       | PROTEIN ZINC FINGER<br>ZINC-FINGER METAL-<br>BINDING NU.          | PD01066 19.43 2.929e-<br>32 9-48  |
| 1011       | PD01066       | PROTEIN ZINC FINGER<br>ZINC-FINGER METAL-<br>BINDING NU.          | PD01066 19.43 2.929e-<br>32 68-107  |
| 1012       | BL00518       | Zinc finger, C3HC4 type<br>(RING finger), proteins.               | BL00518 12.23 6.143e-<br>10 64-73   |
| 1016       | PD01168       | SYNTHETASE LIGASE<br>PROTEIN ALANYL.                              | PD01168H 12.08 1.000e-<br>11 174-194  |
| 1018       | PD00930       | PROTEIN GTPASE DOMAIN<br>ACTIVATION.                              | PD00930B 33.72 1.391e-<br>32 261-302 PD00930A<br>25.62 9.550e-22 157-<br>183  |
| 1022       | BL00175       | Phosphoglycerate mutase<br>family phosphohistidine<br>proteins.   | BL00175A 15.42 5.179e-<br>12 6-26 BL00175C<br>23.75 8.062e-10 79-111  |
| 1025       | PR00305       | 14-3-3 PROTEIN ZETA<br>SIGNATURE                                  | PR00305D 16.34 1.439e-<br>10 158-185  |
| 1026       | BL00353       | HMG1/2 proteins.  | BL00353B 11.47 2.436e-<br>18 238-288 BL00353C<br>14.83 8.844e-11 288-<br>335  |
| 1028       | BL00183       | Ubiquitin-conjugating<br>enzymes proteins.                        | BL00183 28.97 1.310e-<br>33 43-91   |
| 1033       | PF00580       | UvrD/REP helicase.  | PF00580A 13.37 4.720e-<br>09 111-133  |
| 1034       | PR00413       | HALOACID<br>DEHALOGENASE/EPOXIDE<br>HYDROLASE FAMILY<br>SIGNATURE | PR00413E 15.78 3.429e-<br>09 154-171  |
| 1037       | PD01066       | PROTEIN ZINC FINGER<br>ZINC-FINGER METAL-<br>BINDING NU.          | PD01066 19.43 9.657e-<br>09 5-44  |
| 1038       | PD01796       | PROTEIN TRANSMEMBRANE<br>COBALT ZINC CADMIU.                      | PD01796 15.01 4.259e-<br>11 55-82   |
| 1039       | BL00299       | Ubiquitin domain<br>proteins.                                     | BL00299 28.84 9.036e-<br>09 17-69   |
| 1040       | PR00970       | ARGININE ADP-<br>RIBOSYLTRANSFERASE                               | PR00970A 17.73 6.143e-<br>20 56-78 PR00970D   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*   |
|------------|---------------|---|--|
|            |               | SIGNATURE   | 9.96 2.154e-18 154-171<br>PR00970F 12.30 1.000e-16 224-241 PR00970G<br>9.97 9.229e-15 242-258<br>PR00970B 16.37 1.290e-13 86-105 PR00970C<br>11.05 1.643e-11 115-130 PR00970E 11.23<br>9.820e-11 202-218 |
| 1042       | BL00678       | Trp-Asp (WD) repeat proteins proteins.                    | BL00678 9.67 2.200e-10 243-254   |
| 1043       | PR00048       | C2H2-TYPE ZINC FINGER SIGNATURE                           | PR00048A 10.52 6.786e-13 114-128 PR00048A<br>10.52 1.000e-09 172-186   |
| 1045       | BL00615       | C-type lectin domain proteins.                            | BL00615A 16.68 1.720e-11 218-236 BL00615B<br>12.25 1.857e-10 317-331   |
| 1046       | BL01092       | Adenylate cyclases class-I proteins.                      | BL01092N 13.54 8.924e-10 3-40  |
| 1047       | BL01216       | ATP-citrate lyase / succinyl-CoA ligases family proteins. | BL01216D 21.75 4.316e-28 314-344 BL01216A<br>13.91 1.000e-10 97-112  |
| 1049       | DM00031       | IMMUNOGLOBULIN V REGION.                                  | DM00031B 15.41 7.618e-12 102-136   |
| 1050       | BL01073       | Ribosomal protein L24e proteins.                          | BL01073 24.30 1.000e-40 12-62  |
| 1054       | BL00571       | Amidases proteins.  | BL00571 25.69 5.875e-31 160-212  |
| 1055       | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.             | BL00030A 14.39 5.235e-11 98-117 BL00030B<br>7.03 4.316e-09 137-147   |
| 1058       | BL00223       | Annexins repeat proteins domain proteins.                 | BL00223C 24.79 8.754e-23 262-317 BL00223A<br>15.59 9.478e-14 46-80<br>BL00223A 15.59 5.557e-11 118-152   |
| 1060       | BL00027       | 'Homeobox' domain proteins.                               | BL00027 26.43 3.455e-35 158-201  |
| 1064       | BL00455       | Putative AMP-binding domain proteins.                     | BL00455 13.31 6.211e-13 280-296  |
| 1065       | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                             | PR00019A 11.19 2.000e-09 115-129 PR00019B<br>11.36 3.880e-09 87-101  |
| 1066       | PR00326       | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE             | PR00326A 8.75 4.600e-16 151-172 PR00326C<br>9.79 1.290e-14 200-216<br>PR00326B 16.74 8.548e-14 172-191 PR00326D<br>19.09 1.257e-13 217-236   |
| 1071       | PD02870       | RECEPTOR INTERLEUKIN-1 PRECURSOR.                         | PD02870B 18.83 8.518e-11 164-197   |
| 1072       | PF00856       | SET domain proteins.                                      | PF00856A 26.14 5.976e-09 350-387   |
| 1075       | BL01009       | Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.   | BL01009D 14.19 4.300e-20 127-148 BL01009A<br>13.75 6.586e-13 57-75<br>BL01009E 13.50 1.439e-11 159-175   |
| 1077       | PR00724       | CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE | PR00724A 10.91 1.000e-08 366-379   |
| 1078       | BL00215       | Mitochondrial energy transfer proteins.                   | BL00215A 15.82 1.000e-12 170-195 BL00215A<br>15.82 7.529e-10 79-104  |
| 1079       | BL00678       | Trp-Asp (WD) repeat                                       | BL00678 9.67 4.316e-09   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | proteins proteins.   | 298-309  |
| 1081       | BL00326       | Tropomyosins proteins.   | BL00326A 14.01 7.398e-10 23-57   |
| 1094       | BL00460       | Glutathione peroxidases selenocysteine proteins.               | BL00460A 28.67 3.204e-18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e-12 162-182 BL00460C 14.35 5.500e-09 133-156   |
| 1095       | PD02811       | PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.             | PD02811A 20.67 3.017e-22 67-105 PD02811B 17.07 2.263e-21 118-151 PD02811C 13.25 5.696e-13 154-167                                  |
| 1096       | PD02811       | PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.             | PD02811A 20.67 3.017e-22 60-98 PD02811B 17.07 2.263e-21 111-144 PD02811C 13.25 5.696e-13 147-160                                   |
| 1097       | BL00479       | Phorbol esters / diacylglycerol binding domain proteins.       | BL00479B 12.57 6.143e-09 200-216   |
| 1105       | PF00881       | Nitroreductase family.   | PF00881A 27.15 9.229e-13 111-147   |
| 1109       | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                         | PR00449A 13.20 3.077e-10 15-37 PR00449E 13.50 1.857e-09 185-208 PR00449D 10.79 8.364e-09 131-145                                   |
| 1115       | PR00405       | HIV REV INTERACTING PROTEIN SIGNATURE                          | PR00405B 11.83 5.737e-20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e-10 63-85                                       |
| 1116       | BL00355       | HMG14 and HMG17 proteins.                                      | BL00355 5.97 2.528e-25 20-51   |
| 1117       | BL00355       | HMG14 and HMG17 proteins.                                      | BL00355 5.97 2.528e-25 20-51   |
| 1120       | BL00107       | Protein kinases ATP-binding region proteins.                   | BL00107B 13.31 4.857e-10 290-306   |
| 1123       | PR00412       | EPOXIDE HYDROLASE SIGNATURE                                    | PR00412F 18.76 9.526e-12 301-324   |
| 1125       | PR00186       | HEMERYTHRIN SIGNATURE  | PR00186A 13.62 2.800e-09 87-101  |
| 1129       | BL00170       | Cyclophilin-type peptidyl-prolyl cis-trans isomerase signatur. | BL00170C 18.49 3.077e-33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e-15 10-37                                      |
| 1131       | BL00636       | Nt-dnaJ domain proteins.                                       | BL00636A 8.07 5.304e-15 29-46 BL00636B 15.11 1.360e-14 59-80   |
| 1132       | BL00678       | Trp-Asp (WD) repeat proteins proteins.                         | BL00678 9.67 6.211e-09 29-40   |
| 1133       | BL00678       | Trp-Asp (WD) repeat proteins proteins.                         | BL00678 9.67 6.211e-09 29-40   |
| 1136       | BL00990       | Clathrin adaptor complexes medium chain proteins.              | BL00990C 18.78 4.176e-38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e-27 157-187 BL00990D 16.13 5.320e-18 403-422 |
| 1137       | PR00314       | CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE                       | PR00314B 15.68 8.000e-34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               |  | 32 159-188 PR00314A<br>14.53 1.281e-22 13-34   |
| 1139       | BL01115       | GTP-binding nuclear protein ran proteins.                      | BL01115A 10.22 6.364e-13 13-57   |
| 1141       | BL00107       | Protein kinases ATP-binding region proteins.                   | BL00107A 18.39 4.00Ge-19 451-482 BL00107B<br>13.31 3.077e-12 519-535   |
| 1148       | PR00685       | TRANSCRIPTION INITIATION FACTOR IIB SIGNATURE                  | PR00685A 13.62 4.676e-09 21-42   |
| 1155       | PD01652       | RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB.                      | PD01652B 8.50 9.396e-10 522-574 PD01652B<br>8.50 9.463e-10 740-792   |
| 1157       | PD02894       | HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.                     | PD02894A 21.96 7.873e-28 81-127 PD02894B<br>13.93 1.188e-27 178-211  |
| 1159       | BL00623       | GMC oxidoreductases proteins.                                  | BL00623E 15.00 3.531e-20 391-414 BL00623C<br>10.86 4.240e-20 155-176   |
| 1161       | PD01937       | DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-.                      | PD01937A 6.68 3.475e-09 330-341  |
| 1162       | PD01937       | DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-.                      | PD01937A 6.68 3.475e-09 221-232  |
| 1163       | PR00624       | HISTONE H5 SIGNATURE   | PR00624D 11.94 7.455e-10 214-239 PR00624D<br>11.94 1.961e-09 312-337   |
| 1167       | BL00226       | Intermediate filaments proteins.                               | BL00226B 23.86 7.384e-09 302-350   |
| 1177       | BL01032       | Protein phosphatase 2C proteins.                               | BL01032G 8.33 1.422e-10 34-48  |
| 1178       | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                          | PR00320A 16.74 1.794e-10 205-220 PR00320C<br>13.01 7.840e-10 205-220 PR00320B 12.19<br>8.457e-10 35-50<br>PR00320A 16.74 7.146e-09 35-50 PR00320B<br>12.19 9.100e-09 79-94 |
| 1180       | PR00454       | ETS DOMAIN SIGNATURE   | PR00454D 10.89 4.150e-19 765-784   |
| 1181       | BL00291       | Prion protein.   | BL00291A 4.49 8.962e-11 152-187  |
| 1184       | BL00720       | Guanine-nucleotide dissociation stimulators CDC25 family sign. | BL00720B 16.57 4.103e-18 1089-1113   |
| 1185       | BL00215       | Mitochondrial energy transfer proteins.                        | BL00215A 15.82 4.553e-13 204-229 BL00215A<br>15.82 1.429e-12 11-36<br>BL00215A 15.82 9.809e-11 104-129   |
| 1187       | BL00983       | Ly-6 / u-PAR domain proteins.                                  | BL00983C 12.69 2.761e-10 77-93   |
| 1188       | BL00878       | Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si. | BL00878B 10.95 6.000e-16 189-204 BL00878C<br>17.74 8.435e-15 225-245 BL00878F 19.67<br>3.625e-13 379-402<br>BL00878D 16.56 1.621e-09 270-289                               |
| 1191       | PD02939       | PROTEIN GLUTATHIONE SYNTHETASE SY.                             | PD02939B 10.10 2.723e-12 203-220 PD02939C<br>20.01 1.000e-11 224-252   |
| 1193       | PR00345       | STATHMIN FAMILY SIGNATURE                                      | PR00345B 7.12 2.800e-28 72-101 PR00345B  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*  |
|------------|---------------|---|---|
|            |               |   | 8.54 7.652e-28 149-174<br>PR00345C 4.54 9.100e-28 101-125 PR00345D<br>10.97 1.964e-24 125-149 PR00345A 13.46<br>5.645e-16 43-62   |
| 1194       | PR00345       | STATHMIN FAMILY SIGNATURE                               | PR00345B 7.12 2.800e-28 108-137 PR00345E<br>8.54 7.652e-28 185-210<br>PR00345C 4.54 9.100e-28 137-161 PR00345D<br>10.97 1.964e-24 161-185 PR00345A 13.46<br>5.645e-16 79-98 |
| 1195       | PF00995       | Sec1 family.  | PF00995B 17.37 1.120e-13 224-264  |
| 1196       | BL00982       | Bacterial-type phytoene dehydrogenase proteins.         | BL00982A 18.41 6.738e-11 15-47  |
| 1197       | BL01298       | Dihydrodipicolinate reductase proteins.                 | BL01298A 13.90 5.959e-09 51-73  |
| 1203       | BL00061       | Short-chain dehydrogenases/reductase s family proteins. | BL00061B 25.79 1.000e-14 152-190  |
| 1204       | PR00118       | BETA-LACTAMASE CLASS A SIGNATURE                        | PR00118F 16.42 9.386e-09 213-229  |
| 1206       | BL01183       | ubI/COQ5 methyltransferase family proteins.             | BL01183B 21.31 1.429e-37 184-229 BL01183D<br>27.71 8.535e-27 264-307 BL01183A 13.25<br>3.250e-23 51-73<br>BL01183C 10.77 5.295e-09 246-258                                  |
| 1208       | BL00979       | G-protein coupled receptors family 3 proteins.          | BL00979L 20.63 2.485e-09 105-146  |
| 1209       | PFC0023       | Ank repeat proteins.                                    | PF00023A 16.03 4.857e-11 49-65 PF00023B<br>14.20 1.818e-09 45-55  |
| 1212       | PR00048       | C2H2-TYPE ZINC FINGER SIGNATURE                         | PR00048A 10.52 7.750e-14 227-241 PR00048A<br>10.52 4.316e-11 199-213  |
| 1213       | PR00450       | RECOVERIN FAMILY SIGNATURE                              | PR00450C 12.22 1.720e-10 20-42 PR00450C<br>12.22 3.506e-09 56-78<br>PR00450D 16.58 6.769e-09 44-64  |
| 1216       | BL00412       | Neuromodulin (GAP-43) proteins.                         | BL00412D 16.54 5.598e-10 179-230  |
| 1219       | PR00456       | RIBOSOMAL PROTEIN P2 SIGNATURE                          | PR00456E 3.06 5.348e-11 249-264   |
| 1222       | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                        | PD00066 13.92 7.231e-15 295-308 PD00066<br>13.92 7.231e-15 406-419 PD00066 13.92<br>2.286e-12 378-391<br>PD00066 13.92 7.857e-12 434-447 PD00066<br>13.92 3.348e-11 350-363 |
| 1223       | BL50058       | G-protein gamma subunit profile.                        | BL50058 27.23 1.000e-40 13-61   |
| 1226       | BL00412       | Neuromodulin (GAP-43) proteins.                         | BL00412D 16.54 8.439e-09 279-330  |
| 1227       | BL00437       | Catalase proximal heme-ligand proteins.                 | BL00437A 18.82 1.000e-40 49-101 BL00437B<br>16.28 1.000e-40 114-168 BL00437C 21.86  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               |  | 1.000e-40 190-239<br>BL00437D 25.72 1.000e-40 248-301 BL00437E<br>23.95 1.000e-40 327-379                |
| 1230       | BL01160       | Kinesin light chain repeat proteins.                       | BL01160B 19.54 8.297e-10 6-60  |
| 1231       | PR00735       | GLYCOSYL HYDROLASE FAMILY 8 SIGNATURE                      | PR00735A 11.19 6.857e-09 391-405   |
| 1232       | PR00497       | NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE                    | PR00497A 6.92 5.553e-10 158-176  |
| 1233       | PR00497       | NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE                    | PR00497A 6.92 5.553e-10 158-176  |
| 1235       | BL00866       | Carbamoyl-phosphate synthase subdomain proteins.           | BL00866B 36.29 2.776e-09 75-121  |
| 1237       | BL00027       | 'Homeobox' domain proteins.                                | BL00027 26.43 1.818e-21 36-79  |
| 1243       | PR00403       | WW DOMAIN SIGNATURE  | PR00403B 12.19 1.104e-11 10-25   |
| 1246       | PD01168       | SYNTHETASE LIGASE PROTEIN ALANYL.                          | PD01168L 9.47 2.837e-10 31-46 PD01168L<br>9.47 4.490e-10 174-189<br>PD01168L 9.47 7.612e-10 183-198      |
| 1249       | BL00018       | EF-hand calcium-binding domain proteins.                   | BL00018 7.41 2.800e-10 183-196   |
| 1254       | BL00183       | Ubiquitin-conjugating enzymes proteins.                    | BL00183 28.97 2.440e-36 96-144   |
| 1255       | BL01115       | GTP-binding nuclear protein ran proteins.                  | BL01115A 10.22 5.670e-11 8-52  |
| 1256       | BL00373       | Phosphoribosylglycinamide formyltransferase proteins.      | BL00373C 10.35 3.348e-12 143-156   |
| 1258       | PR00011       | TYPE III EGF-LIKE SIGNATURE                                | PR00011B 13.08 3.217e-10 174-193   |
| 1259       | BL00518       | Zinc finger, C3HC4 type (RING finger), proteins.           | BL00518 12.23 8.286e-10 31-40  |
| 1261       | PR00070       | DIHYDROFOLATE REDUCTASE SIGNATURE                          | PR00070D 11.63 1.000e-15 112-127 PR00070C<br>13.09 9.500e-15 51-63<br>PR00070A 12.92 5.500e-12 16-27     |
| 1262       | BL00462       | Gamma-glutamyltranspeptidase proteins.                     | BL00462A 20.89 6.438e-24 140-183 BL00462B<br>17.88 5.500e-20 230-267 BL00462C 27.41<br>2.023e-11 292-347 |
| 1263       | BL00038       | Myc-type, 'helix-loop-helix' dimerization domain proteins. | BL00038B 16.97 9.455e-11 62-83   |
| 1264       | BL01115       | GTP-binding nuclear protein ran proteins.                  | BL01115A 10.22 5.670e-11 17-61   |
| 1266       | PR00837       | ALLERGEN V5/TPX-1 FAMILY SIGNATURE                         | PR00837C 17.21 2.714e-18 165-182 PR00837A<br>14.77 4.512e-12 86-105<br>PR00837D 11.12 7.577e-12 201-215  |
| 1269       | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                     | PR00449C 17.27 9.308e-22 40-63 PR00449E<br>13.50 1.000e-16 137-160 PR00449D 10.79<br>3.520e-11 102-116   |
| 1270       | BL00276       | Channel forming colicins proteins.                         | BL00276A 8.87 1.500e-09 17-29  |
| 1275       | PD02327       | GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.                  | PD02327C 15.47 9.769e-09 228-243   |
| 1276       | PR00412       | EPOXIDE HYDROLASE  | PR00412B 12.59 7.894e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | SIGNATURE  | 12 119-135 PR00412C<br>11.30 1.857e-11 165-<br>179 PR00412A 13.23<br>3.400e-11 100-119                         |
| 1277       | PF00756       | Putative esterase.   | PF00756C 14.12 9.538e-<br>10 127-157   |
| 1279       | BL00134       | Serine proteases,<br>trypsin family,<br>histidine proteins.      | BL00134A 11.96 9.325e-<br>13 128-145   |
| 1280       | BL01220       | Phosphatidylethanolamine<br>-binding protein family<br>proteins. | BL01220C 14.75 9.348e-<br>15 248-276   |
| 1285       | BL00518       | Zinc finger, C3HC4 type<br>(RING finger), proteins.              | BL00518 12.23 2.286e-<br>10 33-42  |
| 1287       | PF00791       | Domain present in ZO-1<br>and Unc5-like netrin<br>receptors.     | PF00791B 28.49 7.182e-<br>11 288-343   |
| 1292       | PR00802       | SERUM ALBUMIN FAMILY<br>SIGNATURE                                | PR00802B 16.51 1.610e-<br>10 81-105  |
| 1297       | PR00716       | M-PHASE INDUCER<br>PHOSPHATASE SIGNATURE                         | PR00716C 17.65 5.696e-<br>09 23-44   |
| 1298       | BL00478       | LIM domain proteins.   | BL00478B 14.79 6.478e-<br>14 268-283   |
| 1301       | BL00127       | Pancreatic ribonuclease<br>family proteins.                      | BL00127C 31.49 3.571e-<br>28 82-126 BL00127B<br>26.57 8.800e-28 23-68  |
| 1302       | PR00637       | TYPE 3 BOMBESIN RECEPTOR<br>SIGNATURE                            | PR00637B 11.27 4.250e-<br>09 290-306   |
| 1307       | BL00215       | Mitochondrial energy<br>transfer proteins.                       | BL00215A 15.82 5.500e-<br>17 13-38 BL00215A<br>15.82 1.000e-16 226-<br>251 BL00215A 15.82<br>2.658e-13 107-132 |
| 1308       | PR00898       | VASOPRESSIN V2 RECEPTOR<br>SIGNATURE                             | PR00898H 11.34 4.682e-<br>09 552-572   |
| 1309       | PD00301       | PROTEIN REPEAT MUSCLE<br>CALCIUM-BI.                             | PD00301B 5.49 2.731e-<br>09 390-401  |
| 1310       | BL00983       | Ly-6 / u-PAR domain<br>proteins.                                 | BL00983C 12.69 9.654e-<br>13 73-89 BL00983B<br>8.19 3.132e-09 12-22  |
| 1313       | BL00194       | Thioredoxin family<br>proteins.                                  | BL00194 12.16 1.900e-<br>11 15-28  |
| 1314       | BL00594       | Aromatic amino acids<br>permeases proteins.                      | BL00594A 16.75 8.969e-<br>10 53-97   |
| 1316       | BL00134       | Serine proteases,<br>trypsin family,<br>histidine proteins.      | BL00134A 11.96 9.325e-<br>13 128-145   |
| 1320       | BL00783       | Ribosomal protein L13<br>proteins.                               | BL00783C 22.43 6.559e-<br>24 87-117 BL00783A<br>14.55 1.600e-19 8-33<br>BL00783B 12.76 3.500e-<br>12 74-86     |
| 1327       | PF00514       | Armadillo/beta-catenin-<br>like repeat proteins.                 | PF00514A 31.30 7.268e-<br>11 82-120  |
| 1329       | BL00030       | Eukaryotic RNA-binding<br>region RNP-1 proteins.                 | BL00030A 14.39 6.294e-<br>11 129-148 BL00030B<br>7.03 4.789e-09 168-178  |
| 1331       | PR00497       | NEUTROPHIL CYTOSOL<br>FACTOR P40 SIGNATURE                       | PR00497A 6.92 7.239e-<br>09 25-43  |
| 1332       | PR00161       | NICKEL-DEPENDENT<br>HYDROGENASE/B-TYPE<br>CYTOCHROME SIGNATURE   | PR00161C 9.51 4.930e-<br>09 317-337  |
| 1333       | PD01066       | PROTEIN ZINC FINGER<br>ZINC-FINGER METAL-<br>BINDING NU.         | PD01066 19.43 6.769e-<br>33 10-49  |
| 1336       | PR00700       | PROTEIN TYROSINE<br>PHOSPHATASE SIGNATURE                        | PR00700D 12.47 2.200e-<br>09 262-281   |
| 1337       | PR00700       | PROTEIN TYROSINE   | PR00700D 12.47 2.200e-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               | PHOSPHATASE SIGNATURE                                      | 09 211-230   |
| 1340       | PR00860       | VERTEBRATE METALLOTHIONEIN SIGNATURE                       | PR00860A 5.46 5.034e-13 5-18   |
| 1341       | BL00893       | mutT domain proteins.                                      | BL00893 18.99 6.750e-16 46-71  |
| 1343       | BL01282       | BIR repeat proteins.                                       | BL01282B 30.49 5.974e-21 383-422   |
| 1344       | DM00099       | 4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.             | DM00099B 14.73 8.313e-09 417-427   |
| 1345       | BL00923       | Aspartate and glutamate racemases proteins.                | BL00923B 11.41 5.935e-10 135-146   |
| 1348       | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.              | PF00651 15.00 7.231e-13 44-57  |
| 1350       | PR00193       | MYOSIN HEAVY CHAIN SIGNATURE                               | PR00193D 14.36 3.571e-32 416-445 PR00193C 12.60 6.318e-31 179-207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e-22 470-499 PR00193A 15.41 1.783e-20 77-97 |
| 1352       | PR00447       | NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN SIGNATURE | PR00447E 9.73 1.554e-15 299-319 PR00447D 13.54 3.408e-15 200-224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e-10 353-373                                   |
| 1353       | BL00303       | S-100/ICaBP type calcium binding protein.                  | BL00303A 21.77 6.667e-26 45-82 BL00303B 26.15 1.000e-24 93-130   |
| 1355       | BL00039       | DEAD-box subfamily ATP-dependent helicases proteins.       | BL00039D 21.67 5.950e-29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e-18 225-249 BL00039B 19.19 3.182e-14 141-167                                 |
| 1357       | PF00615       | Regulator of G protein signalling domain proteins.         | PF00615B 16.25 2.216e-12 84-101 PF00615C 10.06 8.412e-12 162-176   |
| 1360       | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.          | PD01066 19.43 9.234e-29 10-49  |
| 1361       | PR00925       | NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE      | PR00925A 5.47 5.091e-18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e-12 53-64 PR00925D 6.56 1.857e-10 76-87  |
| 1362       | BL01272       | Glucokinase regulatory protein family proteins.            | BL01272B 19.61 6.870e-30 136-171 BL01272C 11.68 3.314e-25 249-274 BL01272A 6.49 1.231e-18 99-117   |
| 1363       | BL01272       | Glucokinase regulatory protein family proteins.            | BL01272B 19.61 6.870e-30 113-148 BL01272C 11.68 3.314e-25 226-251 BL01272A 6.49 1.231e-18 76-94  |
| 1364       | DM00179       | w KINASE ALPHA ADHESION T-CELL.                            | DM00179 13.97 5.304e-09 167-177  |
| 1368       | PR00169       | POTASSIUM CHANNEL SIGNATURE                                | PR00169A 16.77 1.592e-09 76-96   |
| 1370       | PR00988       | URIDINE KINASE SIGNATURE                                   | PR00988A 6.39 1.794e-  |



| SEQ ID NO: | ACCESSION NO. | DESCRIPTION                                       | RESULTS*  |
|------------|---------------|---|---|
|            |               |   | 10 1-19   |
| 1371       | BL00242       | Integrins alpha chain proteins.                   | BL00242B 8.13 8.615e-09 469-479   |
| 1372       | PR00625       | DNAJ PROTEIN FAMILY SIGNATURE                     | PR00625B 13.48 7.353e-19 46-67 PR00625A 12.84 1.391e-16 14-34   |
| 1373       | BL00434       | HSP-type DNA-binding domain proteins.             | BL00434C 23.85 3.770e-09 90-130   |
| 1374       | PR00962       | LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE          | PR00962C 8.00 6.337e-09 505-526   |
| 1375       | PD02475       | MUCIN EPITHELIAL TUMOR-ASSOCIATE.                 | PD02475A 23.18 8.552e-10 1111-1150  |
| 1376       | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 9.571e-32 24-63   |
| 1380       | BL00194       | Thioredoxin family proteins.                      | BL00194 12.16 8.333e-12 48-61   |
| 1381       | DM01970       | 0 kw ZK632.12 YDR313C ENDOSOMAL III.              | DM01970B 8.60 1.458e-15 1123-1136   |
| 1383       | BL00678       | Trp-Asp (WD) repeat proteins proteins.            | BL00678 9.67 7.600e-10 243-254  |
| 1384       | BL00678       | Trp-Asp (WD) repeat proteins proteins.            | BL00678 9.67 7.600e-10 271-282  |
| 1385       | BL00303       | S-100/YCaBP type calcium binding protein.         | BL00303B 26.15 6.203e-10 95-132   |
| 1386       | BL01160       | Kinesin light chain repeat proteins.              | BL01160B 19.54 5.042e-09 1574-1628  |
| 1387       | BL00518       | Zinc finger, C3HC4 type (RING finger), proteins.  | BL00518 12.23 1.000e-11 52-61   |
| 1389       | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 3.600e-30 10-49   |
| 1390       | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 3.512e-31 32-71   |
| 1392       | PR00308       | TYPE I ANTIFREEZE PROTEIN SIGNATURE               | PR00308C 3.83 9.723e-10 127-137   |
| 1393       | PR00380       | KINESIN HEAVY CHAIN SIGNATURE                     | PR00380A 14.18 9.625e-25 88-110 PR00380D 9.93 2.406e-20 304-326 PR00380B 12.64 4.414e-16 208-226 PR00380C 13.18 6.538e-16 243-262                               |
| 1394       | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                  | PD00066 13.92 3.400e-14 462-475 PD00066 13.92 8.800e-14 348-361 PD00066 13.92 9.571e-12 405-418 PD00066 13.92 6.087e-11 490-503 PD00066 13.92 8.043e-11 320-333 |
| 1398       | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 6.786e-32 10-49   |
| 1400       | DM01206       | CORONAVIRUS NUCLEOCAPSID PROTEIN.                 | DM01206B 10.69 7.038e-09 270-290  |
| 1406       | PD00930       | PROTEIN GTPASE DOMAIN ACTIVATION.                 | PD00930A 25.62 7.324e-15 363-389  |
| 1407       | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.     | BL00030A 14.39 7.500e-10 457-476  |
| 1408       | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                     | PR00019A 11.19 9.550e-11 179-193 PR00019A 11.19 8.826e-10 228-242 PR00019B 11.36 1.360e-09 199-213 PR00019B 11.36 4.960e-                                       |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*  |
|------------|---------------|---|---|
|            |               |   | 09 176-190  |
| 1409       | PR00510       | NEBULIN SIGNATURE                                     | PR00510A 9.09 4.150e-12 182-202 PR00510B 12.96 8.767e-12 210-230 PR00510F 9.88 8.172e-10 58-75 PR00510D 9.21 2.367e-09 251-267  |
| 1410       | PD00078       | REPEAT PROTEIN ANK NUCLEAR ANKYR.                     | PD00078B 13.14 5.696e-09 31-44  |
| 1412       | BL00358       | Ribosomal protein L5 proteins.                        | BL00358B 22.76 1.000e-40 57-103 BL00358C 13.75 6.087e-14 122-136 BL00358D 14.26 5.500e-13 143-158 BL00358A 13.06 1.931e-11 33-44  |
| 1414       | BL00282       | Kazal serine protease inhibitors family proteins.     | BL00282 16.88 7.338e-10 511-534   |
| 1415       | BL00023       | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 4.300e-29 40-77   |
| 1417       | PR00681       | RIBOSOMAL PROTEIN S1 SIGNATURE                        | PR00681G 12.54 2.149e-09 38-60  |
| 1418       | DM00973       | 3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.        | DM00973A 21.17 1.462e-09 171-208  |
| 1419       | PR00319       | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE                 | PR00319B 11.47 1.571e-09 428-443  |
| 1420       | PD01941       | TRANSMEMBRANE COTRANSPORTER SYMP.                     | PD01941A 14.81 1.000e-40 142-196 PD01941B 15.02 7.049e-30 400-447 PD01941E 15.92 2.475e-20 817-864 PD01941C 19.96 3.118e-19 488-543 PD01941D 27.18 9.614e-18 641-690 PD01941F 28.52 5.382e-15 1038-1093 |
| 1422       | PR00205       | CADHERIN SIGNATURE                                    | PR00205B 11.39 8.043e-12 199-217  |
| 1423       | PR00209       | ALPHA/BETA GLIADIN FAMILY SIGNATURE                   | PR00209B 4.88 6.318e-11 1009-1028   |
| 1424       | BL50002       | Src homology 3 (SH3) domain proteins profile.         | BL50002A 14.19 8.200e-14 367-386 BL50002A 14.19 9.250e-12 298-317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e-09 244-258   |
| 1425       | PF00628       | PHD-finger.   | PF00628 15.84 3.045e-12 330-345   |
| 1426       | PF00628       | PHD-finger.   | PF00628 15.84 3.045e-12 377-392   |
| 1427       | PR00405       | HIV REV INTERACTING PROTEIN SIGNATURE                 | PR00405B 11.83 5.114e-16 281-299 PR00405A 17.71 4.306e-14 262-282   |
| 1428       | BL00039       | DEAD-box subfamily ATP-dependent helicases. proteins. | BL00039D 21.67 5.219e-34 147-193  |
| 1429       | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                 | PR00320C 13.01 8.920e-10 577-592  |
| 1430       | PR00378       | INOSITOL PHOSPHATASE SIGNATURE                        | PR00378D 16.86 7.563e-12 295-314 PR00378B 13.80 8.650e-10 166-186   |
| 1431       | PR00928       | GRAVES DISEASE CARRIER                                | PR00928B 13.53 3.769e-  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               | PROTEIN SIGNATURE  | 10 103-124  |
| 1433       | BL01113       | C1q domain proteins.   | BL01113B 18.26 7.049e-15 14-50 BL01113C 13.18 7.000e-12 82-102  |
| 1434       | PR00319       | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE                          | PR00319B 11.47 7.983e-10 135-150  |
| 1436       | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.                  | BL00030A 14.39 1.000e-12 84-103   |
| 1438       | BL00290       | Immunoglobulins and major histocompatibility complex proteins. | BL00290B 13.17 2.500e-09 250-268 BL00290A 20.89 4.000e-09 188-211   |
| 1440       | PR00806       | VINCULIN SIGNATURE   | PR00806B 4.28 4.960e-09 38-52   |
| 1441       | PR00806       | VINCULIN SIGNATURE   | PR00806B 4.28 4.960e-09 88-102  |
| 1444       | BL00422       | Granins proteins.  | BL00422D 19.48 1.000e-08 114-138  |
| 1445       | PD01841       | PHOSPHORYLASE KINASE ALPHA MUSCL.                              | PD01841A 21.71 1.000e-40 73-123 PD01841B 14.35 1.000e-40 144-185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e-40 296-345 PD01841G 24.26 1.000e-40 349-403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e-40 895-932 PD01841L 18.42 1.000e-40 1083-1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e-35 1041-1071 PD01841H 21.30 3.189e-31 435-472 PD01841C 13.78 1.000e-25 185-206 PD01841M 10.82 1.250e-20 1175-1194 |
| 1446       | PF00816       | H-NS histone family.   | PF00816B 13.84 8.875e-09 190-220  |
| 1447       | PR00048       | C2H2-TYPE ZINC FINGER SIGNATURE                                | PR00048A 10.52 2.080e-09 402-416  |
| 1448       | DM00315       | 072 RIBONUCLEASE INHIBITOR.                                    | DM00315D 18.40 7.393e-09 23-67  |
| 1451       | BL00030       | Eukaryotic RNA-binding region RNP-1 proteins.                  | BL00030B 7.03 2.800e-10 94-104  |
| 1454       | DM01688       | 2 POLY-IG RECEPTOR.  | DM01688D 13.44 7.146e-09 382-405  |
| 1455       | PF00777       | Sialyltransferase family.                                      | PF00777C 18.60 2.929e-22 4-59   |
| 1457       | BL00927       | Trehalase proteins.  | BL00927C 10.83 8.085e-09 42-53  |
| 1460       | BL00545       | Aldose 1-epimerase proteins.                                   | BL00545C 11.28 7.353e-17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e-09 140-153  |
| 1466       | PR00097       | ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE                   | PR00097C 9.42 9.069e-09 233-245   |
| 1472       | BL01129       | Hypothetical yabO/yceC/sfhB family proteins.                   | BL01129E 13.25 5.250e-22 170-195 BL01129C 25.56 9.526e-18 63-106  |
| 1473       | BL00790       | Receptor tyrosine kinase class V proteins.                     | BL00790I 20.01 2.821e-09 2114-2145  |
| 1475       | PF00686       | Starch binding domain proteins.                                | PF00686A 13.45 9.100e-09 267-277  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
| 1477       | PF00566       | Probable rabGAP domain proteins.                               | PF00566A 12.64 7.333e-10 466-476  |
| 1478       | BL00030       | Eukaryotic RNA-binding region RNP-l proteins.                  | BL00030B 7.03 9.400e-10 43-53   |
| 1479       | DM00406       | GLIADIN.   | DM00406 7.73 8.541e-10 292-305  |
| 1480       | BL00290       | Immunoglobulins and major histocompatibility complex proteins. | BL00290B 13.17 2.385e-15 69-87 BL00290A 20.89 5.091e-11 12-35   |
| 1481       | PR00150       | PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE                      | PR00150F 10.45 9.035e-09 21-51  |
| 1482       | PF00780       | Domain found in NIK1-like kinases, mouse citron and yeast ROM. | PF00780F 14.69 4.825e-09 107-137  |
| 1483       | BL01160       | Kinesin light chain repeat proteins.                           | BL01160B 19.54 1.153e-09 108-162  |
| 1485       | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.              | PD01066 19.43 5.909e-25 17-56   |
| 1486       | BL00107       | Protein kinases ATP-binding region proteins.                   | BL00107B 13.31 1.529e-09 34-50  |
| 1488       | BL00039       | DEAD-box subfamily ATP-dependent helicases proteins.           | BL00039D 21.67 9.586e-10 116-162  |
| 1490       | BL00166       | Bnoyl-CoA hydratase/isomerase proteins.                        | BL00166D 22.87 2.607e-24 190-226 BL00166C 18.93 5.500e-14 140-167 BL00166B 16.92 9.357e-11 93-115                                   |
| 1491       | BL00452       | Guanylate cyclases proteins.                                   | BL00452D 28.59 3.700e-31 63-106 BL00452E 11.92 3.045e-13 115-131  |
| 1492       | PR00019       | LEUCINE-RICH REPEAT SIGNATURE                                  | PR00019A 11.19 3.667e-09 532-546  |
| 1497       | BL00107       | Protein Kinases ATP-binding region proteins.                   | BL00107B 13.31 1.000e-11 384-400 BL00107A 18.39 5.345e-11 322-353   |
| 1500       | PF00876       | Ogre family.   | PF00876E 7.99 1.947e-10 107-117   |
| 1502       | BL00027       | 'Homeobox' domain proteins.                                    | BL00027 26.43 4.789e-24 112-155   |
| 1503       | BL00027       | 'Homeobox' domain proteins.                                    | BL00027 26.43 4.789e-24 112-155   |
| 1505       | BL01177       | Anaphylatoxin domain proteins.                                 | BL01177E 20.64 5.800e-24 448-475 BL01177C 17.39 5.333e-19 402-421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e-15 427-445 |
| 1506       | BL00972       | Ubiquitin carboxyl-terminal hydrolases family 2 proteins.      | BL00972D 22.55 5.500e-14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e-10 341-363                                    |
| 1512       | BL00523       | Sulfatases proteins.   | BL00523E 19.27 4.536e-22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e-09 159-170 BL00523G 9.46 5.333e-09 256-266      |
| 1516       | BL00914       | Syntaxin / epimorphin family proteins.                         | BL00914 24.91 7.045e-14 168-218   |
| 1518       | BL00600       | Aminotransferases class-III pyridoxal-phosphate attachment si. | BL00600A 17.98 6.143e-19 98-122 BL00600E 16.43 1.771e-17 302-   |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*   |
|------------|---------------|---|--|
|            |               |   | 331 BL006C0G 12.43<br>9.625e-17 377-396<br>BL00600B 19.60 5.091e-<br>15 160-186 BL00600C<br>16.18 6.040e-12 190-<br>206 BL006C0F 8.77<br>1.000e-11 343-356<br>BL00600D 8.71 1.000e-<br>10 281-295  |
| 1523       | PDJ0930       | PROTEIN GTPASE DOMAIN<br>ACTIVATION.                              | PD00930B 33.72 9.600e-<br>18 41-82   |
| 1528       | PR00320       | G-PROTEIN BETA WD-40<br>REPEAT SIGNATURE                          | PR00320B 12.19 4.774e-<br>11 192-207 PR00320B<br>12.19 8.839e-11 272-<br>287 PR00320B 12.19<br>9.743e-10 106-121<br>PR00320A 16.74 1.878e-<br>09 192-207 PR00320A<br>16.74 2.317e-09 106-<br>121 PR00320A 16.74<br>8.683e-09 272-287<br>PR00320C 13.01 8.800e-<br>09 106-121   |
| 1538       | DM01970       | 0 kw ZK632.12 YDR313C<br>ENDOSOMAL III.                           | DM01970B 8.60 4.508e-<br>15 171-184  |
| 1539       | PF00781       | Diacylglycerol kinase<br>catalytic domain<br>proteins (presumed). | PF00781D 11.11 7.593e-<br>10 103-127   |
| 1540       | PR00965       | OCULAR ALBINISM TYPE 1<br>PROTEIN SIGNATURE                       | PR00965H 10.73 1.231e-<br>29 312-334 PR00965E<br>12.93 5.846e-29 172-<br>195 PR00965F 5.98<br>1.123e-28 209-231<br>PR00965C 15.04 1.000e-<br>27 131-151 PR00965D<br>5.84 1.000e-27 150-170<br>PR00965G 8.52 2.440e-<br>27 258-279 PR00965B<br>4.80 8.650e-26 88-109<br>PR00965A 12.52 1.000e-<br>25 35-55 PR00965I<br>3.91 6.442e-25 385-406 |
| 1541       | BL01013       | Oxysterol-binding<br>protein family proteins.                     | BL01013D 26.81 9.719e-<br>17 163-207   |
| 1543       | PD02699       | PROTEIN DNA-BINDING<br>BINDING DNA.                               | PD02699C 24.84 1.000e-<br>40 599-646 PD02699A<br>8.91 2.286e-34 219-248<br>PD02699B 18.28 6.143e-<br>21 485-509  |
| 1544       | PR00049       | WILM'S TUMOUR PROTEIN<br>SIGNATURE                                | PR00049D 0.00 7.857e-<br>10 182-197 PR00049D<br>0.00 7.102e-09 67-82   |
| 1547       | BL00951       | ER lumen protein<br>retaining receptor<br>proteins.               | BL00951C 19.35 1.000e-<br>40 93-142 BL00951D<br>13.94 8.714e-40 142-<br>177 BL00951A 15.10<br>1.000e-38 2-38<br>BL00951B 14.23 6.250e-<br>33 38-69   |
| 1548       | BL00536       | Ubiquitin-activating<br>enzyme proteins.                          | BL00536F 13.65 8.920e-<br>30 279-318 BL00536D<br>22.91 5.737e-24 21-65<br>BL00536E 16.94 4.696e-<br>18 248-279   |
| 1549       | PR00139       | ASPARAGINASE/GLUTAMINASE<br>FAMILY SIGNATURE                      | PR00139C 11.72 9.679e-<br>09 550-569   |
| 1553       | PR00049       | WILM'S TUMOUR PROTEIN<br>SIGNATURE                                | PR00049D 0.00 5.119e-<br>09 58-73  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
| 1556       | BL00061       | Short-chain dehydrogenases/reductase s family proteins.  | BL00061B 25.79 6.276e-13 67-105   |
| 1557       | BL01228       | Hypothetical cof family proteins.                        | BL01228D 17.44 8.105e-12 107-132  |
| 1558       | BL01228       | Hypothetical cof family proteins.                        | BL01228D 17.44 8.105e-12 107-132  |
| 1559       | BL01228       | Hypothetical cof family proteins.                        | BL01228D 17.44 8.105e-12 107-132  |
| 1562       | BL00522       | DNA polymerase family X proteins.                        | BL00522C 11.90 6.600e-18 412-436 BL00522B 27.30 1.738e-16 364-410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e-14 502-532 BL00522F 14.90 2.385e-13 551-575  |
| 1563       | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.            | PF00651 15.00 1.947e-11 46-59   |
| 1564       | BL00299       | Ubiquitin domain proteins.                               | BL00299 28.84 2.823e-10 324-376   |
| 1566       | BL01013       | Oxysterol-binding protein family proteins.               | BL01013D 26.81 8.594e-17 184-228 BL01013C 9.97 4.906e-12 14-24  |
| 1567       | BL00678       | Trp-Asp (WD) repeat proteins proteins.                   | BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306  |
| 1570       | BL00479       | Phorbol esters / diacylglycerol binding domain proteins. | BL00479B 12.57 5.235e-17 297-313 BL00479A 19.86 6.625e-15 271-294 BL00479A 19.86 2.667e-14 147-170 BL00479B 12.57 6.294e-12 173-189   |
| 1576       | PR00665       | OXYTOCIN RECEPTOR SIGNATURE                              | PR00665G 12.36 4.673e-24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e-22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e-19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e-15 11-25 |
| 1577       | DM00099       | 4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.           | DM00099B 14.73 9.308e-10 127-137  |
| 1579       | BL00524       | Somatomedin B domain proteins.                           | BL00524A 9.65 6.776e-14 52-73   |
| 1580       | PD02894       | HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.               | PD02894B 13.93 6.959e-16 182-215 PD02894A 21.96 2.125e-10 57-103  |
| 1581       | BL00411       | Kinesin motor domain proteins.                           | BL00411C 15.04 5.292e-12 32-54 BL00411H 15.66 4.441e-11 245-276   |
| 1582       | PR00604       | CLASS IA AND IB CYTOCHROME C SIGNATURE                   | PR00604A 11.13 2.440e-09 79-87  |
| 1584       | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.            | PF00651 15.00 1.000e-10 225-238   |
| 1585       | DM01551       | kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.                   | DM01551C 14.62 9.455e-11 125-145  |
| 1586       | DM01354       | kw TRANSCRIPTASE REVERSE II ORF2.                        | DM01354S 11.61 7.750e-09 474-495  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*  |
|------------|---------------|---|---|
| 1587       | PR00072       | MALIC ENZYME SIGNATURE                                    | PR00072B 13.77 7.955e-33 180-210 PR00072A 12.75 6.040e-25 120-145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e-22 276-295 PR00072E 10.54 1.360e-19 301-318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e-15 332-349 |
| 1589       | BL00191       | Cytochrome b5 family, heme-binding domain proteins.       | BL00191H 15.64 1.537e-22 61-113 BL00191K 17.38 9.027e-12 398-442  |
| 1590       | DM01970       | 0 kw ZK632.12 YDR313C ENDOSOMAL III.                      | DM01970B 8.60 7.716e-13 211-224 DM01970B 8.60 2.157e-12 94-107  |
| 1591       | DM00517       | 5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.                        | DM00517B 10.96 6.625e-16 1175-1193 DM00517A 8.21 1.000e-11 1015-1026  |
| 1592       | BL00037       | Myb DNA-binding domain proteins repeat proteins.          | BL00037H 15.92 3.250e-27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e-12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e-10 146-164   |
| 1595       | BL00028       | Zinc finger, C2H2 type, domain proteins.                  | BL00028 16.07 1.514e-09 110-127   |
| 1598       | PF00628       | PHD-finger.   | PF00628 15.84 3.250e-11 1667-1682   |
| 1599       | PR00014       | FIBRONECTIN TYPE III REPEAT SIGNATURE                     | PR00014D 12.04 5.500e-09 980-995  |
| 1600       | BL00518       | Zinc finger, C3HC4 type (RING finger), proteins.          | BL00518 12.23 6.571e-10 30-39   |
| 1602       | BL00412       | Neuromodulin (GAP-43) proteins.                           | BL00412D 16.54 5.402e-10 136-187  |
| 1605       | PF00651       | BTB (also known as BR-C/Ttk) domain proteins.             | PF00651 15.00 3.571e-10 44-57   |
| 1607       | BL00252       | Interferon alpha, beta and delta family proteins.         | BL00252A 18.49 6.657e-23 20-57 BL00252B 19.78 9.125e-16 58-109  |
| 1610       | DM00215       | PROLINE-RICH PROTEIN 3.                                   | DM00215 19.43 1.000e-08 61-94   |
| 1611       | BL00904       | Protein prenyltransferases alpha subunit repeat proteins. | BL00904C 8.98 7.353e-10 91-125 BL00904D 1.47 6.018e-09 127-168  |
| 1612       | PF00168       | C2 domain proteins.                                       | PF00168C 27.49 3.250e-09 365-391  |
| 1613       | BL00412       | Neuromodulin (GAP-43) proteins.                           | BL00412D 16.54 6.051e-09 932-983 BL00412D 16.54 7.153e-09 933-984   |
| 1614       | BL00559       | Eukaryotic molybdopterin oxidoreductases proteins.        | BL00559I 13.63 3.531e-25 54-83 BL00559K 13.17 2.957e-18 197-224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e-16 266-284   |
| 1615       | PD01427       | TRANSFERASE METHYLTRANSFERASE BI.                         | PD01427B 22.45 3.025e-22 500-541 PD01427A 19.94 8.773e-18 439-  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*  |
|------------|---------------|--|---|
|            |               |  | 472   |
| 1616       | BL00115       | Eukaryotic RNA polymerase II heptapeptide repeat proteins. | BL00115Z 3.12 7.485e-09 152-201 BL00115Z 3.12 9.603e-09 145-194   |
| 1617       | BL00303       | S-100/ICaBP type calcium binding protein.                  | BL00303B 26.15 7.750e-32 51-88 BL00303A 21.77 1.947e-31 4-41  |
| 1618       | BL01254       | Fetuin family proteins.                                    | BL01254F 10.02 8.754e-09 137-147  |
| 1619       | PD01888       | PEPTIDE REDUCTASE PROTEIN METHI.                           | PD01888B 25.10 1.000e-40 47-97 PD01888C 21.56 7.000e-30 125-155 PD01888A 12.84 8.800e-15 7-23   |
| 1621       | PR00239       | MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE              | PR00239E 1.58 3.455e-09 692-704 PR00239E 1.58 4.580e-09 697-709 PR00239E 1.58 4.580e-09 702-714 PR00239E 1.58 5.193e-09 703-715   |
| 1622       | PR00860       | VERTEBRATE METALLOTHIONEIN SIGNATURE                       | PR00860B 7.04 1.900e-18 27-41 PR00860C 9.61 1.474e-14 41-51 PR00860A 5.46 1.720e-14 5-18  |
| 1624       | PR00784       | MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE       | PR00784D 15.86 8.027e-11 77-95  |
| 1626       | BL00325       | Actin-depolymerizing proteins.                             | BL00325B 21.66 1.000e-40 93-139 BL00325A 24.83 6.786e-23 61-93  |
| 1631       | BL00064       | L-lactate dehydrogenase proteins.                          | BL00064B 23.57 1.000e-40 82-130 BL00064C 17.28 1.000e-40 137-182 BL00064E 27.20 1.000e-40 223-275 BL00064F 25.14 7.882e-36 286-331 BL00064A 21.16 1.000e-33 22-60 BL00064D 14.19 6.500e-31 182-212    |
| 1632       | PR00063       | RIBOSOMAL PROTEIN L27 SIGNATURE                            | PR00063B 15.24 9.700e-11 59-84 PR00063A 11.71 1.614e-09 34-59   |
| 1634       | PR00239       | MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE              | PR00239D 0.00 1.105e-11 36-49 PR00239C 3.51 2.538e-09 37-45   |
| 1636       | BL01210       | Caveolins proteins.  | BL01210B 13.92 9.531e-10 133-183  |
| 1637       | BL00982       | Bacterial-type phytoene dehydrogenase proteins.            | BL00982A 18.41 5.388e-11 11-43  |
| 1639       | BL01183       | ubiE/COQ5 methyltransferase family proteins.               | BL01183B 21.31 8.144e-12 132-177  |
| 1640       | PR00015       | GRAM-POSITIVE COCCUS SURFACE PROTEIN ANCHOR SIGNATURE      | PR00015B 9.84 8.468e-10 128-149   |
| 1641       | PR00320       | G-PROTEIN BETA WD-40 REPEAT SIGNATURE                      | PR00320B 12.19 5.935e-11 364-379 PR00320A 16.74 7.828e-11 364-379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e-10 364-379 PR00320B 12.19 5.114e-10 279-294 PR00320A 16.74 1.659e-09 279-294 |



| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
|            |               |  | PR00320A 16.74 2.098e-09 229-244   |
| 1642       | PF00023       | Ank repeat proteins.   | PF00023A 16.03 6.464e-09 114-130   |
| 1643       | PR00169       | POTASSIUM CHANNEL SIGNATURE                                    | PR00169A 16.77 1.806e-11 74-94   |
| 1644       | BL00678       | Trp-Asp (WD) repeat proteins proteins.                         | BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539  |
| 1645       | BL01108       | Ribosomal protein L24 proteins.                                | BL01108A 20.33 7.366e-17 56-89   |
| 1646       | PR00380       | KINESIN HEAVY CHAIN SIGNATURE                                  | PR00380A 14.18 9.270e-21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e-16 332-351 PR00380B 12.64 6.657e-15 292-310                                   |
| 1647       | DM01242       | 3 THREONINE--TRNA LIGASE.                                      | DM01242C 17.15 9.791e-37 340-381 DM01242E 23.00 5.071e-31 463-505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e-18 265-314 DM01242F 10.61 7.618e-14 526-540 |
| 1649       | PD00126       | PROTEIN REPEAT DOMAIN TPR NUCLEA.                              | PD00126A 22.53 5.500e-10 13-34   |
| 1651       | BL01160       | Kinesin light chain repeat proteins.                           | BL01160B 19.54 6.720e-11 431-485   |
| 1652       | BL00933       | FGGY family of carbohydrate kinases proteins.                  | BL00933A 17.50 4.673e-12 11-35 BL00933E 13.80 9.217e-09 456-472  |
| 1653       | BL00795       | Involucrin proteins.   | BL00795C 17.06 2.988e-10 70-115  |
| 1654       | BL00982       | Bacterial-type phytoene dehydrogenase proteins.                | BL00982A 18.41 7.750e-17 302-334   |
| 1655       | BL00982       | Bacterial-type phytoene dehydrogenase proteins.                | BL00982A 18.41 7.750e-17 282-314   |
| 1656       | BL00741       | Guanine-nucleotide dissociation stimulators CDC24 family sign. | BL00741B 14.27 1.391e-16 607-630   |
| 1657       | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                         | PR00449A 13.20 7.938e-11 114-136   |
| 1658       | PR00910       | LUTEOVIRUS ORF6 PROTEIN SIGNATURE                              | PR00910A 2.51 8.889e-10 442-455  |
| 1659       | BL00972       | Ubiquitin carboxyl-terminal hydrolases family 2 proteins.      | BL00972D 22.55 4.140e-12 376-401 BL00972E 20.72 5.629e-09 446-468  |
| 1660       | BL00406       | Actins proteins.   | BL00406D 12.58 8.767e-15 188-243   |
| 1661       | PR00105       | CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE              | PR00105A 10.36 4.900e-13 1140-1157 PR00105B 12.32 2.800e-12 1259-1274 PR00105C 10.86 1.000e-10 1305-1319   |
| 1662       | BL00280       | Pancreatic trypsin inhibitor (Kunitz) family proteins.         | BL00280 24.61 3.172e-33 3119-3163  |
| 1663       | PR00319       | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE                          | PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e-19 51-68 PR00319B 11.47 8.200e-19 70-85                                       |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION                                       | RESULTS*   |
|------------|---------------|---|--|
| 1664       | BL00018       | EF-hand calcium-binding domain proteins.          | BL00018 7.41 5.050e-10 489-502   |
| 1667       | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 8.500e-38 7-46   |
| 1669       | BL01153       | NOL1/NOP2/sun family proteins.                    | BL01153D 19.69 1.188e-17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e-10 13-37   |
| 1671       | PR00678       | PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE       | PR00678H 9.13 3.100e-10 1146-1169  |
| 1672       | BL00598       | Chromo domain proteins.                           | BL00598 14.45 8.500e-20 27-49  |
| 1673       | PR00326       | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE     | PR00326A 8.75 8.329e-09 686-707  |
| 1674       | PR00049       | WILM'S TUMOUR PROTEIN SIGNATURE                   | PR00049D 0.00 7.580e-11 343-358 PR00049D 0.00 1.286e-10 342-357  |
| 1676       | PR00747       | GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE            | PR00747H 12.76 8.636e-19 427-448 PR00747G 14.50 2.286e-18 368-393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747D 15.23 8.759e-17 163-183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 311-328 |
| 1677       | PR00747       | GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE            | PR00747H 12.76 8.636e-19 309-330 PR00747G 14.50 2.286e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 193-210   |
| 1680       | BL00678       | Trp-Asp (WD) repeat proteins proteins.            | BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331  |
| 1681       | BL00678       | Trp-Asp (WD) repeat proteins proteins.            | BL00678 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254  |
| 1683       | PR00326       | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE     | PR00326A 8.75 1.346e-13 389-410  |
| 1685       | PR00646       | RDC1 ORPHAN RECEPTOR SIGNATURE                    | PR00646H 6.32 4.188e-09 755-771  |
| 1690       | BL01160       | Kinesin light chain repeat proteins.              | BL01160B 19.54 6.644e-09 75-129  |
| 1691       | PR00456       | RIBOSOMAL PROTEIN P2 SIGNATURE                    | PR00456E 3.06 7.281e-10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-10 420-435  |
| 1692       | PR00456       | RIBOSOMAL PROTEIN P2 SIGNATURE                    | PR00456E 3.06 7.281e-10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-10 489-504  |
| 1693       | BL00674       | AAA-protein family proteins.                      | BL00674C 22.60 8.043e-24 274-317 BL00674B  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION   | RESULTS*  |
|------------|---------------|---|---|
|            |               |   | 4.46 4.000e-23 241-263<br>BL00674D 23.41 8.560e-18 338-385 BL00674E<br>15.24 1.720e-15 414-434  |
| 1697       | PR00409       | PHthalate dioxygenase reductase family signature                | PR00409F 12.70 4.388e-10 427-447  |
| 1698       | PR00466       | Cytochrome b-245 heavy chain signature                          | PR00466C 10.17 3.443e-13 187-208 PR00466B<br>5.03 5.500e-11 162-186<br>PR00466F 9.16 6.159e-09 498-517  |
| 1699       | BL00028       | Zinc finger, C2H2 type, domain proteins.                        | BL00028 16.07 9.217e-12 283-300 BL00028<br>16.07 3.769e-11 255-272 BL00028 16.07<br>5.154e-11 171-188<br>BL00028 16.07 5.500e-11 227-244 BL00028<br>16.07 1.600e-10 199-216 |
| 1700       | BL01019       | ADP-ribosylation factors family proteins.                       | BL01019A 13.20 3.348e-15 62-102 BL01019B<br>19.49 4.000e-15 107-162   |
| 1703       | PD01066       | Protein zinc finger zinc-finger metal-binding nu.               | PD01066 19.43 2.484e-12 200-239   |
| 1707       | PR00109       | Tyrosine kinase catalytic domain signature                      | PR00109B 12.27 4.558e-14 134-153  |
| 1710       | PR00019       | Leucine-rich repeat signature                                   | PR00019A 11.19 2.565e-10 116-130 PR00019B<br>11.36 4.600e-09 113-127 PR00019B 11.36<br>7.120e-09 204-218  |
| 1711       | BL01159       | WW/rep5/WWP domain proteins.                                    | BL01159 13.85 6.523e-11 232-247 BL01159<br>13.85 5.408e-10 613-628  |
| 1712       | PF00023       | Ank repeat proteins.  | PF00023A 16.03 7.000e-10 187-203  |
| 1713       | PF00642       | Zinc finger C-x8-C-x5-C-x3-H type (and similar).                | PF00642 11.59 9.550e-11 230-241   |
| 1714       | PF00642       | Zinc finger C-x8-C-x5-C-x3-H type (and similar).                | PF00642 11.59 9.550e-11 230-241   |
| 1715       | BL01115       | GTP-binding nuclear protein ran proteins.                       | BL01115A 10.22 7.129e-09 7-51   |
| 1718       | BL00353       | HMG1/2 proteins.  | BL00353C 14.83 6.018e-10 136-183 BL00353B<br>11.47 8.866e-09 86-136   |
| 1719       | BL00412       | Neuromodulin (GAP-43) proteins.                                 | BL00412D 16.54 5.408e-09 432-483  |
| 1721       | BL00038       | Myc-type, 'helix-loop-helix' dimerization domain proteins.      | BL00038B 16.97 8.448e-12 79-100 BL00038A<br>13.61 4.000e-11 52-68   |
| 1723       | PD00567       | Protein RNA-binding RNA repeat hyd.                             | PD00567C 9.17 8.500e-09 418-428   |
| 1724       | BL01279       | Protein-L-isoaspartate (D-aspartate) O-methyltransferase signa. | BL01279A 24.27 5.663e-12 233-281  |
| 1728       | BL00018       | EF-hand calcium-binding domain proteins.                        | BL00018 7.41 2.059e-11 73-86 BL00018 7.41<br>4.176e-11 157-170  |
| 1730       | BL00594       | Aromatic amino acids permeases proteins.                        | BL00594A 16.75 1.089e-09 17-61  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
| 1731       | BL01160       | Kinesin light chain repeat proteins.                           | BL01160B 19.54 9.676e-10 296-350   |
| 1732       | BL01160       | Kinesin light chain repeat proteins.                           | BL01160B 19.54 9.676e-10 316-370   |
| 1733       | PF00850       | Histone deacetylase family.                                    | PF00850F 15.70 4.349e-22 246-279 PF00850D 14.76 6.850e-20 177-201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e-14 281-323 |
| 1734       | BL00354       | HMG-I and HMG-Y DNA-binding domain proteins (Ahook).           | BL00354C 6.61 5.932e-09 292-307  |
| 1735       | DM00179       | w KINASE ALPHA ADHESION T-CELL.                                | DM00179 13.97 5.263e-10 492-502  |
| 1743       | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                         | PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167                                    |
| 1744       | PR00449       | TRANSFORMING PROTEIN P21 RAS SIGNATURE                         | PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167                                    |
| 1745       | BL00720       | Guanine-nucleotide dissociation stimulators CDC25 family sign. | BL00720B 16.57 8.297e-15 136-160   |
| 1746       | PR00081       | GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE                 | PR00081B 10.38 6.727e-11 45-57 PR00081E 17.54 3.935e-10 150-168  |
| 1747       | BL00439       | Acyltransferases ChoActase / COT / CPT family proteins.        | BL00439H 18.24 8.435e-14 65-91 BL00439G 13.40 2.895e-12 3-14   |
| 1749       | PR00819       | CBXX/CFQX SUPERFAMILY SIGNATURE                                | PR00819B 10.83 7.158e-11 4-20  |
| 1751       | PD00066       | PROTEIN ZINC-FINGER METAL-BINDI.                               | PD00066 13.92 3.400e-14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e-13 61-74 PD00066 13.92 6.571e-12 117-130         |
| 1753       | BL01013       | Oxysterol-binding protein family proteins.                     | BL01013D 26.81 6.516e-18 33-77   |
| 1754       | BL00790       | Receptor tyrosine kinase class V proteins.                     | BL00790I 20.01 2.393e-09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e-09 287-318                                   |
| 1756       | PD01066       | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.              | PD01066 19.43 9.750e-35 10-49  |
| 1758       | DM00406       | GLIADIN.   | DM00406 7.73 7.600e-09 653-666   |
| 1762       | PD02929       | ADHESION GLYCOPROTEIN PRECURSOR I.                             | PD02929A 28.27 4.529e-09 224-278   |
| 1765       | PR00326       | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE                  | PR00326A 8.75 5.950e-11 146-167  |
| 1775       | PF00023       | Ank repeat proteins.   | PF00023A 16.03 3.077e-14 523-539   |
| 1776       | BL00942       | glpT family of transporters proteins.                          | BL00942F 15.07 4.343e-10 371-389 BL00942B 20.36 8.040e-09 94-137   |
| 1777       | DM00215       | PROLINE-RICH PROTEIN 3.  | DM00215 19.43 2.373e-09 279-312  |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION  | RESULTS*   |
|------------|---------------|--|--|
| 1778       | BL00084       | Copper type II, ascorbate-dependent monooxygenases proteins.   | BL00084D 25.11 3.700e-20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e-11 107-158                                   |
| 1779       | BL01013       | Oxysterol-binding protein family proteins.                     | BL01013D 26.81 3.758e-18 611-655 BL01013A 25.14 2.891e-15 344-380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e-12 409-420 |
| 1783       | BL00741       | Guanine-nucleotide dissociation stimulators CDC24 family sign. | BL00741B 14.27 8.138e-13 492-515   |
| 1784       | BL00741       | Guanine-nucleotide dissociation stimulators CDC24 family sign. | BL00741B 14.27 8.138e-13 492-515   |

\* results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

TRADOC:1416223.1(%CRJ011.DOC)

TABLE 4

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                  | p-value  | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 2          | ig              | Immunoglobulin domain                        | 2.1e-32  | 109.5      |
| 3          | pkinase         | Eukaryotic protein kinase domain             | 1.3e-29  | 110.7      |
| 4          | zf-C2H2         | Zinc finger, C2H2 type                       | 1.6e-21  | 84.9       |
| 5          | fn3             | Fibronectin type III domain                  | 0        | 1097.1     |
| 6          | fn3             | Fibronectin type III domain                  | 0        | 1035.0     |
| 7          | fn3             | Fibronectin type III domain                  | 0        | 1090.4     |
| 8          | fn3             | Fibronectin type III domain                  | 0        | 1097.1     |
| 9          | TBC             | TBC domain                                   | 4e-40    | 146.7      |
| 10         | p450            | Cytochrome P450                              | 9.5e-17  | 62.0       |
| 12         | ank             | Ank repeat                                   | 6e-20    | 79.7       |
| 14         | ig              | Immunoglobulin domain                        | 1.7e-05  | 22.7       |
| 15         | zf-MYND         | MYND finger                                  | 1.3e-06  | 35.4       |
| 16         | zf-MYND         | MYND finger                                  | 1.3e-06  | 35.4       |
| 17         | zf-C2H2         | Zinc finger, C2H2 type                       | 1.7e-99  | 343.9      |
| 18         | CAP_GLY         | CAP-Gly domain                               | 1.2e-25  | 98.7       |
| 20         | IMPDH_C         | IMP dehydrogenase / GMP reductase C terminus | 1.6e-119 | 410.5      |
| 21         | IMPDH_C         | IMP dehydrogenase / GMP reductase C terminus | 4.3e-102 | 352.6      |
| 22         | pkinase         | Eukaryotic protein kinase domain             | 2.4e-79  | 277.0      |
| 23         | pkinase         | Eukaryotic protein kinase domain             | 8.4e-74  | 258.6      |
| 25         | RNA_pol_A       | RNA polymerase alpha subunit                 | 0        | 1077.7     |
| 26         | Clq             | Clq domain                                   | 1.9e-10  | 44.4       |
| 27         | Ribosomal_L23   | Ribosomal protein L23                        | 7.8e-32  | 111.2      |
| 28         | Ribosomal_L23   | Ribosomal protein L23                        | 1e-29    | 104.2      |
| 30         | zf-A20          | A20-like zinc finger                         | 1.5e-10  | 48.5       |
| 31         | zf-A20          | A20-like zinc finger                         | 1.5e-10  | 48.5       |
| 32         | FMN_dh          | FMN-dependant dehydrogenase                  | 5.4e-179 | 608.1      |
| 34         | PID             | Phosphotyrosine interaction domain (PTB/PID) | 3.8e-59  | 209.9      |
| 35         | ig              | Immunoglobulin domain                        | 1.4e-13  | 48.8       |
| 36         | ig              | Immunoglobulin domain                        | 1.4e-13  | 48.8       |
| 40         | kinesin         | Kinesin motor domain                         | 6.7e-76  | 265.6      |
| 44         | Ets             | Ets-domain                                   | 1.4e-56  | 182.1      |
| 45         | Ets             | Ets-domain                                   | 1.4e-56  | 182.1      |
| 46         | LRR             | Leucine Rich Repeat                          | 1.7e-13  | 58.3       |
| 48         | zf-C2H2         | Zinc finger, C2H2 type                       | 2.3e-162 | 552.8      |
| 49         | ITAM            | Immunoreceptor tyrosine-based activation mot | 1.4e-05  | 31.9       |
| 50         | UCH-2           | Ubiquitin carboxyl-terminal hydrolase family | 1.1e-26  | 102.0      |
| 51         | UCH-2           | Ubiquitin carboxyl-terminal hydrolase family | 1.1e-26  | 102.0      |
| 52         | ras             | Ras family                                   | 8.5e-45  | 162.3      |
| 53         | PRK             | Phosphoribulokinase                          | 2.1e-65  | 230.7      |
| 54         | myb_DNA-binding | Myb-like DNA-binding domain                  | 0.096    | 15.2       |
| 55         | voltage_CLC     | Voltage gated chloride channels              | 3.3e-186 | 631.9      |
| 56         | sugar_tr        | Sugar (and other) transporter                | 0.00015  | -64.3      |
| 57         | TBC             | TBC domain                                   | 2.2e-37  | 137.6      |
| 58         | ank             | Ank repeat                                   | 5.9e-25  | 96.3       |
| 59         | ank             | Ank repeat                                   | 5.9e-25  | 96.3       |
| 67         | PMP22_Claudin   | PMP-22/EMP/MP20/Claudin family               | 7.9e-49  | 175.6      |
| 68         | C2              | C2 domain                                    | 7.9e-54  | 192.2      |
| 69         | C2              | C2 domain                                    | 2.3e-54  | 194.0      |
| 70         | Kelch           | Kelch motif                                  | 9.4e-99  | 341.5      |
| 72         | ig              | Immunoglobulin domain                        | 8.2e-28  | 94.7       |
| 73         | pkinase         | Eukaryotic protein kinase                    | 8e-69    | 242.1      |

| SEQ ID NO: | PFAM NAME        | DESCRIPTION                                  | p-value  | PFAM SCORE |
|------------|------------------|--|----------|------------|
|            |                  | domain                                       |          |            |
| 74         | pkinase          | Eukaryotic protein kinase domain             | 2.8e-38  | 140.6      |
| 76         | zf-C4 Topoisom   | Topoisomerase DNA binding C4 zinc fing       | 5.4e-54  | 192.8      |
| 83         | Peptidase_S9     | Prolyl oligopeptidase family                 | 4.3e-10  | 36.8       |
| 84         | fn3              | Fibronectin type III domain                  | 4.1e-51  | 183.2      |
| 86         | SH2              | Src homology domain 2                        | 3.1e-22  | 67.7       |
| 88         | lg               | Immunoglobulin domain                        | 0.0091   | 14.0       |
| 89         | WD40             | WD domain, G-beta repeat                     | 2.1e-21  | 84.6       |
| 92         | laminin G        | Laminin G domain                             | 6.1e-27  | 98.5       |
| 93         | AMP-binding      | AMP-binding enzyme                           | 2.4e-13  | -37.2      |
| 95         | pkinase          | Eukaryotic protein kinase domain             | 1.4e-59  | 211.4      |
| 96         | pkinase          | Eukaryotic protein kinase domain             | 2.6e-51  | 183.9      |
| 97         | adh_short        | short chain dehydrogenase                    | 2e-61    | 217.5      |
| 98         | kinesin          | Kinesin motor domain                         | 2.2e-86  | 300.4      |
| 101        | IRS              | PTB domain (IRS-1 type)                      | 5.4e-36  | 133.0      |
| 102        | AAA              | ATPases associated with various cellular act | 6.8e-05  | -5.2       |
| 104        | pkinase          | Eukaryotic protein kinase domain             | 2.7e-73  | 256.9      |
| 106        | ras              | Ras family                                   | 8.3e-24  | 92.5       |
| 107        | FYVE             | FYVE zinc finger                             | 5.4e-27  | 100.7      |
| 108        | Cyt_reductas e   | FAD/NAD-binding Cytochrome reductase         | 7.7e-61  | 215.5      |
| 109        | zf-C2H2          | Zinc finger, C2H2 type                       | 2.3e-122 | 420.0      |
| 113        | pkinase          | Eukaryotic protein kinase domain             | 4e-88    | 306.2      |
| 116        | PH               | PH domain                                    | 3.1e-11  | 45.2       |
| 117        | lipocalin        | Lipocalin / cytosolic fatty-acid binding pr  | 2.4e-14  | 53.5       |
| 118        | pkinase          | Eukaryotic protein kinase domain             | 4.5e-20  | 76.3       |
| 120        | WD40             | WD domain, G-beta repeat                     | 2.4e-14  | 61.1       |
| 121        | WD40             | WD domain, G-beta repeat                     | 2.4e-14  | 61.1       |
| 123        | IF5_eIF4_eIF 2   | eIF4-gamma/eIF5/eIF2-epsilon                 | 1e-32    | 122.2      |
| 124        | lg               | Immunoglobulin domain                        | 6.5e-08  | 30.6       |
| 127        | mito_carr        | Mitochondrial carrier proteins               | 3e-16    | 58.6       |
| 128        | PP2C             | Protein phosphatase 2C                       | 2.2e-71  | 250.6      |
| 129        | ATP1G1_PLM_M AT8 | ATP1G1/PLM/MAT8 family                       | 3.1e-20  | 80.6       |
| 130        | pfkB             | pfkB family carbohydrate kinase              | 4.5e-42  | 137.1      |
| 133        | ACBP             | Acyl CoA binding protein                     | 4.6e-22  | 86.7       |
| 134        | rxm              | RNA recognition motif.                       | 1.2e-31  | 118.5      |
| 135        | IQ               | IQ calmodulin-binding motif                  | 2.6e-08  | 41.0       |
| 136        | ATP1G1_PLM_M AT8 | ATP1G1/PLM/MAT8 family                       | 9.3e-22  | 85.7       |
| 139        | WH2              | Wiskott Aldrich syndrome homology region 2   | 0.0067   | 23.1       |
| 140        | zf-C2H2          | Zinc finger, C2H2 type                       | 1.7e-82  | 287.5      |
| 141        | Peptidase_S2 6   | Signal peptidase I                           | 5.7e-10  | 35.7       |
| 143        | arf              | ADP-ribosylation factor family               | 1.2e-39  | 145.2      |
| 146        | KRAB             | KRAB box                                     | 7.3e-30  | 112.6      |
| 148        | DUF6             | Integral membrane protein DUF6               | 0.096    | 8.0        |
| 149        | PDEase           | 3'5'-cyclic nucleotide phosphodiesterase     | 3.8e-80  | 231.1      |
| 151        | S4               | S4 domain                                    | 1.1e-08  | 42.3       |
| 153        | tRNA-synt_1d     | tRNA synthetases class I (R)                 | 3.8e-103 | 356.1      |
| 154        | Cyt_reductas e   | FAD/NAD-binding Cytochrome reductase         | 7.8e-60  | 212.2      |
| 155        | ras              | Ras family                                   | 3.6e-28  | 107.0      |
| 157        | actin            | Actin  | 3.8e-26  | 87.1       |

| SEQ ID NO: | PFAM NAME              | DESCRIPTION                                | p-value  | PFAM SCORE |
|------------|------------------------|--|----------|------------|
| 158        | Jacalin                | Jacalin-like lectin domain                 | 0.09     | -24.9      |
| 160        | Zn_carbopept           | Zinc carboxypeptidase                      | 5e-138   | 471.9      |
| 165        | pkinese                | Eukaryotic protein kinase domain           | 5.1e-67  | 236.1      |
| 167        | zf-C3HC4               | Zinc finger, C3HC4 type (RING finger)      | 5.3e-07  | 27.0       |
| 168        | Ribosomal_S15          | Ribosomal protein S15                      | 1.1e-06  | 29.0       |
| 169        | DEAD                   | DEAD/DEAH box helicase                     | 1e-48    | 157.0      |
| 171        | DUF59                  | Domain of unknown function DUF59           | 0.07     | -17.4      |
| 172        | pkinese                | Eukaryotic protein kinase domain           | 3.7e-15  | 58.6       |
| 173        | globin                 | Globin                                     | 4.6e-18  | 67.4       |
| 174        | NW                     | NW domain                                  | 7.3e-06  | 32.9       |
| 175        | ras                    | Ras family                                 | 1e-31    | 118.8      |
| 178        | ATP1G1_PLM_MAT8        | ATP1G1/PLM/MAT8 family                     | 2.5e-17  | 71.0       |
| 179        | zf-C2H2                | Zinc finger, C2H2 type                     | 1.5e-99  | 344.2      |
| 180        | Clq                    | Clq domain                                 | 8.8e-72  | 251.9      |
| 190        | Y_phosphatase          | Protein-tyrosine phosphatase               | 4.9e-287 | 967.0      |
| 191        | efhand                 | EF hand                                    | 7.5e-16  | 66.1       |
| 193        | pkinese                | Eukaryotic protein kinase domain           | 6.5e-82  | 285.6      |
| 194        | bromodomain            | Bromodomain                                | 5.8e-31  | 111.4      |
| 195        | PALP                   | Pyridoxal-phosphate dependent enzyme       | 2.5e-64  | 227.1      |
| 197        | DnaJ                   | DnaJ domain                                | 1.6e-38  | 141.4      |
| 199        | RrnaAD                 | Ribosomal RNA adenine dimethylases         | 0.00018  | 16.9       |
| 200        | acid_phosphatase       | Histidine acid phosphatase                 | 2.5e-10  | 37.2       |
| 201        | WH2                    | Wiskott Aldrich syndrome homology region 2 | 0.00048  | 26.9       |
| 204        | vATP-synt_AC39         | ATP synthase (C/AC39) subunit              | 1.3e-159 | 543.7      |
| 205        | vATP-synt_AC39         | ATP synthase (C/AC39) subunit              | 1.6e-139 | 476.9      |
| 206        | ldl_recept_a           | Low-density lipoprotein receptor domain    | 2.4e-25  | 97.6       |
| 209        | ank                    | Ank repeat                                 | 1.4e-19  | 78.4       |
| 210        | Rhomboid               | Rhomboid family                            | 0.0035   | 1.2        |
| 211        | Clq                    | Clq domain                                 | 1.6e-70  | 247.7      |
| 212        | UQ_con                 | Ubiquitin-conjugating enzyme               | 7.4e-74  | 258.8      |
| 213        | UQ_con                 | Ubiquitin-conjugating enzyme               | 1e-53    | 191.9      |
| 215        | DEAD                   | DEAD/DEAH box helicase                     | 1.8e-43  | 140.4      |
| 216        | PMP22_Claudin          | PMP-22/EMP/MP20/Claudin family             | 4.5e-21  | 83.4       |
| 218        | Glycosyl transferase 2 | Glycosyl transferases                      | 4e-21    | 83.6       |
| 219        | Ig                     | Immunoglobulin domain                      | 0.092    | 10.7       |
| 222        | WD40                   | WD domain, G-beta repeat                   | 7.4e-23  | 89.4       |
| 224        | TPR                    | TPR Domain                                 | 1.2e-08  | 42.1       |
| 225        | DnaJ_CXXCXGXG          | DnaJ central domain (4 repeats)            | 1.5e-38  | 141.5      |
| 226        | DnaJ_CXXCXGXG          | DnaJ central domain (4 repeats)            | 1.5e-38  | 141.5      |
| 229        | HSP70                  | Hsp70 protein                              | 2.4e-54  | 194.0      |
| 230        | GSHPx                  | Glutathione peroxidases                    | 3.4e-47  | 170.2      |
| 231        | tsp_1                  | Thrombospondin type 1 domain               | 0.0075   | 17.1       |
| 233        | cyclin                 | Cyclin                                     | 4.6e-144 | 492.0      |
| 234        | ras                    | Ras family                                 | 4.8e-50  | 179.7      |
| 235        | LRR                    | Leucine Rich Repeat                        | 1.2e-30  | 115.3      |
| 236        | LRR                    | Leucine Rich Repeat                        | 6.7e-29  | 109.4      |
| 237        | PDZ                    | PDZ domain (Also known as DHR or GLGF).    | 1.7e-09  | 45.0       |



| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                  | p-value  | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 244        | dCMP_cyt_deam   | Cytidine and deoxycytidylate deaminase       | 2.5e-05  | 31.1       |
| 245        | ig              | Immunoglobulin domain                        | 6.7e-08  | 30.5       |
| 248        | wnt             | wnt family of developmental signaling protei | 9.1e-270 | 742.6      |
| 250        | mito_carr       | Mitochondrial carrier proteins               | 1.3e-55  | 193.6      |
| 254        | adenylatekinase | Adenylate kinase                             | 1.8e-14  | 55.7       |
| 255        | Cation_efflux   | Cation efflux family                         | 2.8e-33  | 124.0      |
| 256        | SH3             | SH3 domain                                   | 3.9e-14  | 60.4       |
| 257        | Aa_trans        | Transmembrane amino acid transporter protein | 2.6e-52  | 187.2      |
| 258        | adenylatekinase | Adenylate kinase                             | 2.1e-110 | 380.2      |
| 259        | HIT             | HIT family                                   | 8.2e-07  | 25.3       |
| 260        | Bacterial_PQ    | PQQ enzyme repeat                            | 1.6e-15  | 65.0       |
| 262        | proteasome      | Proteasome A-type and B-type                 | 6.5e-64  | 225.7      |
| 267        | pkinase         | Eukaryotic protein kinase domain             | 6.3e-27  | 101.0      |
| 270        | filament        | Intermediate filament proteins               | 3.2e-150 | 512.5      |
| 271        | Choline_kinase  | Choline/ethanolamine kinase                  | 2e-67    | 237.4      |
| 277        | Ribosomal_S7    | Ribosomal protein S7p/S5e                    | 3.3e-20  | 80.6       |
| 279        | pkinase         | Eukaryotic protein kinase domain             | 3.3e-77  | 269.9      |
| 280        | WD40            | WD domain, G-beta repeat                     | 7.8e-73  | 255.4      |
| 281        | WD40            | WD domain, G-beta repeat                     | 7.8e-73  | 255.4      |
| 284        | zf-DHHC         | DHHC zinc finger domain                      | 4.6e-24  | 93.4       |
| 287        | Exonuclease     | Exonuclease                                  | 1.4e-67  | 238.0      |
| 291        | SAM             | SAM domain (Sterile alpha motif)             | 0.034    | 11.2       |
| 292        | SAM             | SAM domain (Sterile alpha motif)             | 0.034    | 11.2       |
| 294        | zf-C2H2         | Zinc finger, C2H2 type                       | 1.4e-29  | 111.7      |
| 295        | zf-C2H2         | Zinc finger, C2H2 type                       | 2.2e-125 | 430.0      |
| 296        | mito_carr       | Mitochondrial carrier proteins               | 4.1e-59  | 205.5      |
| 297        | HMG_box         | HMG (high mobility group) box                | 6.7e-29  | 109.4      |
| 302        | Glycos_transf_4 | Glycosyl transferase                         | 5e-87    | 302.5      |
| 304        | tRNA-synt_2     | tRNA synthetases class II (D, K and N)       | 1.1e-84  | 294.8      |
| 305        | KRAB            | KRAB box                                     | 2e-44    | 161.0      |
| 306        | rrm             | RNA recognition motif.                       | 2.7e-44  | 160.6      |
| 308        | 7tm_1           | 7 transmembrane receptor (rhodopsin family)  | 5.2e-39  | 126.1      |
| 309        | DNA_polymeraseX | DNA polymerase X family                      | 2.4e-64  | 227.2      |
| 311        | F-box           | F-box domain.                                | 9.5e-08  | 39.2       |
| 312        | ig              | Immunoglobulin domain                        | 6.8e-19  | 65.9       |
| 313        | Ets             | Ets-domain                                   | 8.1e-60  | 192.3      |
| 315        | Kelch           | Kelch motif                                  | 1.3e-106 | 367.6      |
| 317        | arf             | ADP-ribosylation factor family               | 3.2e-35  | 130.4      |
| 318        | sugar_tr        | Sugar (and other) transporter                | 0.0003   | -73.1      |
| 320        | pkinase         | Eukaryotic protein kinase domain             | 8.1e-83  | 288.6      |
| 322        | pkinase         | Eukaryotic protein kinase domain             | 4.9e-81  | 282.6      |
| 324        | Xlink           | Extracellular link domain                    | 4.5e-143 | 331.5      |
| 326        | ARID            | ARID DNA binding domain                      | 5.1e-37  | 136.4      |
| 327        | HMG_box         | HMG (high mobility group) box                | 6.7e-29  | 109.4      |
| 328        | cadherin        | Cadherin domain                              | 8.1e-81  | 281.9      |
| 331        | chromo          | 'chromo' (CHRRomatin Organization Modifier)  | 4e-18    | 66.7       |
| 333        | Peptidase_M2_2  | Glycoprotease family                         | 1.2e-136 | 467.4      |

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                  | p-value  | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 335        | vwa             | von Willebrand factor type A domain          | 2.3e-07  | 37.9       |
| 339        | ras             | Ras family                                   | 7.8e-07  | -59.1      |
| 340        | zf-C2H2         | Zinc finger, C2H2 type                       | 8.2e-64  | 225.4      |
| 342        | zf-C2H2         | Zinc finger, C2H2 type                       | 2.4e-85  | 297.0      |
| 343        | ig              | Immunoglobulin domain                        | 0.0005   | 18.0       |
| 346        | pkinase         | Eukaryotic protein kinase domain             | 6.5e-65  | 229.1      |
| 347        | pkinase         | Eukaryotic protein kinase domain             | 6.5e-65  | 229.1      |
| 351        | EGF             | EGF-like domain                              | 8.5e-20  | 79.2       |
| 352        | ank             | Ank repeat                                   | 2.5e-101 | 350.0      |
| 354        | TBC             | TBC domain                                   | 5.1e-15  | 63.3       |
| 355        | PHD             | PHD-finger                                   | 3.2e-07  | 37.4       |
| 358        | DUF6            | Integral membrane protein DUF6               | 0.033    | 15.8       |
| 359        | zf-C2H2         | Zinc finger, C2H2 type                       | 7.4e-20  | 79.4       |
| 361        | ank             | Ank repeat                                   | 6.6e-34  | 126.1      |
| 362        | ArfGap          | Putative GTP-ase activating protein for Arf  | 4.7e-53  | 189.7      |
| 363        | efhand          | EF hand                                      | 5.4e-10  | 46.6       |
| 367        | LRR             | Leucine Rich Repeat                          | 8.8e-44  | 158.9      |
| 368        | laminin_G       | Laminin G domain                             | 1.5e-33  | 121.7      |
| 369        | PP2C            | Protein phosphatase 2C                       | 5.3e-20  | 73.9       |
| 372        | LIM             | LIM domain containing proteins               | 9.9e-15  | 57.1       |
| 373        | KRAB            | KRAB box                                     | 4.8e-23  | 90.0       |
| 376        | ion_trans       | Ion transport protein                        | 2.9e-09  | -4.2       |
| 377        | Beach           | Beige/BEACH domain                           | 4.9e-208 | 704.5      |
| 380        | pkinase         | Eukaryotic protein kinase domain             | 1.6e-94  | 327.5      |
| 381        | AMP-binding     | AMP-binding enzyme                           | 1.4e-07  | -140.3     |
| 382        | HECT            | HECT-domain (ubiquitin-transferase).         | 1.3e-07  | -13.5      |
| 384        | ank             | Ank repeat                                   | 2.5e-101 | 350.0      |
| 386        | ig              | Immunoglobulin domain                        | 9.5e-05  | 23.6       |
| 388        | zf-C2H2         | Zinc finger, C2H2 type                       | 1.7e-42  | 154.6      |
| 389        | ig              | Immunoglobulin domain                        | 2.8e-15  | 54.3       |
| 390        | mito_carr       | Mitochondrial carrier proteins               | 3.5e-67  | 233.2      |
| 392        | TPR             | TPR Domain                                   | 6.1e-17  | 69.7       |
| 393        | SH3             | SH3 domain                                   | 3.5e-09  | 43.9       |
| 394        | AAA             | ATPases associated with various cellular act | 4.1e-21  | 83.6       |
| 396        | spectrin        | Spectrin repeat                              | 2.1e-67  | 237.3      |
| 397        | zf-C2H2         | Zinc finger, C2H2 type                       | 0.0066   | 23.1       |
| 399        | fn3             | Fibronectin type III domain                  | 4.1e-102 | 352.6      |
| 400        | WD40            | WD domain, G-beta repeat                     | 0.00049  | 26.8       |
| 401        | E1_dehydrog     | Dehydrogenase E1 component                   | 3e-119   | 409.6      |
| 402        | fn3             | Fibronectin type III domain                  | 0        | 1719.6     |
| 404        | LRR             | Leucine Rich Repeat                          | 2.1e-10  | 48.0       |
| 405        | cadherin        | Cadherin domain                              | 8.1e-81  | 281.9      |
| 406        | zf-CXXC         | CXXC zinc finger                             | 5e-15    | 63.4       |
| 410        | RhoGEF          | RhoGEF domain                                | 1.1e-23  | 92.1       |
| 411        | F-box           | F-box domain.                                | 4.2e-06  | 33.7       |
| 412        | SNF2_N          | SNF2 and others N-terminal domain            | 5.0e-16  | 61.6       |
| 415        | CPSase_L_cha in | Carbamoyl-phosphate synthase (CPSase)        | 1.5e-172 | 586.6      |
| 418        | LRR             | Leucine Rich Repeat                          | 3.8e-24  | 93.6       |
| 419        | DENN            | DENN (AEX-3) domain                          | 2e-58    | 207.5      |
| 420        | RasGEF          | RasGEF domain                                | 8.1e-43  | 155.7      |
| 421        | ank             | Ank repeat                                   | 1.4e-153 | 523.7      |
| 424        | G-patch         | G-patch domain                               | 1e-19    | 78.9       |
| 425        | pkinase         | Eukaryotic protein kinase domain             | 2.2e-31  | 117.1      |
| 426        | Plexin_repeat   | Plexin repeat                                | 0.0023   | 24.6       |
| 427        | Plexin_repca    | Plexin repeat                                | 0.0023   | 24.6       |

| SEQ ID NO: | PFAM NAME           | DESCRIPTION                                  | p-value  | PFAM SCORE |
|------------|---------------------|--|----------|------------|
|            | t                   |  |          |            |
| 429        | zf-C3HC4            | Zinc finger, C3HC4 type (RING finger)        | 8.6e-11  | 39.2       |
| 431        | DEAD                | DEAD/DEAH box helicase                       | 1e-66    | 214.0      |
| 432        | SH3                 | SH3 domain                                   | 3.4e-16  | 67.2       |
| 433        | GTP_CDC             | Cell division protein                        | 2.1e-114 | 393.5      |
| 436        | Collagen            | Collagen triple helix repeat (20 copies)     | 4.6e-194 | 658.1      |
| 438        | Ricin_B_lectin      | Similarity to lectin domain of ricin b       | 0.0085   | 10.5       |
| 441        | Alpha_adaptin_C     | Alpha adaptin carboxyl-terminal domain       | 1.2e-256 | 866.0      |
| 442        | Alpha_adaptin_C     | Alpha adaptin carboxyl-terminal domain       | 1.8e-235 | 795.7      |
| 443        | PDZ                 | PDZ domain (Also known as DHR or GLGF).      | 1.9e-65  | 230.9      |
| 445        | LON                 | ATP-dependent protease La (LON) domain       | 0.00012  | -17.1      |
| 446        | ig                  | Immunoglobulin domain                        | 0.00011  | 20.1       |
| 451        | sushi               | Sushi domain (SCR repeat)                    | 1.4e-18  | 75.2       |
| 452        | fn3                 | Fibronectin type III domain                  | 1.5e-06  | 35.2       |
| 454        | pyridoxal_dependent | Pyridoxal-dependent decarboxylase conse      | 8.3e-14  | 50.3       |
| 456        | kinesin             | Kinesin motor domain                         | 4.9e-217 | 734.4      |
| 457        | neur_chan           | Neurotransmitter-gated ion-channel           | 1e-175   | 597.1      |
| 458        | Josephin            | Josephin                                     | 0.0002   | 18.7       |
| 468        | bZIP                | bZIP transcription factor                    | 1.7e-07  | 31.8       |
| 470        | NTP_transferase     | Nucleotidyl transferase                      | 6.3e-06  | -26.3      |
| 471        | WD40                | WD domain, G-beta repeat                     | 2e-28    | 107.9      |
| 473        | LIM                 | LIM domain containing proteins               | 0.00021  | 20.7       |
| 477        | zf-RanBP            | Zn-finger in Ran binding protein and others. | 0.028    | 21.0       |
| 479        | WD40                | WD domain, G-beta repeat                     | 6.5e-18  | 73.0       |
| 480        | KRAB                | KRAB box                                     | 1e-31    | 118.8      |
| 481        | ArfGap              | Putative GTP-ase activating protein for Arf  | 8.4e-66  | 232.0      |
| 485        | SH2                 | Src homology domain 2                        | 0.011    | 11.4       |
| 486        | Clg                 | Clg domain                                   | 4.3e-74  | 259.6      |
| 487        | darm                | Double-stranded RNA binding motif            | 1.1e-47  | 171.9      |
| 489        | zf-C2H2             | Zinc finger, C2H2 type                       | 4.8e-153 | 521.9      |
| 490        | Alpha_adaptin_C     | Alpha adaptin carboxyl-terminal domain       | 3.4e-222 | 751.6      |
| 492        | SKI                 | Shikimate kinase                             | 1.2e-10  | 48.8       |
| 497        | ENV_polyprotein     | ENV polyprotein (coat polyprotein)           | 2.6e-22  | 77.6       |
| 498        | abhydrolase_2       | Phospholipase/Carboxylesterase               | 0.041    | -48.1      |
| 500        | rrm                 | RNA recognition motif.                       | 5.4e-34  | 126.4      |
| 501        | WW                  | WW domain                                    | 4.6e-18  | 73.4       |
| 502        | ig                  | Immunoglobulin domain                        | 1.1e-10  | 39.5       |
| 504        | abhydrolase         | alpha/beta hydrolase fold                    | 0.045    | -3.6       |
| 505        | vwa                 | von Willebrand factor type A domain          | 7.1e-62  | 219.0      |
| 508        | Na_K_ATPase_C       | Na+/K+ ATPase C-terminus                     | 2.3e-145 | 496.3      |
| 509        | Exonuclease         | Exonuclease                                  | 1.3e-56  | 201.5      |
| 510        | Glycosyl_transf_1   | Glycosyl transferases group 1                | 2.9e-06  | 27.0       |
| 511        | Glycosyl_transf_1   | Glycosyl transferases group 1                | 2.9e-06  | 27.0       |
| 512        | Glycosyl_transf_1   | Glycosyl transferases group 1                | 1.9e-09  | 38.5       |
| 514        | pro_isomerase       | Cyclophilin type peptidyl-prolyl cis-tr      | 1.8e-63  | 221.4      |

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                   | p-value  | PFAM SCORE |
|------------|-----------------|---|----------|------------|
| 515        | EGF             | EGF-like domain                               | 1.9e-18  | 74.7       |
| 516        | Surp            | Surp module                                   | 4.3e-38  | 140.0      |
| 523        | ig              | Immunoglobulin domain                         | 3.3e-06  | 25.0       |
| 526        | UBX             | UBX domain                                    | 1.1e-34  | 128.6      |
| 528        | adh_zinc        | Zinc-binding dehydrogenases                   | 2.7e-34  | 127.4      |
| 530        | SAM             | SAM domain (Sterile alpha motif)              | 0.046    | 10.0       |
| 531        | adh_short       | short chain dehydrogenase                     | 0.0025   | -34.1      |
| 532        | mito_carr       | Mitochondrial carrier proteins                | 2.5e-81  | 281.7      |
| 533        | mito_carr       | Mitochondrial carrier proteins                | 2e-61    | 213.5      |
| 534        | thiolase        | Thiolase                                      | 3.5e-183 | 622.0      |
| 535        | PMO-like        | Flavin-binding monooxygenase-like             | 0        | 1153.7     |
| 536        | SCAN            | SCAN domain                                   | 4e-55    | 196.6      |
| 537        | tRNA-synt_1     | tRNA synthetases class I (I, L, M and V)      | 3.1e-136 | 466.0      |
| 538        | tRNA-synt_1     | tRNA synthetases class I (I, L, M and V)      | 3.1e-136 | 466.0      |
| 539        | tRNA-synt_1     | tRNA synthetases class I (I, L, M and V)      | 1.9e-117 | 403.6      |
| 540        | tRNA-synt_1     | tRNA synthetases class I (I, L, M and V)      | 3.1e-136 | 466.0      |
| 541        | vATP-synt_E     | ATP synthase (E/31 kDa) subunit               | 5.9e-85  | 295.7      |
| 543        | zf-C2H2         | Zinc finger, C2H2 type                        | 5.5e-69  | 242.6      |
| 544        | DUF101          | Protein of unknown function DUF101            | 8.5e-38  | 139.0      |
| 545        | TGFb_propeptide | TGF-beta propeptide                           | 1.1e-67  | 238.2      |
| 547        | WD40            | WD domain, G-beta repeat                      | 2.6e-32  | 120.8      |
| 548        | RHD             | Rel homology domain (RHD)                     | 1.6e-238 | 686.2      |
| 549        | MMR_HSR1        | GTPase of unknown function                    | 5.4e-67  | 236.0      |
| 551        | HECT            | HECT-domain (ubiquitin-transferase)           | 4.3e-127 | 435.6      |
| 554        | MHC_II_alpha    | Class II histocompatibility antigen, alp      | 3.5e-74  | 259.8      |
| 555        | zf-UBR1         | Putative zinc finger in N-recogin             | 3.3e-16  | 67.3       |
| 556        | Kelch           | Kelch motif                                   | 5.5e-29  | 109.7      |
| 561        | AMP-binding     | AMP-binding enzyme                            | 2.8e-06  | -163.7     |
| 562        | PABP            | Poly-adenylate binding protein, unique domain | 4.9e-38  | 139.8      |
| 564        | Gag_p30         | Gag P30 core shell protein                    | 1.2e-67  | 238.2      |
| 566        | PWWP            | PWWP domain                                   | 8.1e-16  | 66.0       |
| 567        | SCAN            | SCAN domain                                   | 7.3e-68  | 238.9      |
| 569        | pkinase         | Eukaryotic protein kinase domain              | 1.5e-84  | 294.3      |
| 570        | pkinase         | Eukaryotic protein kinase domain              | 1.5e-84  | 294.3      |
| 571        | CN_hydrolase    | Carbon-nitrogen hydrolase                     | 0.00081  | -79.7      |
| 572        | myosin_head     | Myosin head (motor domain)                    | 0        | 1495.2     |
| 573        | myosin_head     | Myosin head (motor domain)                    | 0        | 1490.4     |
| 575        | Surp            | Surp module                                   | 1.7e-23  | 91.5       |
| 576        | Surp            | Surp module                                   | 1.7e-23  | 91.5       |
| 577        | DNA_pol_B       | DNA polymerase family B                       | 0        | 1138.6     |
| 578        | PDZ             | PDZ domain (Also known as DHR or GLGF)        | 8.3e-09  | 42.7       |
| 579        | LRR             | Leucine Rich Repeat                           | 4.9e-21  | 83.3       |
| 580        | neur_chan       | Neurotransmitter-gated ion-channel            | 5.9e-177 | 601.3      |
| 583        | sushi           | Sushi domain (SCR repeat)                     | 0        | 1673.0     |
| 584        | DEAD            | DEAD/DEAH box, helicase                       | 7.3e-36  | 116.3      |
| 586        | KH-domain       | KH domain                                     | 2.9e-13  | 57.5       |
| 587        | G-patch         | G-patch domain                                | 2.3e-14  | 61.2       |
| 589        | LIM             | LIM domain containing proteins                | 2.3e-36  | 133.4      |
| 590        | bromodomain     | Bromodomain                                   | 6.6e-32  | 114.7      |
| 591        | bromodomain     | Bromodomain                                   | 6.6e-32  | 114.7      |

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                | p-value  | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 592        | hormone_rec     | Ligand-binding domain of nuclear hormone   | 3.5e-22  | 87.1       |
| 593        | PHD             | PHD-finger                                 | 3.8e-12  | 53.8       |
| 594        | cadherin        | Cadherin domain                            | 4.2e-99  | 342.7      |
| 596        | pkinase         | Eukaryotic protein kinase domain           | 5e-92    | 319.2      |
| 597        | WD40            | WD domain, G-beta repeat                   | 0.00054  | 26.7       |
| 600        | FG-GAP          | FG-GAP repeat                              | 4.3e-75  | 262.9      |
| 602        | G_Adapt_CT      | Gamma-adaptin, C-terminus                  | 1.1e-53  | 191.8      |
| 603        | pkinase         | Eukaryotic protein kinase domain           | 2.3e-86  | 300.4      |
| 605        | Collagen        | Collagen triple helix repeat (20 copies)   | 8e-42    | 152.4      |
| 606        | mito_carr       | Mitochondrial carrier proteins             | 6.3e-67  | 232.3      |
| 608        | PWWP            | PWWP domain                                | 2.6e-28  | 107.5      |
| 609        | PWWP            | PWWP domain                                | 2.6e-28  | 107.5      |
| 613        | CAP_GLY         | CAP-Gly domain                             | 0.0046   | 20.1       |
| 615        | RFX_DNA_binding | RFX DNA-binding domain                     | 5.2e-54  | 192.9      |
| 616        | kinesin         | Kinesin motor domain                       | 1.1e-81  | 284.8      |
| 617        | kinesin         | Kinesin motor domain                       | 8.4e-80  | 278.5      |
| 618        | zf-C3HC4        | Zinc finger, C3HC4 type (RING finger)      | 0.0098   | 13.1       |
| 620        | MATH            | MATH domain                                | 7.8e-05  | 22.2       |
| 621        | Y_phosphatase   | Protein-tyrosine phosphatase               | 1.4e-32  | 121.6      |
| 622        | pkinase         | Eukaryotic protein kinase domain           | 4.4e-40  | 146.6      |
| 623        | BNR             | BNR repeat                                 | 2.1e-11  | 51.3       |
| 624        | molybdopterin   | Prokaryotic molybdopterine oxidoreductase  | 1.4e-12  | 42.2       |
| 625        | TPR             | TPR Domain                                 | 1.1e-17  | 72.2       |
| 627        | cNMP_binding    | Cyclic nucleotide-binding domain           | 3.7e-58  | 206.6      |
| 630        | adh_short       | short chain dehydrogenase                  | 5e-17    | 70.0       |
| 631        | zf-C2H2         | Zinc finger, C2H2 type                     | 2.1e-88  | 307.1      |
| 632        | rrm             | RNA recognition motif                      | 4e-05    | 30.5       |
| 635        | pkinase         | Eukaryotic protein kinase domain           | 1.6e-104 | 360.7      |
| 636        | Fork_head       | Fork head domain                           | 5.9e-27  | 103.0      |
| 637        | pkinase         | Eukaryotic protein kinase domain           | 3.8e-70  | 246.5      |
| 642        | TPR             | TPR Domain                                 | 4.8e-08  | 40.1       |
| 643        | efhand          | EF hand                                    | 1.9e-27  | 104.6      |
| 647        | SNF2_N          | SNF2 and others N-terminal domain          | 1.2e-101 | 351.1      |
| 648        | PseudoU_synth_2 | RNA pseudouridylate synthase               | 1.9e-55  | 197.6      |
| 650        | zf-C2H2         | Zinc finger, C2H2 type                     | 0.0087   | 22.7       |
| 651        | ank             | Ank repeat                                 | 1.3e-17  | 71.9       |
| 652        | I_LWEQ          | I/LWEQ domain                              | 9.5e-101 | 341.0      |
| 653        | neur_chan       | Neurotransmitter-gated ion-channel         | 4.1e-171 | 581.8      |
| 654        | tsp_1           | Thrombospondin type 1 domain               | 4.1e-47  | 169.9      |
| 659        | FH2             | Formin Homology 2 Domain                   | 1e-107   | 371.2      |
| 661        | pou             | Pou domain - N-terminal to homeobox domain | 5.3e-45  | 162.9      |
| 662        | C2              | C2 domain                                  | 6.7e-19  | 76.2       |
| 663        | C2              | C2 domain                                  | 6.7e-19  | 76.2       |
| 664        | C2              | C2 domain                                  | 6.7e-19  | 76.2       |
| 667        | GST             | Glutathione S-transferases                 | 9.3e-34  | 114.4      |
| 668        | LRR             | Leucine Rich Repeat                        | 9.3e-31  | 115.6      |
| 670        | spectrin        | Spectrin repeat                            | 4e-57    | 203.2      |
| 671        | I_LWEQ          | I/LWEQ domain                              | 9.5e-101 | 341.0      |
| 672        | ABC_tran        | ABC transporter                            | 5.3e-60  | 212.8      |
| 674        | WD40            | WD domain, G-beta repeat                   | 4.8e-24  | 93.3       |

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                  | p-value  | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 675        | WD40            | WD domain, G-beta repeat                     | 4.8e-24  | 93.3       |
| 676        | LRR             | Leucine Rich Repeat                          | 0.0015   | 25.2       |
| 679        | zf-CCCH         | Zinc finger C-x8-C-x5-C-x3-H type            | 2.6e-29  | 107.7      |
| 680        | zf-C2H2         | Zinc finger, C2H2 type                       | 5.2e-05  | 30.1       |
| 681        | CH              | Calponin homology (CH) domain                | 2.4e-17  | 71.1       |
| 682        | DSPc            | Dual specificity phosphatase, catalytic doma | 4.3e-43  | 156.6      |
| 683        | zf-C3HC4        | Zinc finger, C3HC4 type (RING finger)        | 0.051    | 10.8       |
| 687        | Synapsin        | Synapsin                                     | 0        | 1890.8     |
| 689        | PR55            | Protein phosphatase 2A regulatory subunit PR | 0        | 1038.8     |
| 691        | homeobox        | Homeobox domain                              | 8.5e-30  | 112.4      |
| 696        | Peptidase_M24   | metallopeptidase family M24                  | 2.6e-59  | 210.5      |
| 697        | RhoGEF          | RhoGEF domain                                | 9.5e-35  | 128.9      |
| 698        | PHD             | PHD-finger                                   | 0.008    | 9.3        |
| 701        | zf-C2H2         | Zinc finger, C2H2 type                       | 5.5e-123 | 422.0      |
| 702        | Sulfatase       | Sulfatase                                    | 3e-231   | 781.6      |
| 703        | zf-C2H2         | Zinc finger, C2H2 type                       | 5.7e-20  | 79.8       |
| 707        | Acyl_transf     | Acyl transferase domain                      | 1.1e-22  | 88.8       |
| 708        | WD40            | WD domain, G-beta repeat                     | 4.8e-19  | 76.7       |
| 710        | Ran_BP1         | RanBP1 domain.                               | 8.4e-06  | -7.3       |
| 713        | DEAD            | DEAD/DEAH box helicase                       | 9.9e-42  | 134.9      |
| 714        | PH              | PH domain                                    | 1.6e-09  | 39.0       |
| 715        | DSPc            | Dual specificity phosphatase, catalytic doma | 1.5e-37  | 138.2      |
| 717        | Sialyltransf    | Sialyltransferase family                     | 7.5e-31  | 115.9      |
| 718        | ig              | Immunoglobulin domain                        | 1e-29    | 100.8      |
| 719        | integrin_B      | Integrins, beta chain                        | 0        | 1125.4     |
| 720        | zf-C3HC4        | Zinc finger, C3HC4 type (RING finger)        | 1.1e-08  | 32.4       |
| 722        | Peptidase_C2    | Calpain family cysteine protease             | 3e-145   | 495.9      |
| 723        | ig              | Immunoglobulin domain                        | 2.2e-05  | 22.4       |
| 724        | F-box           | F-box domain.                                | 0.007    | 23.0       |
| 725        | Nop             | Putative snRNA binding domain                | 8.1e-58  | 205.5      |
| 726        | Nop             | Putative snRNA binding domain                | 8.1e-58  | 205.5      |
| 727        | WD40            | WD domain, G-beta repeat                     | 7.5e-26  | 99.3       |
| 730        | darm            | Double-stranded RNA binding motif            | 0.027    | 12.1       |
| 731        | dynamin         | Dynamin family                               | 4.2e-16  | 66.9       |
| 733        | zf-CCCH         | Zinc finger C-x8-C-x5-C-x3-H type            | 2.8e-10  | 41.7       |
| 735        | CDP-OH_P_transf | CDP-alcohol phosphatidyltransferase          | 4.2e-26  | 100.1      |
| 738        | DEAD            | DEAD/DEAH box helicase                       | 8.6e-57  | 182.5      |
| 739        | TSC22           | TSC-22/dip/bun family                        | 6.5e-32  | 119.5      |
| 742        | ras             | Ras family                                   | 2.2e-100 | 346.9      |
| 743        | PMI_typeI       | Phosphomannose isomerase type I              | 1.2e-243 | 822.9      |
| 747        | trypsin         | Trypsin                                      | 6.4e-88  | 279.4      |
| 748        | kazal           | Kazal-type serine protease inhibitor domain  | 2.2e-52  | 187.4      |
| 749        | efhand          | EF hand                                      | 6.3e-06  | 33.1       |
| 751        | PHD             | PHD-finger                                   | 4.9e-16  | 66.7       |
| 752        | zf-C2H2         | Zinc finger, C2H2 type                       | 3.2e-21  | 83.9       |
| 753        | Hydrolase       | haloacid dehalogenase-like hydrolase         | 6.1e-11  | 49.8       |
| 754        | Ribosomal_L39   | Ribosomal L39 protein                        | 0.00018  | 26.7       |
| 755        | PH              | PH domain                                    | 3.6e-14  | 55.7       |
| 758        | SCAN            | SCAN domain                                  | 1.4e-53  | 191.5      |
| 759        | PA              | PA domain                                    | 0.0065   | 23.1       |
| 760        | arf             | ADP-ribosylation factor family               | 2.2e-19  | 77.8       |
| 761        | CIDE-N          | CIDE-N domain                                | 2.2e-40  | 147.6      |

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                 | p-value  | PFAM SCORE |
|------------|-----------------|---|----------|------------|
| 762        | histone         | Core histone H2A/H2B/H3/H4                  | 9.9e-53  | 188.6      |
| 763        | zf-MYND         | MYND finger                                 | 4.1e-14  | 60.3       |
| 764        | pou             | Pou domain - N-terminal to homeobox domain  | 1e-52    | 188.6      |
| 767        | vwc             | von Willebrand factor type C domain         | 2.9e-34  | 127.3      |
| 769        | efhand          | EF hand                                     | 4.8e-11  | 50.1       |
| 770        | zf-C4           | Zinc finger, C4 type (two domains)          | 2.4e-53  | 181.6      |
| 772        | ras             | Ras family                                  | 7e-90    | 312.0      |
| 773        | Sulfatase       | Sulfatase                                   | 1e-142   | 487.5      |
| 775        | zf-C2H2         | Zinc finger, C2H2 type                      | 1.1e-12  | 55.5       |
| 776        | zf-C2H2         | Zinc finger, C2H2 type                      | 1.1e-12  | 55.5       |
| 777        | zf-C2H2         | Zinc finger, C2H2 type                      | 1.1e-12  | 55.5       |
| 778        | rrm             | RNA recognition motif.                      | 2.1e-32  | 121.1      |
| 779        | G6PD            | Glucose-6-phosphate dehydrogenase           | 1.5e-76  | 236.6      |
| 780        | spectrin        | Spectrin repeat                             | 3.7e-29  | 110.3      |
| 781        | mito_carr       | Mitochondrial carrier proteins              | 4.6e-57  | 198.5      |
| 782        | SCAN            | SCAN domain                                 | 1.3e-24  | 95.2       |
| 783        | PDZ             | PDZ domain (Also known as DHR or GLGF).     | 4.1e-07  | 37.1       |
| 785        | DEAD            | DEAD/DEAH box helicase                      | 6e-06    | 21.7       |
| 786        | ras             | Ras family                                  | 5.3e-39  | 143.0      |
| 787        | RNase HII       | Ribonuclease HII                            | 2.5e-67  | 237.1      |
| 790        | PI3_PI4_kinase  | Phosphatidylinositol 3- and 4-kinases       | 5.4e-108 | 372.2      |
| 795        | cadherin        | Cadherin domain                             | 2.5e-40  | 147.4      |
| 796        | ARID            | ARID DNA binding domain                     | 1.6e-20  | 81.6       |
| 797        | trypsin         | Trypsin                                     | 9.9e-20  | 64.8       |
| 799        | CH              | Calponin homology (CH) domain               | 3.7e-15  | 63.8       |
| 801        | Gal-bind_lectin | Vertebrate galactoside-binding lectin       | 4.1e-25  | 88.7       |
| 803        | WD40            | WD domain, G-beta repeat                    | 0.00082  | 26.1       |
| 806        | TBC             | TBC domain                                  | 1.8e-26  | 101.4      |
| 807        | TBC             | TBC domain                                  | 1.8e-26  | 101.4      |
| 808        | CN_hydrolase    | Carbon-nitrogen hydrolase                   | 8.8e-80  | 278.5      |
| 811        | CBFD_NFYB_HMF   | Histone-like transcription factor           | 6e-14    | 59.8       |
| 812        | adh_short       | short chain dehydrogenase                   | 8.1e-20  | 79.3       |
| 814        | IMP4            | Domain of unknown function                  | 3.3e-71  | 250.0      |
| 815        | zf-C2H2         | Zinc finger, C2H2 type                      | 8.2e-66  | 232.1      |
| 816        | Pept_tRNA_hydro | Peptidyl-tRNA hydrolase                     | 1.6e-37  | 138.0      |
| 817        | ARID            | ARID DNA binding domain                     | 2.5e-18  | 74.3       |
| 826        | IF5_eIF4_eIF2   | eIF4-gamma/eIF5/eIF2-epsilon                | 1.6e-32  | 121.5      |
| 830        | ArfGap          | Putative GTP-ase activating protein for Arf | 1.5e-53  | 191.3      |
| 831        | LRR             | Leucine Rich Repeat                         | 2.1e-26  | 101.1      |
| 832        | laminin_EGF     | Laminin EGF-like (Domains III and V)        | 2e-57    | 204.2      |
| 839        | rrm             | RNA recognition motif.                      | 1.3e-22  | 88.5       |
| 840        | Y_phosphatase   | Protein-tyrosine phosphatase                | 2.6e-119 | 409.8      |
| 841        | pkinase         | Eukaryotic protein kinase domain            | 3.4e-100 | 346.3      |
| 844        | Ribosomal_L22e  | Ribosomal L22e protein family               | 1e-64    | 228.4      |
| 846        | IBR             | IBR domain                                  | 9e-15    | 62.5       |
| 849        | zf-C3HC4        | Zinc finger, C3HC4 type (RING finger)       | 7.4e-07  | 26.5       |
| 850        | zf-C3HC4        | Zinc finger, C3HC4 type (RING finger)       | 0.00016  | 18.9       |
| 851        | SET             | SET domain                                  | 5e-30    | 113.2      |
| 852        | SRCR            | Scavenger receptor cysteine-                | 0        | 1025.4     |

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                | p-value  | PFAM SCORE |
|------------|-----------------|--|----------|------------|
|            |                 | rich domain                                |          |            |
| 853        | SRCR            | Scavenger receptor cysteine-rich domain    | 0        | 1025.4     |
| 857        | lactamase_B     | Metallo-beta-lactamase superfamily         | 0.012    | -6.0       |
| 858        | COX6A           | Cytochrome c oxidase subunit VIa           | 3.4e-58  | 206.7      |
| 859        | rrm             | RNA recognition motif                      | 5.4e-45  | 162.9      |
| 861        | PRK             | Phosphoribulokinase                        | 5.1e-62  | 219.4      |
| 863        | mito_carr       | Mitochondrial carrier proteins             | 2.9e-53  | 185.5      |
| 864        | HSP90           | Hsp90 protein                              | 4.7e-158 | 538.5      |
| 866        | lg              | Immunoglobulin domain                      | 4e-12    | 44.1       |
| 867        | zf-C2H2         | Zinc finger, C2H2 type                     | 7e-135   | 461.5      |
| 872        | histone         | Core histone H2A/H2B/H3/H4                 | 4.9e-41  | 149.8      |
| 874        | CPSase_L_chain  | Carbamoyl-phosphate synthase (CPSase)      | 2.1e-218 | 739.0      |
| 879        | Ribosomal_S12e  | Ribosomal protein S12e                     | 2.1e-98  | 340.3      |
| 882        | serpin          | Serpins (serine protease inhibitors)       | 2.5e-42  | 145.7      |
| 883        | Patatin         | Patatin                                    | 1.2e-51  | 182.0      |
| 884        | RA              | Ras association (RalGDS/AF-6) domain       | 0.044    | 8.0        |
| 887        | DUF92           | Integral membrane protein DUF92            | 2.7e-12  | 54.3       |
| 889        | sugar_tr        | Sugar (and other) transporter              | 8.2e-63  | 222.1      |
| 893        | DUF28           | Domain of unknown function DUF28           | 1.3e-43  | 158.3      |
| 896        | IP_trans        | Phosphatidylinositol transfer protein      | 6.5e-98  | 338.7      |
| 898        | DEAD            | DEAD/DEAH box helicase                     | 1.5e-48  | 156.5      |
| 899        | KE2             | KE2 family protein                         | 7e-61    | 215.7      |
| 900        | KE2             | KE2 family protein                         | 4.3e-51  | 183.2      |
| 901        | zf-C2H2         | Zinc finger, C2H2 type                     | 2.7e-57  | 203.8      |
| 902        | ras             | Ras family                                 | 2.3e-75  | 263.8      |
| 904        | TPR             | TPR Domain                                 | 3.2e-22  | 87.2       |
| 906        | GBP             | Guanylate-binding protein                  | 8.9e-253 | 853.1      |
| 907        | GBP             | Guanylate-binding protein                  | 1.1e-239 | 809.6      |
| 908        | WD40            | WD domain, G-beta repeat                   | 2.6e-26  | 100.8      |
| 909        | PH              | PH domain                                  | 1.3e-09  | 39.4       |
| 910        | zf-C2H2         | Zinc finger, C2H2 type                     | 2.5e-39  | 144.1      |
| 913        | Epimerase       | NAD dependent epimerase/dehydratase family | 5e-07    | -88.5      |
| 921        | TBC             | TBC domain                                 | 1.5e-09  | 30.7       |
| 922        | WD40            | WD domain, G-beta repeat                   | 1.6e-25  | 98.2       |
| 923        | WD40            | WD domain, G-beta repeat                   | 8.2e-07  | 36.1       |
| 924        | Hydrolase       | haloacid dehalogenase-like hydrolase       | 2.9e-05  | 29.1       |
| 925        | UQ_con          | Ubiquitin-conjugating enzyme               | 0.00033  | -27.6      |
| 926        | CH              | Calponin homology (CH) domain              | 3.3e-53  | 190.2      |
| 928        | WD40            | WD domain, G-beta repeat                   | 5.9e-48  | 172.7      |
| 929        | zf-C3HC4        | Zinc finger, C3HC4 type (RING finger)      | 3.1e-10  | 37.4       |
| 930        | Ribul_P_3_epim  | Ribulose-phosphate 3 epimerase family      | 7.2e-105 | 361.8      |
| 931        | Ribul_P_3_epim  | Ribulose-phosphate 3 epimerase family      | 1.2e-96  | 334.4      |
| 936        | C2              | C2 domain                                  | 2.2e-62  | 220.7      |
| 937        | NAP_family      | Nucleosome assembly protein (NAP)          | 1.1e-22  | 84.6       |
| 940        | abhydrolase     | alpha/beta hydrolase fold                  | 0.011    | 3.1        |
| 944        | Tropomyosin     | Tropomyosins                               | 3.2e-07  | 25.1       |
| 948        | pkinase         | Eukaryotic protein kinase domain           | 3.4e-75  | 263.2      |
| 949        | WD40            | WD domain, G-beta repeat                   | 1.8e-27  | 104.7      |
| 950        | Acyltransferase | Acyltransferase                            | 1.6e-07  | 38.4       |



| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                 | p-value  | PFAM SCORE |
|------------|-----------------|---|----------|------------|
| 951        | SAM             | SAM domain (Sterile alpha motif)            | 0.014    | 14.5       |
| 954        | GFO_IDH_MocA    | Oxidoreductase family                       | 1.3e-11  | 52.0       |
| 955        | BTB             | BTB/POZ domain                              | 7e-22    | 86.1       |
| 956        | BTB             | BTB/POZ domain                              | 7e-22    | 86.1       |
| 957        | CDP-OH_P_transf | CDP-alcohol phosphatidyltransferase         | 0.053    | -22.2      |
| 959        | ras             | Ras family                                  | 2.4e-97  | 336.8      |
| 960        | ras             | Ras family                                  | 8.4e-43  | 155.6      |
| 961        | Acetyltransf    | Acetyltransferase (GNAT) family             | 1.2e-08  | 42.2       |
| 962        | adh_short       | short chain dehydrogenase                   | 2.4e-31  | 117.6      |
| 963        | mutT            | Bacterial mutT protein                      | 5.6e-06  | 26.2       |
| 969        | IF-2B           | Initiation factor 2 subunit family          | 8.4e-193 | 653.9      |
| 970        | RNase_PH        | 3' exoribonuclease family                   | 9e-24    | 92.4       |
| 975        | WW              | WW domain                                   | 5.7e-25  | 96.4       |
| 977        | PDZ             | PDZ domain (Also known as DHR or GLGF).     | 3.6e-21  | 83.7       |
| 978        | Ribosomal_L17   | Ribosomal protein L17                       | 2.4e-20  | 81.0       |
| 979        | LIM             | LIM domain containing proteins              | 5.8e-42  | 152.8      |
| 980        | Calsequestrin   | Calsequestrin                               | 1.7e-297 | 1001.7     |
| 982        | HSP20           | Hsp20/alpha crystallin family               | 1.2e-10  | 43.2       |
| 983        | oxidored_q6     | NADH ubiquinone oxidoreductase, 20 Kd sub   | 4.8e-63  | 222.9      |
| 988        | TBC             | TBC domain                                  | 2.2e-50  | 180.8      |
| 989        | TBC             | TBC domain                                  | 2.2e-50  | 180.8      |
| 993        | trRNA_int_endo  | trRNA intron endonuclease                   | 0.0017   | -34.2      |
| 994        | homeobox        | Homeobox domain                             | 4e-18    | 73.6       |
| 997        | pyr_redox       | Pyridine nucleotide-disulphide oxidoreducta | 0.012    | 11.6       |
| 1000       | mito_carr       | Mitochondrial carrier proteins              | 9.7e-123 | 421.2      |
| 1001       | RA              | Ras association (RalGDS/AF-6) domain        | 1.2e-15  | 65.4       |
| 1004       | DUF81           | Domain of unknown function DUF81            | 0.099    | 10.2       |
| 1005       | actin           | Actin                                       | 1.3e-174 | 574.3      |
| 1006       | actin           | Actin                                       | 3.1e-130 | 428.6      |
| 1007       | cpn60_TCP1      | TCP-1/cpn60 chaperonin family               | 3.7e-195 | 661.8      |
| 1008       | TPR             | TPR Domain                                  | 8.1e-44  | 159.0      |
| 1009       | zf-C2H2         | Zinc finger, C2H2 type                      | 3.6e-61  | 216.6      |
| 1011       | zf-C2H2         | Zinc finger, C2H2 type                      | 3.6e-61  | 216.6      |
| 1012       | zf-C3HC4        | Zinc finger, C3HC4 type (RING finger)       | 4.7e-15  | 53.1       |
| 1016       | trRNA-synt_2c   | trRNA synthetases class II (A)              | 2.3e-15  | 55.2       |
| 1018       | RhoGAP          | RhoGAP domain                               | 1.6e-78  | 274.3      |
| 1022       | PGAM            | Phosphoglycerate mutase family              | 3.8e-18  | 69.7       |
| 1026       | HMG_box         | HMG (high mobility group) box               | 8.4e-20  | 79.2       |
| 1027       | TBC             | TBC domain                                  | 7.3e-45  | 162.5      |
| 1028       | UQ_con          | Ubiquitin-conjugating enzyme                | 1.4e-49  | 178.1      |
| 1032       | PDZ             | PDZ domain (Also known as DHR or GLGF).     | 0.028    | 16.3       |
| 1034       | Hydrolase       | haloacid dehalogenase-like hydrolase        | 2e-21    | 84.6       |
| 1037       | KRAB            | KRAB box                                    | 4.8e-06  | 32.4       |
| 1038       | Cation_efflux   | Cation efflux family                        | 7.1e-42  | 152.5      |
| 1040       | ART             | NAD:arginine ADP-ribosyltransferase         | 4.7e-47  | 169.1      |
| 1042       | WD40            | WD domain, G-beta repeat                    | 1.9e-18  | 74.7       |
| 1043       | zf-C2H2         | Zinc finger, C2H2 type                      | 3.7e-24  | 93.7       |
| 1045       | lectin_c        | Lectin C-type domain                        | 1.9e-28  | 108.0      |
| 1046       | Glucosamine_iso | Glucosamine-6-phosphate isomerase           | 0.00013  | -25.1      |

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                    | p-value  | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 1047       | ligase-CoA      | CoA-ligases                                    | 4.5e-80  | 279.4      |
| 1049       | ig              | Immunoglobulin domain                          | 1.7e-09  | 35.6       |
| 1050       | Ribosomal_L24e  | Ribosomal protein L24e                         | 2e-33    | 124.5      |
| 1054       | Amidase         | Amidase  | 4.3e-152 | 518.7      |
| 1055       | rrm             | RNA recognition motif.                         | 3.8e-26  | 100.3      |
| 1058       | annexin         | Annexin  | 6.9e-44  | 159.2      |
| 1059       | PMP22_Claudin   | PMP-22/EMP/MP20/Claudin family                 | 0.023    | -23.6      |
| 1060       | homeobox        | Homeobox domain                                | 3.2e-31  | 117.2      |
| 1062       | Acyltransferase | Acyltransferase                                | 0.00065  | 10.5       |
| 1064       | AMP-binding     | AMP-binding enzyme                             | 6.6e-100 | 345.3      |
| 1065       | LRR             | Leucine Rich Repeat                            | 3.3e-14  | 60.6       |
| 1066       | GTP1_OBG        | GTP1/OBG family                                | 4.8e-41  | 141.8      |
| 1071       | ig              | Immunoglobulin domain                          | 8.4e-48  | 159.1      |
| 1072       | PHD             | PHD-finger                                     | 6.8e-07  | 36.3       |
| 1074       | DENN            | DENN (AEK-3) domain                            | 8.3e-33  | 121.5      |
| 1075       | SCP             | SCP-like extracellular protein                 | 4.7e-41  | 149.8      |
| 1077       | OLF             | Olfactomedin-like domain                       | 2.2e-66  | 234.0      |
| 1078       | mito_carr       | Mitochondrial carrier proteins                 | 1e-42    | 149.3      |
| 1079       | WD40            | WD domain, G-beta repeat                       | 6.2e-45  | 162.7      |
| 1087       | START           | START domain                                   | 1.5e-48  | 174.7      |
| 1093       | DSPc            | Dual specificity phosphatase, catalytic domain | 3.3e-63  | 223.4      |
| 1094       | GSHPx           | Glutathione peroxidases                        | 9.6e-41  | 148.8      |
| 1095       | DUF25           | Domain of unknown function DUF25               | 2e-75    | 264.0      |
| 1096       | DUF25           | Domain of unknown function DUF25               | 6e-75    | 262.4      |
| 1105       | Nitroreductase  | Nitroreductase family                          | 1.3e-13  | 58.6       |
| 1106       | PTE             | Phosphotriesterase family                      | 1.3e-179 | 610.1      |
| 1107       | DAGKc           | Diacylglycerol kinase catalytic domain         | 0.00049  | 19.6       |
| 1109       | ras             | Ras family                                     | 1.3e-15  | 40.7       |
| 1115       | ArfGap          | Putative GTP-ase activating protein for Arf    | 9.7e-47  | 168.7      |
| 1116       | HMG14_17        | HMG14 and HMG17                                | 4.4e-21  | 83.5       |
| 1117       | HMG14_17        | HMG14 and HMG17                                | 9.9e-12  | 52.4       |
| 1119       | FAA_hydrolase   | Fumarylacetoacetate (FAA) hydrolase fam        | 2e-83    | 290.6      |
| 1120       | pkinase         | Eukaryotic protein kinase domain               | 1.4e-94  | 327.6      |
| 1123       | abhydrolase     | alpha/beta hydrolase fold                      | 9.2e-23  | 89.0       |
| 1129       | pro_isomerase   | Cyclophilin type peptidyl-prolyl cis-tr        | 2.2e-56  | 197.1      |
| 1131       | DnaJ            | DnaJ domain                                    | 1.6e-30  | 114.9      |
| 1132       | WD40            | WD domain, G-beta repeat                       | 1.3e-19  | 78.6       |
| 1133       | WD40            | WD domain, G-beta repeat                       | 1.8e-15  | 64.9       |
| 1134       | PH              | PH domain                                      | 0.0015   | 17.8       |
| 1136       | Adap_comp_sub   | Adaptor complexes medium subunit family        | 1.2e-256 | 866.0      |
| 1137       | Adap_comp_sub   | Adaptor complexes medium subunit family        | 2.5e-209 | 708.8      |
| 1139       | ras             | Ras family                                     | 1.5e-86  | 301.0      |
| 1141       | pkinase         | Eukaryotic protein kinase domain               | 9.4e-74  | 258.4      |
| 1152       | Acyltransferase | Acyltransferase                                | 1.2e-05  | 29.9       |
| 1153       | IRS             | PTB domain (IRS-I.type)                        | 5.4e-55  | 196.1      |
| 1155       | ig              | Immunoglobulin domain                          | 1.3e-31  | 106.9      |
| 1157       | Asparaginase_2  | Asparaginase                                   | 6.4e-72  | 252.3      |
| 1159       | GMC_oxred       | GMC oxidoreductases                            | 4.7e-142 | 485.3      |
| 1160       | zf-AN1          | AN1-like Zinc finger                           | 0.00021  | 27.9       |

| SEQ ID NO: | PFAM NAME        | DESCRIPTION                                 | p-value  | PFAM SCORE |
|------------|------------------|---|----------|------------|
| 1163       | linker_histo ne  | linker histone H1 and H5 family             | 3.8e-14  | 60.4       |
| 1164       | DED              | Death effector domain                       | 3.9e-05  | 30.5       |
| 1165       | IRS              | PTB domain (IRS-1 type)                     | 2.6e-43  | 157.3      |
| 1166       | IRS              | PTB domain (IRS-1 type)                     | 2.6e-43  | 157.3      |
| 1168       | SAM              | SAM domain (Sterile alpha motif)            | 0.04     | 10.5       |
| 1170       | abhydrolase      | alpha/beta hydrolase fold                   | 0.098    | -7.5       |
| 1174       | SAP              | SAP domain                                  | 3.9e-10  | 47.1       |
| 1177       | PP2C             | Protein phosphatase 2C                      | 5.3e-31  | 112.5      |
| 1178       | WD40             | WD domain, G-beta repeat                    | 4.7e-35  | 129.9      |
| 1180       | Ets              | Ets-domain                                  | 1.8e-09  | 33.3       |
| 1181       | Collagen         | Collagen triple helix repeat (20 copies)    | 0.00016  | 24.7       |
| 1182       | TCL1_MTCP1       | TCL1/MTCP1 family                           | 9.5e-56  | 198.6      |
| 1184       | RasGEF           | RasGEF domain                               | 1.7e-88  | 307.4      |
| 1185       | mito_carr        | Mitochondrial carrier proteins              | 1.5e-62  | 217.3      |
| 1187       | UPAR_LY6         | u-PAR/Ly-6 domain                           | 0.0042   | 15.6       |
| 1188       | Orn_DAP_Arg_deC  | Pyridoxal-dependent decarboxylase           | 6.2e-128 | 430.6      |
| 1193       | Stathmin         | Stathmin family                             | 1.8e-90  | 314.0      |
| 1194       | Stathmin         | Stathmin family                             | 1.8e-90  | 314.0      |
| 1195       | Sec1             | Sec1 family                                 | 3.2e-183 | 622.1      |
| 1196       | pyr_redox        | Pyridine nucleotide-disulphide oxidoreducta | 3.1e-32  | 111.8      |
| 1197       | Glyco_transf_8   | Glycosyl transferase family 8               | 1.2e-09  | 45.5       |
| 1202       | K_tetra          | K+ channel tetramerisation domain           | 0.022    | -16.8      |
| 1203       | adh_short        | short chain dehydrogenase                   | 8.3e-45  | 162.3      |
| 1206       | Ubie_methylt ran | ubie/COQ5 methyltransferase family          | 1.3e-121 | 417.4      |
| 1208       | 7tm_3            | 7 transmembrane receptor                    | 7.2e-09  | 29.0       |
| 1209       | ank              | Ank repeat                                  | 3.9e-15  | 63.7       |
| 1210       | vATP-synt_AC39   | ATP synthase (C/AC39) subunit               | 2.5e-128 | 439.7      |
| 1212       | zf-C2H2          | Zinc finger, C2H2 type                      | 5.5e-17  | 69.9       |
| 1213       | efhand           | EF hand                                     | 3.2e-07  | 37.4       |
| 1219       | rrm              | RNA recognition motif                       | 2.1e-40  | 147.7      |
| 1220       | DUF6             | Integral membrane protein DUF6              | 0.015    | 21.5       |
| 1222       | SCAN             | SCAN domain                                 | 1.5e-71  | 251.1      |
| 1223       | G-gamma          | GGL domain                                  | 3.6e-36  | 129.5      |
| 1227       | catalase         | Catalase                                    | 0        | 1158.9     |
| 1232       | PX               | PX domain                                   | 2.2e-15  | 64.5       |
| 1233       | PX               | PX domain                                   | 2.2e-15  | 64.5       |
| 1236       | FCH              | Fes/CIP4 homology domain                    | 3.3e-09  | 44.0       |
| 1241       | Peptidase_M20    | Peptidase family M20/M25/M40                | 2e-63    | 224.1      |
| 1243       | WW               | WW domain                                   | 0.044    | 17.9       |
| 1247       | UPF0006          | Metalloenzyme of unknown function UPF0006   | 6.3e-61  | 215.8      |
| 1248       | Glycos_transf_2  | Glycosyl transferases                       | 4.5e-10  | 46.9       |
| 1249       | efhand           | EF hand                                     | 4e-11    | 50.4       |
| 1254       | UQ_con           | Ubiquitin-conjugating enzyme                | 2.1e-73  | 257.3      |
| 1255       | ras              | Ras family                                  | 2.2e-62  | 220.7      |
| 1256       | formyl_transf    | Formyl transferase                          | 4.9e-30  | 108.3      |
| 1259       | zf-C3HC4         | Zinc finger, C3HC4 type (RING finger)       | 5.3e-13  | 46.4       |
| 1261       | Dihfolate_re d   | Dihydrofolate reductase                     | 2.1e-69  | 241.7      |
| 1262       | G_glu_transp ept | Gamma-glutamyltranspeptidase                | 1.8e-110 | 380.4      |
| 1263       | PAS              | PAS domain                                  | 1.3e-08  | 36.9       |
| 1265       | LRR              | Leucine Rich Repeat                         | 4.2e-22  | 86.9       |

| SEQ ID NO: | PFAM NAME     | DESCRIPTION                                   | p-value  | PFAM SCORE |
|------------|---------------|---|----------|------------|
| 1266       | SCP           | SCP-like extracellular protein                | 6e-29    | 108.0      |
| 1267       | K_tetra       | K <sup>+</sup> channel tetramerisation domain | 2.8e-27  | 104.0      |
| 1269       | ras           | Ras family                                    | 1.3e-85  | 297.9      |
| 1275       | zf-C3HC4      | Zinc finger, C3HC4 type (RING finger)         | 4.2e-10  | 37.0       |
| 1276       | abhydrolase   | alpha/beta hydrolase fold                     | 5.4e-23  | 89.8       |
| 1277       | abhydrolase   | alpha/beta hydrolase fold                     | 5.6e-21  | 83.1       |
| 1279       | trypsin       | Trypsin                                       | 4.4e-41  | 132.0      |
| 1280       | PBP           | Phosphatidylethanolamine-binding protein      | 1.3e-13  | 58.7       |
| 1285       | zf-C3HC4      | Zinc finger, C3HC4 type (RING finger)         | 5.6e-14  | 49.6       |
| 1287       | ank           | Ank repeat                                    | 1.7e-52  | 187.8      |
| 1294       | fn3           | Fibronectin type III domain                   | 0.026    | 20.9       |
| 1295       | GBP           | Guanylate-binding protein                     | 0.00026  | -70.0      |
| 1296       | PMP22_Claudin | PMP-22/EMP/MP20/Claudin family                | 6.9e-41  | 149.3      |
| 1297       | Rhodanese     | Rhodanese-like domain                         | 3.2e-14  | 60.7       |
| 1298       | LIM           | LIM domain containing proteins                | 5.8e-21  | 79.1       |
| 1301       | rnaseA        | Pancreatic ribonucleases                      | 4.9e-43  | 145.2      |
| 1307       | mito_carr     | Mitochondrial carrier proteins                | 2.1e-53  | 186.0      |
| 1308       | WD40          | WD domain, G-beta repeat                      | 1.6e-17  | 71.6       |
| 1310       | UPAR_LY6      | u-PAR/Ly-6 domain                             | 7.1e-20  | 75.5       |
| 1313       | thioredo      | Thioredoxin                                   | 3.6e-05  | 21.6       |
| 1314       | Aa_trans      | Transmembrane amino acid transporter protein  | 1.5e-67  | 237.9      |
| 1316       | trypsin       | Trypsin                                       | 4.4e-41  | 132.0      |
| 1320       | Ribosomal_L13 | Ribosomal protein L13                         | 3.9e-62  | 219.8      |
| 1327       | Armadillo_se  | Armadillo/beta-catenin-like repeats           | 0.0054   | 23.4       |
| 1328       | KRAB          | KRAB box                                      | 0.052    | -5.6       |
| 1329       | rrm           | RNA recognition motif.                        | 2.1e-40  | 147.7      |
| 1330       | Bcl-2         | Apoptosis regulator proteins, Bcl-2 family    | 0.014    | -1.6       |
| 1331       | PX            | PX domain                                     | 2.1e-10  | 48.0       |
| 1333       | KRAB          | KRAB box                                      | 1.8e-36  | 134.6      |
| 1334       | UPP_syntheta  | Putative undecaprenyl diphosphate synt        | 2.3e-89  | 310.3      |
| 1335       | UPP_syntheta  | Putative undecaprenyl diphosphate synt        | 1.8e-59  | 211.0      |
| 1336       | DSPc          | Dual specificity phosphatase, catalytic doma  | 1.2e-31  | 118.6      |
| 1337       | DSPc          | Dual specificity phosphatase, catalytic doma  | 2.3e-12  | 54.5       |
| 1338       | TPR           | TPR Domain                                    | 0.00021  | 28.1       |
| 1340       | metalthio     | Metallothionein                               | 0.013    | 20.3       |
| 1341       | mutT          | Bacterial mutT protein                        | 5.8e-09  | 36.5       |
| 1343       | Band 41       | FERM domain (Band 4.1 family)                 | 1.3e-38  | 122.5      |
| 1344       | Kelch         | Kelch motif                                   | 1.4e-44  | 161.5      |
| 1345       | Antifreeze    | Antifreeze protein                            | 1.2e-10  | 48.8       |
| 1347       | 3Beta_HSD     | 3-beta hydroxysteroid dehydrogenase/isomera   | 0.086    | -177.2     |
| 1348       | BTB           | BTB/POZ domain                                | 5.3e-28  | 106.5      |
| 1349       | DUF6          | Integral membrane protein DUF6                | 0.033    | 15.8       |
| 1350       | myosin_head   | Myosin head (motor domain)                    | 0        | 1088.7     |
| 1352       | Nramp         | Natural resistance-associated macrophage pro  | 1.2e-202 | 686.6      |
| 1353       | S_100         | S-100/ICaBP type calcium binding domain       | 5.3e-23  | 89.9       |
| 1355       | DEAD          | DEAD/DEAH box helicase                        | 3.6e-65  | 209.0      |
| 1356       | C2            | C2 domain                                     | 2.4e-15  | 64.4       |
| 1357       | RBD           | Raf-like Ras-binding domain                   | 4.2e-57  | 203.1      |
| 1360       | zf-C2H2       | Zinc finger, C2H2 type                        | 7.4e-141 | 481.4      |
| 1361       | HMG14_17      | HMG14 and HMG17                               | 7.9e-40  | 145.7      |

| SEQ ID NO: | PFAM NAME          | DESCRIPTION                                   | p-value  | PFAM SCORE |
|------------|--------------------|---|----------|------------|
| 1362       | SIS                | SIS domain                                    | 3.8e-30  | 113.6      |
| 1363       | SIS                | SIS domain                                    | 1.3e-28  | 108.5      |
| 1364       | ig                 | Immunoglobulin domain                         | 0.00026  | 19.0       |
| 1368       | K_tetra            | K <sup>+</sup> channel tetramerisation domain | 1.1e-16  | 68.9       |
| 1371       | Collagen           | Collagen triple helix repeat (20 copies)      | 2.2e-113 | 390.1      |
| 1372       | DnaJ               | DnaJ domain                                   | 6.6e-36  | 132.7      |
| 1376       | KRAB               | KRAB box                                      | 2.1e-38  | 141.0      |
| 1378       | ELM2               | ELM2 domain                                   | 2e-23    | 91.3       |
| 1380       | Thioredoxin        | Thioredoxin                                   | 1.2e-23  | 82.8       |
| 1381       | ank                | Ank repeat                                    | 2.3e-83  | 290.4      |
| 1382       | BTB                | BTB/POZ domain                                | 3e-11    | 50.8       |
| 1383       | WD40               | WD domain, G-beta repeat                      | 1.6e-19  | 78.3       |
| 1384       | WD40               | WD domain, G-beta repeat                      | 6.3e-24  | 92.9       |
| 1387       | zf-C3HC4           | Zinc finger, C3HC4 type (RING finger)         | 1.1e-09  | 35.6       |
| 1389       | zf-C2H2            | Zinc finger, C2H2 type                        | 5.5e-50  | 179.5      |
| 1390       | zf-C2H2            | Zinc finger, C2H2 type                        | 2.5e-85  | 296.9      |
| 1393       | kinesin            | Kinesin motor domain                          | 7.8e-188 | 637.4      |
| 1394       | zf-C2H2            | Zinc finger, C2H2 type                        | 1.2e-49  | 178.4      |
| 1398       | KRAB               | KRAB box                                      | 5.1e-22  | 86.6       |
| 1402       | bZIP               | bZIP transcription factor                     | 0.035    | 13.1       |
| 1405       | sugar_tr           | Sugar (and other) transporter                 | 0.003    | -101.5     |
| 1406       | RhoGAP             | RhoGAP domain                                 | 8.9e-47  | 168.8      |
| 1407       | rrm                | RNA recognition motif.                        | 1e-35    | 132.1      |
| 1408       | LRR                | Leucine Rich Repeat                           | 2.1e-13  | 58.0       |
| 1409       | Nebulin_repe<br>at | Nebulin repeat                                | 6e-54    | 192.6      |
| 1410       | ank                | Ank repeat                                    | 1.6e-17  | 71.6       |
| 1412       | Ribosomal_LS<br>C  | ribosomal L5P family C-terminus               | 8.2e-58  | 205.5      |
| 1415       | trypsin            | Trypsin                                       | 4.7e-85  | 270.4      |
| 1416       | aminotran_1        | Aminotransferases class-I                     | 4.4e-05  | -91.2      |
| 1417       | S1                 | S1 RNA binding domain                         | 1.6e-07  | 33.1       |
| 1419       | WD40               | WD domain, G-beta repeat                      | 2.2e-09  | 44.6       |
| 1422       | cadherin           | Cadherin domain                               | 8.3e-42  | 152.3      |
| 1424       | SH3                | SH3 domain                                    | 2.5e-80  | 280.3      |
| 1425       | PHD                | PHD-finger                                    | 3.2e-17  | 70.6       |
| 1426       | PHD                | PHD-finger                                    | 3.2e-17  | 70.6       |
| 1427       | ArfGAP             | Putative GTP-ase activating protein for Arf   | 1e-37    | 138.8      |
| 1428       | helicase_C         | Helicases conserved C-terminal domain         | 1e-26    | 102.2      |
| 1429       | WD40               | WD domain, G-beta repeat                      | 3.9e-07  | 37.2       |
| 1430       | inositol_P         | Inositol monophosphatase family               | 2.5e-10  | 40.2       |
| 1431       | mito_carr          | Mitochondrial carrier proteins                | 4.3e-83  | 287.7      |
| 1433       | Clq                | Clq domain                                    | 2.9e-16  | 66.2       |
| 1434       | WD40               | WD domain, G-beta repeat                      | 1.6e-13  | 58.3       |
| 1435       | Inos-1-<br>P_synth | Myo-inositol-1-phosphate synthase             | 7e-228   | 770.4      |
| 1436       | rrm                | RNA recognition motif.                        | 1.4e-34  | 128.3      |
| 1438       | ig                 | Immunoglobulin domain                         | 1.3e-12  | 45.6       |
| 1440       | G_Adapt_CT         | Gamma-adaptin, C-terminus                     | 3.4e-67  | 236.7      |
| 1441       | G_Adapt_CT         | Gamma-adaptin, C-terminus                     | 3.4e-67  | 236.7      |
| 1443       | Kelch              | Kelch motif                                   | 0.00013  | 28.7       |
| 1446       | ARID               | ARID DNA binding domain                       | 1.8e-21  | 84.7       |
| 1447       | zf-C2H2            | Zinc finger, C2H2 type                        | 9.4e-28  | 105.6      |
| 1448       | AMP-binding        | AMP-binding enzyme                            | 2.6e-07  | -145.1     |
| 1451       | rrm                | RNA recognition motif.                        | 6.5e-21  | 82.9       |
| 1454       | ig                 | Immunoglobulin domain                         | 5.6e-44  | 146.7      |
| 1455       | Sialyltransf       | Sialyltransferase family                      | 5.4e-21  | 83.2       |
| 1460       | Aldose_epim        | Aldose 1-epimerase                            | 1.9e-35  | 131.2      |
| 1461       | C2                 | C2 domain                                     | 4e-18    | 73.6       |
| 1470       | TIG                | IPT/TIG domain                                | 3.1e-19  | 77.3       |
| 1472       | PseudoU_synt       | RNA pseudouridylate synthase                  | 4.3e-16  | 66.9       |

| SEQ ID NO: | PFAM NAME       | DESCRIPTION                                  | p-value  | PFAM SCORE |
|------------|-----------------|--|----------|------------|
|            | h_2             |  |          |            |
| 1474       | DENN            | DENN (AEX-3) domain                          | 1.3e-44  | 161.6      |
| 1475       | Cation_efflux   | Cation efflux family                         | 4.6e-49  | 176.4      |
| 1477       | TBC             | TBC domain                                   | 8e-47    | 169.0      |
| 1478       | rrm             | RNA recognition motif.                       | 2e-21    | 84.6       |
| 1480       | lg              | Immunoglobulin domain                        | 5.5e-06  | 24.3       |
| 1484       | Telo_bind_alpha | Telomere-binding protein alpha subunit       | 0.028    | -225.9     |
| 1485       | zf-C2H2         | Zinc finger, C2H2 type                       | 1.8e-68  | 240.9      |
| 1486       | pkinase         | Eukaryotic protein kinase domain             | 9.5e-13  | 49.9       |
| 1488       | helicase_C      | Helicases conserved C-terminal domain        | 1.4e-15  | 65.2       |
| 1489       | DUF89           | Protein of unknown function DUF89            | 0.079    | -132.4     |
| 1490       | ECH             | Enoyl-CoA hydratase/isomerase family         | 5.2e-41  | 149.7      |
| 1491       | guanylate_cyc   | Adenylate and Guanylate cyclase catalyt      | 5.9e-46  | 166.1      |
| 1492       | LRR             | Leucine Rich Repeat                          | 3.4e-19  | 77.2       |
| 1495       | zf-C3HC4        | Zinc finger, C3HC4 type (RING finger)        | 7.1e-10  | 36.3       |
| 1497       | pkinase         | Eukaryotic protein kinase domain             | 1e-22    | 85.8       |
| 1500       | SH3             | SH3 domain                                   | 9.3e-05  | 27.2       |
| 1502       | homeobox        | Homeobox domain                              | 0.084    | 13.8       |
| 1503       | homeobox        | Homeobox domain                              | 0.084    | 13.8       |
| 1505       | EGF             | EGF-like domain                              | 2.7e-23  | 90.8       |
| 1506       | UCH-2           | Ubiquitin carboxyl-terminal hydrolase family | 2.7e-21  | 84.2       |
| 1508       | Peptidase_M20   | Peptidase family M20/M25/M40                 | 2.8e-28  | 101.8      |
| 1511       | PX              | PX domain                                    | 1.9e-11  | 51.5       |
| 1512       | Sulfatase       | Sulfatase                                    | 2.8e-35  | 130.7      |
| 1516       | Syntaxin        | Syntaxin                                     | 0.011    | -62.3      |
| 1518       | aminotran_3     | Aminotransferases class-III pyridoxal-pho    | 9.7e-106 | 305.6      |
| 1520       | lg              | Immunoglobulin domain                        | 0.075    | 11.0       |
| 1521       | RA              | Ras association (RalGDS/AF-6) domain         | 0.013    | 13.3       |
| 1523       | RhoGAP          | RhoGAP domain                                | 2.5e-05  | 10.7       |
| 1528       | WD40            | WD domain, G-beta repeat                     | 5.4e-24  | 93.1       |
| 1535       | IMS             | impB/mucB/samB family                        | 7.8e-95  | 328.5      |
| 1538       | FYVE            | FYVE zinc finger                             | 3.2e-27  | 101.5      |
| 1539       | DAGKc           | Diacylglycerol kinase catalytic domain       | 6e-07    | 36.5       |
| 1540       | Ocular_alb      | Ocular albinism type 1 protein               | 0        | 1184.7     |
| 1653       | SAP             | SAP domain                                   | 6e-06    | 33.2       |
| 1654       | Amino_oxidase   | Flavin containing amine oxidase              | 3.2e-43  | 157.0      |
| 1655       | Amino_oxidase   | Flavin containing amine oxidase              | 3.2e-43  | 157.0      |
| 1656       | RhoGEF          | RhoGEF domain                                | 1.4e-24  | 95.1       |
| 1657       | MMR_HSR1        | GTPase of unknown function                   | 0.0011   | -45.5      |
| 1659       | UCH-2           | Ubiquitin carboxyl-terminal hydrolase family | 2.5e-11  | 51.1       |
| 1660       | actin           | Actin  | 6.6e-21  | 69.9       |
| 1661       | BAH             | BAH domain                                   | 1.7e-82  | 287.5      |
| 1662       | vwa             | von Willebrand factor type A domain          | 0        | 1909.4     |
| 1663       | WD40            | WD domain, G-beta repeat                     | 1.4e-67  | 237.9      |
| 1667       | zf-C2H2         | Zinc finger, C2H2 type                       | 1.3e-93  | 324.4      |
| 1669       | Nol1_Nop2_Sun   | NOL1/NOP2/sun family                         | 1.3e-23  | 84.3       |
| 1671       | SH2             | Src homology domain 2                        | 5.4e-15  | 46.9       |

| SEQ ID NO: | PFAM NAME      | DESCRIPTION                                  | p-value  | PFAM SCORE |
|------------|----------------|--|----------|------------|
| 1672       | chromo         | 'chromo' (CHRromatin Organization Modifier)  | 2.1e-18  | 67.7       |
| 1674       | zf-CCCH        | Zinc finger C-x8-C-x5-C-x3-H type            | 0.0025   | 17.6       |
| 1676       | Glyco_hydro_47 | Glycosyl hydrolase family 47                 | 1.8e-187 | 636.2      |
| 1677       | Glyco_hydro_47 | Glycosyl hydrolase family 47                 | 4.5e-74  | 259.5      |
| 1680       | WD40           | WD domain, G-beta repeat                     | 1.1e-27  | 105.5      |
| 1681       | WD40           | WD domain, G-beta repeat                     | 1.1e-27  | 105.5      |
| 1683       | MMR_HSR1       | GTPase of unknown function                   | 1.8e-78  | 274.1      |
| 1691       | rrm            | RNA recognition motif.                       | 1.8e-37  | 137.9      |
| 1692       | rrm            | RNA recognition motif.                       | 1.8e-37  | 137.9      |
| 1693       | AAA            | ATPases associated with various cellular act | 1.3e-81  | 284.5      |
| 1697       | Ferric_reduc t | Ferric reductase like transmembrane com      | 8.4e-82  | 285.2      |
| 1698       | Ferric_reduc t | Ferric reductase like transmembrane com      | 3.5e-53  | 190.1      |
| 1699       | zf-C2H2        | Zinc finger, C2H2 type                       | 4.4e-34  | 126.6      |
| 1700       | arf            | ADP-ribosylation factor family               | 9e-19    | 75.8       |
| 1702       | GTP_EFTU       | Elongation factor Tu family                  | 0.014    | 11.4       |
| 1703       | SCAN           | SCAN domain                                  | 1.8e-54  | 194.4      |
| 1707       | pkinase        | Eukaryotic protein kinase domain             | 1.2e-88  | 307.9      |
| 1709       | WD40           | WD domain, G-beta repeat                     | 0.0035   | 24.0       |
| 1710       | LRR            | Leucine Rich Repeat                          | 1.2e-30  | 115.3      |
| 1711       | WW             | WW domain                                    | 7.6e-12  | 52.8       |
| 1712       | ank            | Ank repeat                                   | 4.2e-34  | 126.7      |
| 1713       | zf-CCCH        | Zinc finger C-x8-C-x5-C-x3-H type            | 2.6e-09  | 38.3       |
| 1714       | zf-CCCH        | Zinc finger C-x8-C-x5-C-x3-H type            | 2.6e-09  | 38.3       |
| 1715       | ras            | Ras family                                   | 4.4e-41  | 149.9      |
| 1718       | HMG_box        | HMG (high mobility group) box                | 8.3e-21  | 82.6       |
| 1719       | TBC            | TBC domain                                   | 1.1e-45  | 165.2      |
| 1721       | HLH            | Helix-loop-helix DNA-binding domain          | 9.2e-10  | 45.9       |
| 1723       | garm           | Double-stranded RNA binding motif            | 2.9e-05  | 30.9       |
| 1724       | RrnaAD         | Ribosomal RNA adenine dimethylases           | 0.045    | 9.2        |
| 1725       | CIDE-N         | CIDE-N domain                                | 5.9e-40  | 146.2      |
| 1726       | HAT            | HAT (Half-A-TPR) repeats                     | 2.9e-44  | 160.5      |
| 1728       | efhand         | EF hand                                      | 5.1e-20  | 79.9       |
| 1733       | Hist_deacety l | Histone deacetylase family                   | 1.7e-104 | 360.6      |
| 1735       | LRR            | Leucine Rich Repeat                          | 4.6e-34  | 126.6      |
| 1739       | PI-PLC-X       | Phosphatidylinositol-specific phospholipase  | 0.0023   | 16.1       |
| 1743       | ras            | Ras family                                   | 3.7e-10  | -21.3      |
| 1744       | ras            | Ras family                                   | 3.7e-10  | -21.3      |
| 1745       | RasGEF         | RasGEF domain                                | 3.2e-49  | 176.9      |
| 1746       | adh_short      | short chain dehydrogenase                    | 7.1e-08  | 34.6       |
| 1751       | zf-C2H2        | Zinc finger, C2H2 type                       | 9e-39    | 142.2      |
| 1754       | fn3            | Fibronectin type III domain                  | 5.5e-101 | 348.9      |
| 1756       | zf-C2H2        | Zinc finger, C2H2 type                       | 6.3e-93  | 322.1      |
| 1758       | rrm            | RNA recognition motif.                       | 0.017    | 21.2       |
| 1760       | Nop            | Putative snoRNA binding domain               | 6.1e-95  | 328.8      |
| 1761       | Nop            | Putative snoRNA binding domain               | 6.1e-95  | 328.8      |
| 1765       | MMR_HSR1       | GTPase of unknown function                   | 6.4e-41  | 149.4      |
| 1769       | CN hydrolase   | Carbon-nitrogen hydrolase                    | 3e-06    | -43.9      |
| 1775       | ank            | Ank repeat                                   | 4.1e-07  | 37.1       |
| 1779       | Oxysterol_BP   | Oxysterol-binding protein                    | 4.7e-56  | 199.6      |
| 1783       | RhoGEF         | RhoGEF domain                                | 1.6e-23  | 91.6       |
| 1784       | RhoGEF         | RhoGEF domain                                | 1.6e-23  | 91.6       |

| SEQ ID<br>NO: | PFAM NAME | DESCRIPTION            | p-value | PFAM<br>SCORE |
|---------------|-----------|------------------------|---------|---------------|
| 1785          | rrm       | RNA recognition motif. | 6.4e-14 | 59.7          |

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TABLE 5

| SEQ ID NO: | POSITION OF<br>SIGNAL IN AMINO<br>ACID SEQUENCE | MaxS (MAXIMUM<br>SCORE) | MeanS (MEAN<br>SCORE) |
|------------|---|-------------------------|-----------------------|
| 1          | 1-21  | 0.991                   | 0.955                 |
| 2          | 1-31  | 0.995                   | 0.944                 |
| 3          | 1-33  | 0.949                   | 0.736                 |
| 4          | 1-19  | 0.970                   | 0.951                 |
| 5          | 1-26  | 0.971                   | 0.863                 |
| 6          | 1-26  | 0.971                   | 0.863                 |
| 7          | 1-26  | 0.971                   | 0.863                 |
| 8          | 1-26  | 0.971                   | 0.863                 |
| 9          | 1-46  | 0.982                   | 0.901                 |
| 10         | 1-21  | 0.991                   | 0.955                 |
| 11         | 1-23  | 0.989                   | 0.899                 |
| 12         | 1-25  | 0.955                   | 0.803                 |
| 13         | 1-18  | 0.932                   | 0.625                 |
| 14         | 1-18  | 0.938                   | 0.876                 |
| 15         | 1-25  | 0.941                   | 0.811                 |
| 16         | 1-17  | 0.972                   | 0.939                 |
| 17         | 1-27  | 0.964                   | 0.777                 |
| 18         | 1-16  | 0.914                   | 0.657                 |
| 19         | 1-19  | 0.953                   | 0.840                 |
| 20         | 1-20  | 0.935                   | 0.701                 |
| 21         | 1-22  | 0.974                   | 0.850                 |
| 22         | 1-33  | 0.961                   | 0.895                 |
| 23         | 1-19  | 0.991                   | 0.959                 |
| 24         | 1-31  | 0.995                   | 0.944                 |
| 25         | 1-22  | 0.976                   | 0.935                 |
| 26         | 1-27  | 0.996                   | 0.928                 |
| 27         | 1-24  | 0.953                   | 0.739                 |
| 28         | 1-21  | 0.906                   | 0.688                 |
| 29         | 1-31  | 0.986                   | 0.841                 |
| 30         | 1-28  | 0.980                   | 0.893                 |
| 31         | 1-19  | 0.993                   | 0.976                 |
| 32         | 1-22  | 0.998                   | 0.909                 |
| 35         | 1-33  | 0.949                   | 0.736                 |
| 36         | 1-33  | 0.949                   | 0.736                 |
| 46         | 1-19  | 0.970                   | 0.951                 |
| 67         | 1-25  | 0.968                   | 0.848                 |
| 71         | 1-18  | 0.949                   | 0.845                 |
| 72         | 1-30  | 0.991                   | 0.919                 |
| 75         | 1-29  | 0.958                   | 0.854                 |
| 88         | 1-20  | 0.986                   | 0.945                 |
| 94         | 1-33  | 0.994                   | 0.943                 |
| 97         | 1-46  | 0.964                   | 0.595                 |
| 103        | 1-49  | 0.983                   | 0.570                 |
| 108        | 1-26  | 0.978                   | 0.885                 |
| 111        | 1-23  | 0.989                   | 0.899                 |
| 126        | 1-25  | 0.955                   | 0.803                 |
| 129        | 1-19  | 0.963                   | 0.918                 |
| 138        | 1-29  | 0.971                   | 0.844                 |
| 143        | 1-18  | 0.914                   | 0.628                 |
| 148        | 1-20  | 0.969                   | 0.904                 |
| 156        | 1-25  | 0.941                   | 0.811                 |
| 158        | 1-22  | 0.979                   | 0.927                 |
| 160        | 1-17  | 0.972                   | 0.939                 |
| 161        | 1-48  | 0.903                   | 0.571                 |
| 162        | 1-25  | 0.937                   | 0.729                 |
| 168        | 1-16  | 0.939                   | 0.826                 |
| 171        | 1-27  | 0.964                   | 0.777                 |
| 178        | 1-21  | 0.945                   | 0.825                 |
| 180        | 1-27  | 0.981                   | 0.941                 |
| 187        | 1-28  | 0.982                   | 0.936                 |
| 190        | 1-19  | 0.953                   | 0.840                 |
| 196        | 1-22  | 0.975                   | 0.916                 |
| 197        | 1-22  | 0.963                   | 0.936                 |

| SEQ ID NO: | POSITION OF<br>SIGNAL IN AMINO<br>ACID SEQUENCE | MaxS (MAXIMUM<br>SCORE) | MeanS (MEAN<br>SCORE) |
|------------|---|-------------------------|-----------------------|
| 199        | 1-20  | 0.935                   | 0.701                 |
| 200        | 1-23  | 0.977                   | 0.773                 |
| 206        | 1-30  | 0.984                   | 0.890                 |
| 207        | 1-19  | 0.990                   | 0.924                 |
| 208        | 1-22  | 0.974                   | 0.850                 |
| 210        | 1-40  | 0.940                   | 0.670                 |
| 211        | 1-28  | 0.971                   | 0.849                 |
| 216        | 1-24  | 0.986                   | 0.956                 |
| 218        | 1-33  | 0.961                   | 0.895                 |
| 219        | 1-19  | 0.970                   | 0.871                 |
| 221        | 1-19  | 0.904                   | 0.553                 |
| 222        | 1-21  | 0.917                   | 0.555                 |
| 230        | 1-19  | 0.991                   | 0.959                 |
| 231        | 1-26  | 0.953                   | 0.800                 |
| 232        | 1-25  | 0.988                   | 0.826                 |
| 239        | 1-23  | 0.969                   | 0.828                 |
| 240        | 1-17  | 0.982                   | 0.955                 |
| 241        | 1-17  | 0.982                   | 0.955                 |
| 245        | 1-30  | 0.970                   | 0.722                 |
| 248        | 1-22  | 0.976                   | 0.935                 |
| 249        | 1-23  | 0.968                   | 0.940                 |
| 252        | 1-18  | 0.971                   | 0.923                 |
| 261        | 1-24  | 0.883                   | 0.587                 |
| 265        | 1-18  | 0.939                   | 0.868                 |
| 272        | 1-24  | 0.953                   | 0.739                 |
| 283        | 1-21  | 0.906                   | 0.688                 |
| 284        | 1-29  | 0.997                   | 0.854                 |
| 290        | 1-31  | 0.986                   | 0.841                 |
| 302        | 1-28  | 0.980                   | 0.893                 |
| 304        | 1-16  | 0.907                   | 0.635                 |
| 312        | 1-19  | 0.993                   | 0.976                 |
| 313        | 1-17  | 0.930                   | 0.753                 |
| 323        | 1-22  | 0.998                   | 0.909                 |
| 324        | 1-17  | 0.982                   | 0.954                 |
| 328        | 1-19  | 0.971                   | 0.865                 |
| 329        | 1-22  | 0.963                   | 0.924                 |
| 330        | 1-33  | 0.978                   | 0.841                 |
| 331        | 1-24  | 0.920                   | 0.712                 |
| 332        | 1-24  | 0.975                   | 0.881                 |
| 333        | 1-19  | 0.984                   | 0.941                 |
| 334        | 1-20  | 0.899                   | 0.567                 |
| 335        | 1-27  | 0.942                   | 0.813                 |
| 336        | 1-20  | 0.952                   | 0.850                 |
| 337        | 1-38  | 0.942                   | 0.653                 |
| 338        | 1-27  | 0.973                   | 0.772                 |
| 339        | 1-36  | 0.979                   | 0.804                 |
| 340        | 1-27  | 0.888                   | 0.597                 |
| 343        | 1-19  | 0.971                   | 0.865                 |
| 344        | 1-22  | 0.994                   | 0.928                 |
| 345        | 1-17  | 0.966                   | 0.687                 |
| 346        | 1-19  | 0.936                   | 0.822                 |
| 347        | 1-22  | 0.963                   | 0.924                 |
| 349        | 1-24  | 0.982                   | 0.966                 |
| 351        | 1-21  | 0.918                   | 0.815                 |
| 352        | 1-31  | 0.988                   | 0.912                 |
| 354        | 1-31  | 0.974                   | 0.839                 |
| 355        | 1-29  | 0.932                   | 0.632                 |
| 356        | 1-15  | 0.994                   | 0.969                 |
| 357        | 1-33  | 0.935                   | 0.726                 |
| 360        | 1-27  | 0.938                   | 0.827                 |
| 361        | 1-25  | 0.954                   | 0.674                 |
| 362        | 1-22  | 0.929                   | 0.788                 |
| 363        | 1-21  | 0.881                   | 0.715                 |
| 364        | 1-33  | 0.978                   | 0.841                 |
| 365        | 1-33  | 0.978                   | 0.841                 |

| SEQ ID NO: | POSITION OF<br>SIGNAL IN AMINO<br>ACID SEQUENCE | MaxS (MAXIMUM<br>SCORE) | MeanS (MEAN<br>SCORE) |
|------------|---|-------------------------|-----------------------|
| 366        | 1-21  | 0.916                   | 0.820                 |
| 367        | 1-19  | 0.936                   | 0.822                 |
| 368        | 1-29  | 0.972                   | 0.874                 |
| 370        | 1-24  | 0.920                   | 0.712                 |
| 371        | 1-24  | 0.961                   | 0.773                 |
| 372        | 1-27  | 0.919                   | 0.768                 |
| 373        | 1-19  | 0.986                   | 0.945                 |
| 375        | 1-32  | 0.994                   | 0.932                 |
| 376        | 1-34  | 0.987                   | 0.810                 |
| 377        | 1-17  | 0.995                   | 0.950                 |
| 378        | 1-49  | 0.971                   | 0.749                 |
| 380        | 1-20  | 0.968                   | 0.874                 |
| 381        | 1-20  | 0.928                   | 0.782                 |
| 382        | 1-19  | 0.986                   | 0.934                 |
| 383        | 1-28  | 0.965                   | 0.829                 |
| 384        | 1-39  | 0.970                   | 0.551                 |
| 386        | 1-24  | 0.975                   | 0.881                 |
| 388        | 1-30  | 0.989                   | 0.868                 |
| 389        | 1-19  | 0.984                   | 0.941                 |
| 390        | 1-26  | 0.971                   | 0.782                 |
| 392        | 1-20  | 0.981                   | 0.900                 |
| 393        | 1-16  | 0.968                   | 0.890                 |
| 394        | 1-23  | 0.937                   | 0.701                 |
| 397        | 1-22  | 0.985                   | 0.854                 |
| 399        | 1-46  | 0.977                   | 0.698                 |
| 401        | 1-20  | 0.899                   | 0.567                 |
| 402        | 1-22  | 0.967                   | 0.931                 |
| 403        | 1-27  | 0.992                   | 0.934                 |
| 404        | 1-19  | 0.991                   | 0.973                 |
| 405        | 1-23  | 0.994                   | 0.921                 |
| 407        | 1-35  | 0.987                   | 0.658                 |
| 408        | 1-39  | 0.976                   | 0.551                 |
| 409        | 1-33  | 0.897                   | 0.570                 |
| 410        | 1-25  | 0.990                   | 0.962                 |
| 411        | 1-38  | 0.977                   | 0.827                 |
| 412        | 1-20  | 0.944                   | 0.768                 |
| 413        | 1-20  | 0.988                   | 0.965                 |
| 414        | 1-46  | 0.993                   | 0.638                 |
| 415        | 1-23  | 0.981                   | 0.940                 |
| 417        | 1-29  | 0.941                   | 0.672                 |
| 418        | 1-20  | 0.952                   | 0.850                 |
| 419        | 1-19  | 0.986                   | 0.967                 |
| 420        | 1-29  | 0.965                   | 0.861                 |
| 421        | 1-22  | 0.889                   | 0.785                 |
| 422        | 1-48  | 0.982                   | 0.862                 |
| 424        | 1-19  | 0.979                   | 0.933                 |
| 428        | 1-38  | 0.942                   | 0.653                 |
| 430        | 1-18  | 0.947                   | 0.595                 |
| 432        | 1-33  | 0.957                   | 0.789                 |
| 433        | 1-26  | 0.979                   | 0.904                 |
| 434        | 1-27  | 0.962                   | 0.777                 |
| 435        | 1-24  | 0.998                   | 0.977                 |
| 436        | 1-27  | 0.973                   | 0.772                 |
| 443        | 1-15  | 0.966                   | 0.940                 |
| 448        | 1-36  | 0.979                   | 0.804                 |
| 453        | 1-41  | 0.958                   | 0.609                 |
| 455        | 1-33  | 0.943                   | 0.606                 |
| 457        | 1-27  | 0.888                   | 0.597                 |
| 462        | 1-16  | 0.925                   | 0.681                 |
| 486        | 1-27  | 0.972                   | 0.845                 |
| 495        | 1-24  | 0.917                   | 0.636                 |
| 498        | 1-26  | 0.993                   | 0.890                 |
| 505        | 1-20  | 0.976                   | 0.926                 |
| 507        | 1-17  | 0.966                   | 0.687                 |
| 510        | 1-23  | 0.930                   | 0.593                 |

| SEQ ID NO: | POSITION OF<br>SIGNAL IN AMINO<br>ACID SEQUENCE | MaxS (MAXIMUM<br>SCORE) | MeanS (MEAN<br>SCORE) |
|------------|---|-------------------------|-----------------------|
| 511        | 1-23  | 0.930                   | 0.593                 |
| 512        | 1-23  | 0.930                   | 0.593                 |
| 515        | 1-18  | 0.978                   | 0.956                 |
| 523        | 1-19  | 0.936                   | 0.822                 |
| 529        | 1-22  | 0.963                   | 0.924                 |
| 545        | 1-24  | 0.982                   | 0.966                 |
| 550        | 1-30  | 0.933                   | 0.713                 |
| 552        | 1-21  | 0.973                   | 0.912                 |
| 554        | 1-23  | 0.969                   | 0.784                 |
| 571        | 1-21  | 0.918                   | 0.815                 |
| 574        | 1-31  | 0.988                   | 0.912                 |
| 580        | 1-39  | 0.525                   | 0.556                 |
| 594        | 1-31  | 0.974                   | 0.839                 |
| 608        | 1-29  | 0.932                   | 0.632                 |
| 609        | 1-29  | 0.932                   | 0.632                 |
| 610        | 1-21  | 0.990                   | 0.948                 |
| 621        | 1-15  | 0.994                   | 0.969                 |
| 623        | 1-33  | 0.935                   | 0.726                 |
| 653        | 1-27  | 0.938                   | 0.827                 |
| 668        | 1-22  | 0.929                   | 0.788                 |
| 677        | 1-16  | 0.948                   | 0.807                 |
| 685        | 1-21  | 0.881                   | 0.715                 |
| 699        | 1-22  | 0.975                   | 0.816                 |
| 702        | 1-31  | 0.968                   | 0.898                 |
| 707        | 1-16  | 0.880                   | 0.562                 |
| 713        | 1-25  | 0.966                   | 0.743                 |
| 718        | 1-19  | 0.936                   | 0.822                 |
| 719        | 1-20  | 0.961                   | 0.824                 |
| 729        | 1-29  | 0.972                   | 0.874                 |
| 735        | 1-46  | 0.903                   | 0.598                 |
| 746        | 1-14  | 0.916                   | 0.730                 |
| 747        | 1-22  | 0.965                   | 0.876                 |
| 748        | 1-29  | 0.968                   | 0.785                 |
| 759        | 1-24  | 0.961                   | 0.773                 |
| 767        | 1-27  | 0.919                   | 0.768                 |
| 768        | 1-33  | 0.900                   | 0.585                 |
| 773        | 1-42  | 0.959                   | 0.702                 |
| 779        | 1-19  | 0.986                   | 0.945                 |
| 797        | 1-19  | 0.944                   | 0.759                 |
| 798        | 1-19  | 0.900                   | 0.568                 |
| 820        | 1-17  | 0.995                   | 0.950                 |
| 827        | 1-49  | 0.971                   | 0.749                 |
| 848        | 1-20  | 0.968                   | 0.874                 |
| 864        | 1-20  | 0.928                   | 0.782                 |
| 866        | 1-19  | 0.986                   | 0.934                 |
| 873        | 1-23  | 0.948                   | 0.886                 |
| 881        | 1-28  | 0.965                   | 0.829                 |
| 887        | 1-39  | 0.970                   | 0.551                 |
| 927        | 1-30  | 0.985                   | 0.868                 |
| 934        | 1-48  | 0.988                   | 0.777                 |
| 939        | 1-39  | 0.994                   | 0.889                 |
| 944        | 1-26  | 0.971                   | 0.782                 |
| 950        | 1-29  | 0.957                   | 0.845                 |
| 963        | 1-20  | 0.981                   | 0.900                 |
| 964        | 1-20  | 0.886                   | 0.558                 |
| 973        | 1-16  | 0.968                   | 0.890                 |
| 980        | 1-34  | 0.961                   | 0.749                 |
| 981        | 1-20  | 0.953                   | 0.822                 |
| 984        | 1-12  | 0.938                   | 0.780                 |
| 1015       | 1-22  | 0.985                   | 0.854                 |
| 1040       | 1-46  | 0.977                   | 0.698                 |
| 1052       | 1-18  | 0.969                   | 0.842                 |
| 1059       | 1-20  | 0.927                   | 0.867                 |
| 1065       | 1-33  | 0.983                   | 0.918                 |
| 1069       | 1-22  | 0.993                   | 0.935                 |

| SEQ ID NO: | POSITION OF<br>SIGNAL IN AMINO<br>ACID SEQUENCE | MaxS (MAXIMUM<br>SCORE) | Means (MEAN<br>SCORE) |
|------------|---|-------------------------|-----------------------|
| 1075       | 1-27  | 0.992                   | 0.934                 |
| 1080       | 1-19  | 0.931                   | 0.829                 |
| 1092       | 1-19  | 0.991                   | 0.973                 |
| 1094       | 1-46  | 0.992                   | 0.653                 |
| 1095       | 1-30  | 0.974                   | 0.929                 |
| 1105       | 1-23  | 0.994                   | 0.921                 |
| 1123       | 1-35  | 0.987                   | 0.658                 |
| 1138       | 1-32  | 0.954                   | 0.613                 |
| 1140       | 1-38  | 0.989                   | 0.789                 |
| 1142       | 1-33  | 0.897                   | 0.570                 |
| 1152       | 1-25  | 0.990                   | 0.962                 |
| 1170       | 1-38  | 0.977                   | 0.827                 |
| 1176       | 1-20  | 0.944                   | 0.768                 |
| 1187       | 1-20  | 0.988                   | 0.965                 |
| 1189       | 1-35  | 0.967                   | 0.839                 |
| 1192       | 1-46  | 0.993                   | 0.638                 |
| 1193       | 1-16  | 0.925                   | 0.710                 |
| 1197       | 1-29  | 0.985                   | 0.853                 |
| 1208       | 1-23  | 0.981                   | 0.940                 |
| 1225       | 1-29  | 0.941                   | 0.672                 |
| 1245       | 1-19  | 0.986                   | 0.967                 |
| 1258       | 1-29  | 0.965                   | 0.861                 |
| 1265       | 1-22  | 0.889                   | 0.785                 |
| 1266       | 1-20  | 0.944                   | 0.809                 |
| 1276       | 1-48  | 0.982                   | 0.862                 |
| 1292       | 1-19  | 0.979                   | 0.933                 |
| 1296       | 1-21  | 0.984                   | 0.944                 |
| 1297       | 1-19  | 0.984                   | 0.953                 |
| 1332       | 1-38  | 0.942                   | 0.653                 |
| 1358       | 1-18  | 0.947                   | 0.595                 |
| 1371       | 1-33  | 0.957                   | 0.789                 |
| 1380       | 1-26  | 0.979                   | 0.904                 |
| 1397       | 1-27  | 0.962                   | 0.777                 |
| 1399       | 1-23  | 0.997                   | 0.960                 |
| 1404       | 1-24  | 0.998                   | 0.977                 |
| 1410       | 1-15  | 0.946                   | 0.845                 |
| 1414       | 1-24  | 0.913                   | 0.588                 |
| 1415       | 1-19  | 0.982                   | 0.929                 |
| 1416       | 1-12  | 0.931                   | 0.891                 |
| 1418       | 1-30  | 0.933                   | 0.563                 |
| 1420       | 1-20  | 0.881                   | 0.561                 |
| 1421       | 1-19  | 0.990                   | 0.968                 |
| 1423       | 1-17  | 0.968                   | 0.863                 |
| 1424       | 1-21  | 0.885                   | 0.591                 |
| 1425       | 1-24  | 0.913                   | 0.588                 |
| 1426       | 1-24  | 0.913                   | 0.588                 |
| 1428       | 1-25  | 0.957                   | 0.899                 |
| 1430       | 1-34  | 0.977                   | 0.819                 |
| 1431       | 1-28  | 0.979                   | 0.923                 |
| 1432       | 1-36  | 0.957                   | 0.613                 |
| 1433       | 1-32  | 0.921                   | 0.753                 |
| 1434       | 1-39  | 0.983                   | 0.621                 |
| 1435       | 1-25  | 0.910                   | 0.631                 |
| 1436       | 1-42  | 0.988                   | 0.868                 |
| 1437       | 1-22  | 0.998                   | 0.980                 |
| 1442       | 1-20  | 0.918                   | 0.753                 |
| 1448       | 1-12  | 0.931                   | 0.891                 |
| 1462       | 1-18  | 0.968                   | 0.888                 |
| 1490       | 1-20  | 0.881                   | 0.561                 |
| 1518       | 1-17  | 0.968                   | 0.863                 |
| 1525       | 1-21  | 0.885                   | 0.591                 |
| 1547       | 1-28  | 0.974                   | 0.891                 |
| 1561       | 1-25  | 0.967                   | 0.899                 |
| 1580       | 1-17  | 0.923                   | 0.824                 |
| 1593       | 1-28  | 0.979                   | 0.923                 |

| SEQ ID NO: | POSITION OF<br>SIGNAL IN AMINO<br>ACID SEQUENCE | MaxS (MAXIMUM<br>SCORE) | MeanS (MEAN<br>SCORE) |
|------------|---|-------------------------|-----------------------|
| 1596       | 1-16  | 0.929                   | 0.709                 |
| 1601       | 1-36  | 0.957                   | 0.613                 |
| 1606       | 1-22  | 0.979                   | 0.831                 |
| 1607       | 1-20  | 0.974                   | 0.770                 |
| 1608       | 1-32  | 0.921                   | 0.753                 |
| 1614       | 1-33  | 0.969                   | 0.829                 |
| 1616       | 1-20  | 0.959                   | 0.869                 |
| 1625       | 1-39  | 0.983                   | 0.621                 |
| 1632       | 1-25  | 0.910                   | 0.631                 |
| 1636       | 1-33  | 0.897                   | 0.591                 |
| 1639       | 1-42  | 0.988                   | 0.868                 |
| 1645       | 1-20  | 0.927                   | 0.568                 |
| 1647       | 1-17  | 0.923                   | 0.742                 |
| 1648       | 1-22  | 0.998                   | 0.980                 |

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TABLE 6

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 1  | 1787   | 3573  | 5359  | 784CIP2_1   | 1103                                       |
| 2  | 1788   | 3574  | 5360  | 784CIP2_2   | 2673                                       |
| 3  | 1789   | 3575  | 5361  | 784CIP2_3   | 4117                                       |
| 4  | 1790   | 3576  | 5362  | 784CIP2_4   | 5556                                       |
| 5  | 1791   | 3577  | 5363  | 784CIP2_5   | 5562                                       |
| 6  | 1792   | 3578  | 5364  | 784CIP2_6   | 5562                                       |
| 7  | 1793   | 3579  | 5365  | 784CIP2_7   | 5562                                       |
| 8  | 1794   | 3580  | 5366  | 784CIP2_8   | 5562                                       |
| 9  | 1795   | 3581  | 5367  | 784CIP2_9   | 5563                                       |
| 10   | 1796   | 3582  | 5368  | 784CIP2_10  | 5564                                       |
| 11   | 1797   | 3583  | 5369  | 784CIP2_11  | 5565                                       |
| 12   | 1798   | 3584  | 5370  | 784CIP2_12  | 5689                                       |
| 13   | 1799   | 3585  | 5371  | 784CIP2_13  | 5729                                       |
| 14   | 1800   | 3586  | 5372  | 784CIP2_14  | 5745                                       |
| 15   | 1801   | 3587  | 5373  | 784CIP2_15  | 5777                                       |
| 16   | 1802   | 3588  | 5374  | 784CIP2_16  | 5777                                       |
| 17   | 1803   | 3589  | 5375  | 784CIP2_17  | 5789                                       |
| 18   | 1804   | 3590  | 5376  | 784CIP2_18  | 5792                                       |
| 19   | 1805   | 3591  | 5377  | 784CIP2_19  | 5804                                       |
| 20   | 1806   | 3592  | 5378  | 784CIP2_20  | 5805                                       |
| 21   | 1807   | 3593  | 5379  | 784CIP2_21  | 5805                                       |
| 22   | 1808   | 3594  | 5380  | 784CIP2_22  | 5844                                       |
| 23   | 1809   | 3595  | 5381  | 784CIP2_23  | 5844                                       |
| 24   | 1810   | 3596  | 5382  | 784CIP2_24  | 5850                                       |
| 25   | 1811   | 3597  | 5383  | 784CIP2_25  | 5867                                       |
| 26   | 1812   | 3598  | 5384  | 784CIP2_26  | 5973                                       |
| 27   | 1813   | 3599  | 5385  | 784CIP2_27  | 5995                                       |
| 28   | 1814   | 3600  | 5386  | 784CIP2_28  | 5995                                       |
| 29   | 1815   | 3601  | 5387  | 784CIP2_29  | 6005                                       |
| 30   | 1816   | 3602  | 5388  | 784CIP2_30  | 6007                                       |
| 31   | 1817   | 3603  | 5389  | 784CIP2_31  | 6007                                       |
| 32   | 1818   | 3604  | 5390  | 784CIP2_32  | 6009                                       |
| 33   | 1819   | 3605  | 5391  | 784CIP2_33  | 6012                                       |
| 34   | 1820   | 3606  | 5392  | 784CIP2_34  | 6015                                       |
| 35   | 1821   | 3607  | 5393  | 784CIP2_35  | 6016                                       |
| 36   | 1822   | 3608  | 5394  | 784CIP2_36  | 6016                                       |
| 37   | 1823   | 3609  | 5395  | 784CIP2_37  | 6018                                       |
| 38   | 1824   | 3610  | 5396  | 784CIP2_38  | 6018                                       |
| 39   | 1825   | 3611  | 5397  | 784CIP2_39  | 6018                                       |
| 40   | 1826   | 3612  | 5398  | 784CIP2_40  | 6023                                       |
| 41   | 1827   | 3613  | 5399  | 784CIP2_41  | 6070                                       |
| 42   | 1828   | 3614  | 5400  | 784CIP2_42  | 6081                                       |
| 43   | 1829   | 3615  | 5401  | 784CIP2_43  | 6089                                       |
| 44   | 1830   | 3616  | 5402  | 784CIP2_44  | 6118                                       |
| 45   | 1831   | 3617  | 5403  | 784CIP2_45  | 6118                                       |
| 46   | 1832   | 3618  | 5404  | 784CIP2_46  | 6130                                       |
| 47   | 1833   | 3619  | 5405  | 784CIP2_47  | 6177                                       |
| 48   | 1834   | 3620  | 5406  | 784CIP2_48  | 6189                                       |
| 49   | 1835   | 3621  | 5407  | 784CIP2_49  | 6191                                       |
| 50   | 1836   | 3622  | 5408  | 784CIP2_50  | 6204                                       |
| 51   | 1837   | 3623  | 5409  | 784CIP2_51  | 6204                                       |
| 52   | 1838   | 3624  | 5410  | 784CIP2_52  | 6284                                       |
| 53   | 1839   | 3625  | 5411  | 784CIP2_53  | 6367                                       |
| 54   | 1840   | 3626  | 5412  | 784CIP2_54  | 6436                                       |
| 55   | 1841   | 3627  | 5413  | 784CIP2_55  | 6442                                       |
| 56   | 1842   | 3628  | 5414  | 784CIP2_56  | 6445                                       |
| 57   | 1843   | 3629  | 5415  | 784CIP2_57  | 6457                                       |
| 58   | 1844   | 3630  | 5416  | 784CIP2_58  | 6458                                       |
| 59   | 1845   | 3631  | 5417  | 784CIP2_59  | 6458                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding_<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|--|--|
| 60   | 1846   | 3632  | 5418  | 784CIP2_60   | 6462                                       |
| 61   | 1847   | 3633  | 5419  | 784CIP2_61   | 6472                                       |
| 62   | 1848   | 3634  | 5420  | 784CIP2_62   | 6499                                       |
| 63   | 1849   | 3635  | 5421  | 784CIP2_63   | 6499                                       |
| 64   | 1850   | 3636  | 5422  | 784CIP2_64   | 6505                                       |
| 65   | 1851   | 3637  | 5423  | 784CIP2_65   | 6534                                       |
| 66   | 1852   | 3638  | 5424  | 784CIP2_66   | 6534                                       |
| 67   | 1853   | 3639  | 5425  | 784CIP2_67   | 6540                                       |
| 68   | 1854   | 3640  | 5426  | 784CIP2_68   | 6550                                       |
| 69   | 1855   | 3641  | 5427  | 784CIP2_69   | 6550                                       |
| 70   | 1856   | 3642  | 5428  | 784CIP2_70   | 6592                                       |
| 71   | 1857   | 3643  | 5429  | 784CIP2_71   | 6645                                       |
| 72   | 1858   | 3644  | 5430  | 784CIP2_72   | 6671                                       |
| 73   | 1859   | 3645  | 5431  | 784CIP2_73   | 6763                                       |
| 74   | 1860   | 3646  | 5432  | 784CIP2_74   | 6763                                       |
| 75   | 1861   | 3647  | 5433  | 784CIP2_75   | 6786                                       |
| 76   | 1862   | 3648  | 5434  | 784CIP2_76   | 6824                                       |
| 77   | 1863   | 3649  | 5435  | 784CIP2_77   | 6830                                       |
| 78   | 1864   | 3650  | 5436  | 784CIP2_78   | 6831                                       |
| 79   | 1865   | 3651  | 5437  | 784CIP2_79   | 6832                                       |
| 80   | 1866   | 3652  | 5438  | 784CIP2_80   | 6834                                       |
| 81   | 1867   | 3653  | 5439  | 784CIP2_81   | 6834                                       |
| 82   | 1868   | 3654  | 5440  | 784CIP2_82   | 6835                                       |
| 83   | 1869   | 3655  | 5441  | 784CIP2_83   | 6837                                       |
| 84   | 1870   | 3656  | 5442  | 784CIP2_84   | 6843                                       |
| 85   | 1871   | 3657  | 5443  | 784CIP2_85   | 6859                                       |
| 86   | 1872   | 3658  | 5444  | 784CIP2_86   | 6915                                       |
| 87   | 1873   | 3659  | 5445  | 784CIP2_87   | 6932                                       |
| 88   | 1874   | 3660  | 5446  | 784CIP2_88   | 6957                                       |
| 89   | 1875   | 3661  | 5447  | 784CIP2_89   | 6961                                       |
| 90   | 1876   | 3662  | 5448  | 784CIP2_90   | 6973                                       |
| 91   | 1877   | 3663  | 5449  | 784CIP2_91   | 6973                                       |
| 92   | 1878   | 3664  | 5450  | 784CIP2_93   | 7007                                       |
| 93   | 1879   | 3665  | 5451  | 784CIP2_94   | 7018                                       |
| 94   | 1880   | 3666  | 5452  | 784CIP2_95   | 7019                                       |
| 95   | 1881   | 3667  | 5453  | 784CIP2_96   | 7020                                       |
| 96   | 1882   | 3668  | 5454  | 784CIP2_97   | 7020                                       |
| 97   | 1883   | 3669  | 5455  | 784CIP2_98   | 7021                                       |
| 98   | 1884   | 3670  | 5456  | 784CIP2_99   | 7023                                       |
| 99   | 1885   | 3671  | 5457  | 784CIP2_100  | 7027                                       |
| 100  | 1886   | 3672  | 5458  | 784CIP2_101  | 7028                                       |
| 101  | 1887   | 3673  | 5459  | 784CIP2_102  | 7029                                       |
| 102  | 1888   | 3674  | 5460  | 784CIP2_103  | 7031                                       |
| 103  | 1889   | 3675  | 5461  | 784CIP2_104  | 7032                                       |
| 104  | 1890   | 3676  | 5462  | 784CIP2_105  | 7033                                       |
| 105  | 1891   | 3677  | 5463  | 784CIP2_106  | 7035                                       |
| 106  | 1892   | 3678  | 5464  | 784CIP2_107  | 7036                                       |
| 107  | 1893   | 3679  | 5465  | 784CIP2_108  | 7039                                       |
| 108  | 1894   | 3680  | 5466  | 784CIP2_109  | 7043                                       |
| 109  | 1895   | 3681  | 5467  | 784CIP2_110  | 7044                                       |
| 110  | 1896   | 3682  | 5468  | 784CIP2_111  | 7046                                       |
| 111  | 1897   | 3683  | 5469  | 784CIP2_112  | 7054                                       |
| 112  | 1898   | 3684  | 5470  | 784CIP2_113  | 7061                                       |
| 113  | 1899   | 3685  | 5471  | 784CIP2_114  | 7077                                       |
| 114  | 1900   | 3686  | 5472  | 784CIP2_115  | 7092                                       |
| 115  | 1901   | 3687  | 5473  | 784CIP2_116  | 7094                                       |
| 116  | 1902   | 3688  | 5474  | 784CIP2_117  | 7106                                       |
| 117  | 1903   | 3689  | 5475  | 784CIP2_118  | 7107                                       |
| 118  | 1904   | 3690  | 5476  | 784CIP2_119  | 7111                                       |
| 119  | 1905   | 3691  | 5477  | 784CIP2_120  | 7123                                       |
| 120  | 1906   | 3692  | 5478  | 784CIP2_121  | 7142                                       |
| 121  | 1907   | 3693  | 5479  | 784CIP2_122  | 7142                                       |



| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 122  | 1908   | 3694  | 5480  | 784CIP2_123   | 7154                                       |
| 123  | 1909   | 3695  | 5481  | 784CIP2_124   | 7160                                       |
| 124  | 1910   | 3696  | 5482  | 784CIP2_125   | 7169                                       |
| 125  | 1911   | 3697  | 5483  | 784CIP2_126   | 7185                                       |
| 126  | 1912   | 3698  | 5484  | 784CIP2_127   | 7197                                       |
| 127  | 1913   | 3699  | 5485  | 784CIP2_128   | 7219                                       |
| 128  | 1914   | 3700  | 5486  | 784CIP2_129   | 7226                                       |
| 129  | 1915   | 3701  | 5487  | 784CIP2_130   | 7229                                       |
| 130  | 1916   | 3702  | 5488  | 784CIP2_131   | 7234                                       |
| 131  | 1917   | 3703  | 5489  | 784CIP2_132   | 7235                                       |
| 132  | 1918   | 3704  | 5490  | 784CIP2_133   | 7238                                       |
| 133  | 1919   | 3705  | 5491  | 784CIP2_134   | 7247                                       |
| 134  | 1920   | 3706  | 5492  | 784CIP2_135   | 7261                                       |
| 135  | 1921   | 3707  | 5493  | 784CIP2_136   | 7262                                       |
| 136  | 1922   | 3708  | 5494  | 784CIP2_137   | 7267                                       |
| 137  | 1923   | 3709  | 5495  | 784CIP2_138   | 7272                                       |
| 138  | 1924   | 3710  | 5496  | 784CIP2_139   | 7273                                       |
| 139  | 1925   | 3711  | 5497  | 784CIP2_140   | 7282                                       |
| 140  | 1926   | 3712  | 5498  | 784CIP2_141   | 7288                                       |
| 141  | 1927   | 3713  | 5499  | 784CIP2_142   | 7291                                       |
| 142  | 1928   | 3714  | 5500  | 784CIP2_143   | 7293                                       |
| 143  | 1929   | 3715  | 5501  | 784CIP2_144   | 7294                                       |
| 144  | 1930   | 3716  | 5502  | 784CIP2_145   | 7299                                       |
| 145  | 1931   | 3717  | 5503  | 784CIP2_146   | 7300                                       |
| 146  | 1932   | 3718  | 5504  | 784CIP2_147   | 7312                                       |
| 147  | 1933   | 3719  | 5505  | 784CIP2_148   | 7313                                       |
| 148  | 1934   | 3720  | 5506  | 784CIP2_149   | 7315                                       |
| 149  | 1935   | 3721  | 5507  | 784CIP2_150   | 7318                                       |
| 150  | 1936   | 3722  | 5508  | 784CIP2_151   | 7321                                       |
| 151  | 1937   | 3723  | 5509  | 784CIP2_152   | 7330                                       |
| 152  | 1938   | 3724  | 5510  | 784CIP2_153   | 7331                                       |
| 153  | 1939   | 3725  | 5511  | 784CIP2_154   | 7333                                       |
| 154  | 1940   | 3726  | 5512  | 784CIP2_155   | 7350                                       |
| 155  | 1941   | 3727  | 5513  | 784CIP2_156   | 7352                                       |
| 156  | 1942   | 3728  | 5514  | 784CIP2_157   | 7384                                       |
| 157  | 1943   | 3729  | 5515  | 784CIP2_158   | 7403                                       |
| 158  | 1944   | 3730  | 5516  | 784CIP2_159   | 7431                                       |
| 159  | 1945   | 3731  | 5517  | 784CIP2_160   | 7441                                       |
| 160  | 1946   | 3732  | 5518  | 784CIP2_161   | 7453                                       |
| 161  | 1947   | 3733  | 5519  | 784CIP2_162   | 7467                                       |
| 162  | 1948   | 3734  | 5520  | 784CIP2_163   | 7471                                       |
| 163  | 1949   | 3735  | 5521  | 784CIP2_164   | 7493                                       |
| 164  | 1950   | 3736  | 5522  | 784CIP2_165   | 7502                                       |
| 165  | 1951   | 3737  | 5523  | 784CIP2_166   | 7511                                       |
| 166  | 1952   | 3738  | 5524  | 784CIP2_167   | 7514                                       |
| 167  | 1953   | 3739  | 5525  | 784CIP2_168   | 7520                                       |
| 168  | 1954   | 3740  | 5526  | 784CIP2_169   | 7541                                       |
| 169  | 1955   | 3741  | 5527  | 784CIP2_170   | 7570                                       |
| 170  | 1956   | 3742  | 5528  | 784CIP2_171   | 7578                                       |
| 171  | 1957   | 3743  | 5529  | 784CIP2_172   | 7583                                       |
| 172  | 1958   | 3744  | 5530  | 784CIP2_173   | 7592                                       |
| 173  | 1959   | 3745  | 5531  | 784CIP2_174   | 7601                                       |
| 174  | 1960   | 3746  | 5532  | 784CIP2_175   | 7602                                       |
| 175  | 1961   | 3747  | 5533  | 784CIP2_176   | 7608                                       |
| 176  | 1962   | 3748  | 5534  | 784CIP2_177   | 7615                                       |
| 177  | 1963   | 3749  | 5535  | 784CIP2_178   | 7617                                       |
| 178  | 1964   | 3750  | 5536  | 784CIP2_179   | 7624                                       |
| 179  | 1965   | 3751  | 5537  | 784CIP2_181   | 7626                                       |
| 180  | 1966   | 3752  | 5538  | 784CIP2_182   | 7640                                       |
| 181  | 1967   | 3753  | 5539  | 784CIP2_183   | 7641                                       |
| 182  | 1968   | 3754  | 5540  | 784CIP2_184   | 7641                                       |
| 183  | 1969   | 3755  | 5541  | 784CIP2_185   | 7641                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|--|--|
| 184  | 1970   | 3756  | 5542  | 784CIP2_186  | 7641                                       |
| 185  | 1971   | 3757  | 5543  | 784CIP2_187  | 7642                                       |
| 186  | 1972   | 3758  | 5544  | 784CIP2_188  | 7649                                       |
| 187  | 1973   | 3759  | 5545  | 784CIP2_189  | 7656                                       |
| 188  | 1974   | 3760  | 5546  | 784CIP2_190  | 7657                                       |
| 189  | 1975   | 3761  | 5547  | 784CIP2_191  | 7657                                       |
| 190  | 1976   | 3762  | 5548  | 784CIP2_192  | 7662                                       |
| 191  | 1977   | 3763  | 5549  | 784CIP2_193  | 7668                                       |
| 192  | 1978   | 3764  | 5550  | 784CIP2_194  | 7673                                       |
| 193  | 1979   | 3765  | 5551  | 784CIP2_195  | 7690                                       |
| 194  | 1980   | 3766  | 5552  | 784CIP2_196  | 7700                                       |
| 195  | 1981   | 3767  | 5553  | 784CIP2_197  | 7709                                       |
| 196  | 1982   | 3768  | 5554  | 784CIP2_198  | 7736                                       |
| 197  | 1983   | 3769  | 5555  | 784CIP2_199  | 7737                                       |
| 198  | 1984   | 3770  | 5556  | 784CIP2_200  | 7744                                       |
| 199  | 1985   | 3771  | 5557  | 784CIP2_201  | 7771                                       |
| 200  | 1986   | 3772  | 5558  | 784CIP2_202  | 7786                                       |
| 201  | 1987   | 3773  | 5559  | 784CIP2_203  | 7791                                       |
| 202  | 1988   | 3774  | 5560  | 784CIP2_204  | 7797                                       |
| 203  | 1989   | 3775  | 5561  | 784CIP2_205  | 7806                                       |
| 204  | 1990   | 3776  | 5562  | 784CIP2_206  | 7812                                       |
| 205  | 1991   | 3777  | 5563  | 784CIP2_207  | 7812                                       |
| 206  | 1992   | 3778  | 5564  | 784CIP2_208  | 7818                                       |
| 207  | 1993   | 3779  | 5565  | 784CIP2_209  | 7822                                       |
| 208  | 1994   | 3780  | 5566  | 784CIP2_210  | 7827                                       |
| 209  | 1995   | 3781  | 5567  | 784CIP2_211  | 7830                                       |
| 210  | 1995   | 3782  | 5568  | 784CIP2_212  | 7835                                       |
| 211  | 1997   | 3783  | 5569  | 784CIP2_214  | 7840                                       |
| 212  | 1998   | 3784  | 5570  | 784CIP2_215  | 7858                                       |
| 213  | 1999   | 3785  | 5571  | 784CIP2_216  | 7858                                       |
| 214  | 2000   | 3786  | 5572  | 784CIP2_217  | 7861                                       |
| 215  | 2001   | 3787  | 5573  | 784CIP2_218  | 7866                                       |
| 216  | 2002   | 3788  | 5574  | 784CIP2_219  | 7868                                       |
| 217  | 2003   | 3789  | 5575  | 784CIP2_220  | 7896                                       |
| 218  | 2004   | 3790  | 5576  | 784CIP2_221  | 7898                                       |
| 219  | 2005   | 3791  | 5577  | 784CIP2_222  | 7900                                       |
| 220  | 2006   | 3792  | 5578  | 784CIP2_223  | 7906                                       |
| 221  | 2007   | 3793  | 5579  | 784CIP2_224  | 7908                                       |
| 222  | 2008   | 3794  | 5580  | 784CIP2_225  | 7909                                       |
| 223  | 2009   | 3795  | 5581  | 784CIP2_226  | 7917                                       |
| 224  | 2010   | 3796  | 5582  | 784CIP2_227  | 7932                                       |
| 225  | 2011   | 3797  | 5583  | 784CIP2_228  | 7940                                       |
| 226  | 2012   | 3798  | 5584  | 784CIP2_229  | 7940                                       |
| 227  | 2013   | 3799  | 5585  | 784CIP2_230  | 7984                                       |
| 228  | 2014   | 3800  | 5586  | 784CIP2_231  | 7984                                       |
| 229  | 2015   | 3801  | 5587  | 784CIP2_232  | 8001                                       |
| 230  | 2016   | 3802  | 5588  | 784CIP2_233  | 8021                                       |
| 231  | 2017   | 3803  | 5589  | 784CIP2_234  | 8029                                       |
| 232  | 2018   | 3804  | 5590  | 784CIP2_235  | 8033                                       |
| 233  | 2019   | 3805  | 5591  | 784CIP2_236  | 8040                                       |
| 234  | 2020   | 3806  | 5592  | 784CIP2_237  | 8052                                       |
| 235  | 2021   | 3807  | 5593  | 784CIP2_238  | 8096                                       |
| 236  | 2022   | 3808  | 5594  | 784CIP2_239  | 8096                                       |
| 237  | 2023   | 3809  | 5595  | 784CIP2_240  | 8113                                       |
| 238  | 2024   | 3810  | 5596  | 784CIP2_241  | 8126                                       |
| 239  | 2025   | 3811  | 5597  | 784CIP2_242  | 8132                                       |
| 240  | 2026   | 3812  | 5598  | 784CIP2_243  | 8137                                       |
| 241  | 2027   | 3813  | 5599  | 784CIP2_244  | 8137                                       |
| 242  | 2028   | 3814  | 5600  | 784CIP2_245  | 8159                                       |
| 243  | 2029   | 3815  | 5601  | 784CIP2_246  | 8159                                       |
| 244  | 2030   | 3816  | 5602  | 784CIP2_247  | 8161                                       |
| 245  | 2031   | 3817  | 5603  | 784CIP2_248  | 8176                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number,<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 246  | 2032   | 3818  | 5604  | 784CIP2_249   | 8196                                       |
| 247  | 2033   | 3819  | 5605  | 784CIP2_250   | 8200                                       |
| 248  | 2034   | 3820  | 5606  | 784CIP2_251   | 8212                                       |
| 249  | 2035   | 3821  | 5607  | 784CIP2_252   | 8220                                       |
| 250  | 2036   | 3822  | 5608  | 784CIP2_253   | 8238                                       |
| 251  | 2037   | 3823  | 5609  | 784CIP2_254   | 8254                                       |
| 252  | 2038   | 3824  | 5610  | 784CIP2_255   | 8255                                       |
| 253  | 2039   | 3825  | 5611  | 784CIP2_256   | 8288                                       |
| 254  | 2040   | 3826  | 5612  | 784CIP2_257   | 8296                                       |
| 255  | 2041   | 3827  | 5613  | 784CIP2_258   | 8329                                       |
| 256  | 2042   | 3828  | 5614  | 784CIP2_259   | 8362                                       |
| 257  | 2043   | 3829  | 5615  | 784CIP2_260   | 8429                                       |
| 258  | 2044   | 3830  | 5616  | 784CIP2_261   | 8436                                       |
| 259  | 2045   | 3831  | 5617  | 784CIP2_262   | 8448                                       |
| 260  | 2046   | 3832  | 5618  | 784CIP2_263   | 8472                                       |
| 261  | 2047   | 3833  | 5619  | 784CIP2_264   | 8502                                       |
| 262  | 2048   | 3834  | 5620  | 784CIP2_265   | 8504                                       |
| 263  | 2049   | 3835  | 5621  | 784CIP2_266   | 8507                                       |
| 264  | 2050   | 3836  | 5622  | 784CIP2_268   | 8509                                       |
| 265  | 2051   | 3837  | 5623  | 784CIP2_269   | 8515                                       |
| 266  | 2052   | 3838  | 5624  | 784CIP2_270   | 8519                                       |
| 267  | 2053   | 3839  | 5625  | 784CIP2_271   | 8530                                       |
| 268  | 2054   | 3840  | 5626  | 784CIP2_272   | 8532                                       |
| 269  | 2055   | 3841  | 5627  | 784CIP2_273   | 8532                                       |
| 270  | 2056   | 3842  | 5628  | 784CIP2_274   | 8539                                       |
| 271  | 2057   | 3843  | 5629  | 784CIP2_275   | 8541                                       |
| 272  | 2058   | 3844  | 5630  | 784CIP2_276   | 8543                                       |
| 273  | 2059   | 3845  | 5631  | 784CIP2_277   | 8593                                       |
| 274  | 2060   | 3846  | 5632  | 784CIP2_278   | 8595                                       |
| 275  | 2061   | 3847  | 5633  | 784CIP2_279   | 8615                                       |
| 276  | 2062   | 3848  | 5634  | 784CIP2_280   | 8620                                       |
| 277  | 2063   | 3849  | 5635  | 784CIP2_281   | 8621                                       |
| 278  | 2064   | 3850  | 5636  | 784CIP2_282   | 8623                                       |
| 279  | 2065   | 3851  | 5637  | 784CIP2_283   | 8625                                       |
| 280  | 2066   | 3852  | 5638  | 784CIP2_284   | 8628                                       |
| 281  | 2067   | 3853  | 5639  | 784CIP2_285   | 8628                                       |
| 282  | 2068   | 3854  | 5640  | 784CIP2_286   | 8629                                       |
| 283  | 2069   | 3855  | 5641  | 784CIP2_287   | 8630                                       |
| 284  | 2070   | 3856  | 5642  | 784CIP2_288   | 8631                                       |
| 285  | 2071   | 3857  | 5643  | 784CIP2_289   | 8633                                       |
| 286  | 2072   | 3858  | 5644  | 784CIP2_290   | 8634                                       |
| 287  | 2073   | 3859  | 5645  | 784CIP2_291   | 8635                                       |
| 288  | 2074   | 3860  | 5646  | 784CIP2_292   | 8636                                       |
| 289  | 2075   | 3861  | 5647  | 784CIP2_293   | 8659                                       |
| 290  | 2076   | 3862  | 5648  | 784CIP2_294   | 8660                                       |
| 291  | 2077   | 3863  | 5649  | 784CIP2_295   | 8667                                       |
| 292  | 2078   | 3864  | 5650  | 784CIP2_296   | 8667                                       |
| 293  | 2079   | 3865  | 5651  | 784CIP2_297   | 8685                                       |
| 294  | 2080   | 3866  | 5652  | 784CIP2_298   | 8805                                       |
| 295  | 2081   | 3867  | 5653  | 784CIP2_299   | 8896                                       |
| 296  | 2082   | 3868  | 5654  | 784CIP2_300   | 8978                                       |
| 297  | 2083   | 3869  | 5655  | 784CIP2_301   | 9046                                       |
| 298  | 2084   | 3870  | 5656  | 784CIP2_302   | 9048                                       |
| 299  | 2085   | 3871  | 5657  | 784CIP2_303   | 9116                                       |
| 300  | 2086   | 3872  | 5658  | 784CIP2_304   | 9195                                       |
| 301  | 2087   | 3873  | 5659  | 784CIP2_305   | 9201                                       |
| 302  | 2088   | 3874  | 5660  | 784CIP2_306   | 9307                                       |
| 303  | 2089   | 3875  | 5661  | 784CIP2_307   | 9321                                       |
| 304  | 2090   | 3876  | 5662  | 784CIP2_308   | 9397                                       |
| 305  | 2091   | 3877  | 5663  | 784CIP2_309   | 9405                                       |
| 306  | 2092   | 3878  | 5664  | 784CIP2_310   | 9406                                       |
| 307  | 2093   | 3879  | 5665  | 784CIP2_311   | 9422                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 308  | 2094   | 3880  | 5666  | 784CIP2_312   | 9494                                       |
| 309  | 2095   | 3881  | 5667  | 784CIP2_313   | 9512                                       |
| 310  | 2096   | 3882  | 5668  | 784CIP2_314   | 9632                                       |
| 311  | 2097   | 3883  | 5669  | 784CIP2_315   | 9661                                       |
| 312  | 2098   | 3884  | 5670  | 784CIP2_316   | 9664                                       |
| 313  | 2099   | 3885  | 5671  | 784CIP2_317   | 9691                                       |
| 314  | 2100   | 3886  | 5672  | 784CIP2_318   | 9700                                       |
| 315  | 2101   | 3887  | 5673  | 784CIP2_319   | 9716                                       |
| 316  | 2102   | 3888  | 5674  | 784CIP2_320   | 9721                                       |
| 317  | 2103   | 3889  | 5675  | 784CIP2_321   | 9870                                       |
| 318  | 2104   | 3890  | 5676  | 784CIP2_322   | 9887                                       |
| 319  | 2105   | 3891  | 5677  | 784CIP2_323   | 9923                                       |
| 320  | 2106   | 3892  | 5678  | 784CIP2_324   | 9938                                       |
| 321  | 2107   | 3893  | 5679  | 784CIP2_325   | 9964                                       |
| 322  | 2108   | 3894  | 5680  | 784CIP2_326   | 10007                                      |
| 323  | 2109   | 3895  | 5681  | 784CIP2_327   | 10009                                      |
| 324  | 2110   | 3896  | 5682  | 784CIP2_328   | 10046                                      |
| 325  | 2111   | 3897  | 5683  | 784CIP2_329   | 10156                                      |
| 326  | 2112   | 3898  | 5684  | 784CIP2_330   | 10276                                      |
| 327  | 2113   | 3899  | 5685  | 784CIP2_331   | 10283                                      |
| 328  | 2114   | 3900  | 5686  | 784CIP2B_1  | 152  |
| 329  | 2115   | 3901  | 5687  | 784CIP2B_2  | 167  |
| 330  | 2116   | 3902  | 5688  | 784CIP2B_3  | 205  |
| 331  | 2117   | 3903  | 5689  | 784CIP2B_4  | 210  |
| 332  | 2118   | 3904  | 5690  | 784CIP2B_5  | 225  |
| 333  | 2119   | 3905  | 5691  | 784CIP2B_6  | 226  |
| 334  | 2120   | 3906  | 5692  | 784CIP2B_7  | 264  |
| 335  | 2121   | 3907  | 5693  | 784CIP2B_8  | 268  |
| 336  | 2122   | 3908  | 5694  | 784CIP2B_9  | 293  |
| 337  | 2123   | 3909  | 5695  | 784CIP2B_10   | 293  |
| 338  | 2124   | 3910  | 5696  | 784CIP2B_11   | 293  |
| 339  | 2125   | 3911  | 5697  | 784CIP2B_12   | 302  |
| 340  | 2126   | 3912  | 5698  | 784CIP2B_13   | 311  |
| 341  | 2127   | 3913  | 5699  | 784CIP2B_14   | 352  |
| 342  | 2128   | 3914  | 5700  | 784CIP2B_15   | 358  |
| 343  | 2129   | 3915  | 5701  | 784CIP2B_16   | 368  |
| 344  | 2130   | 3916  | 5702  | 784CIP2B_17   | 393  |
| 345  | 2131   | 3917  | 5703  | 784CIP2B_18   | 477  |
| 346  | 2132   | 3918  | 5704  | 784CIP2B_19   | 508  |
| 347  | 2133   | 3919  | 5705  | 784CIP2B_20   | 508  |
| 348  | 2134   | 3920  | 5706  | 784CIP2B_21   | 515  |
| 349  | 2135   | 3921  | 5707  | 784CIP2B_22   | 578  |
| 350  | 2136   | 3922  | 5708  | 784CIP2B_23   | 588  |
| 351  | 2137   | 3923  | 5709  | 784CIP2B_24   | 591  |
| 352  | 2138   | 3924  | 5710  | 784CIP2B_25   | 593  |
| 353  | 2139   | 3925  | 5711  | 784CIP2B_26   | 594  |
| 354  | 2140   | 3926  | 5712  | 784CIP2B_27   | 619  |
| 355  | 2141   | 3927  | 5713  | 784CIP2B_28   | 620  |
| 356  | 2142   | 3928  | 5714  | 784CIP2B_29   | 654  |
| 357  | 2143   | 3929  | 5715  | 784CIP2B_30   | 692  |
| 358  | 2144   | 3930  | 5716  | 784CIP2B_31   | 753  |
| 359  | 2145   | 3931  | 5717  | 784CIP2B_32   | 758  |
| 360  | 2146   | 3932  | 5718  | 784CIP2B_33   | 787  |
| 361  | 2147   | 3933  | 5719  | 784CIP2B_34   | 833  |
| 362  | 2148   | 3934  | 5720  | 784CIP2B_35   | 838  |
| 363  | 2149   | 3935  | 5721  | 784CIP2B_36   | 870  |
| 364  | 2150   | 3936  | 5722  | 784CIP2B_37   | 891  |
| 365  | 2151   | 3937  | 5723  | 784CIP2B_38   | 891  |
| 366  | 2152   | 3938  | 5724  | 784CIP2B_39   | 921  |
| 367  | 2153   | 3939  | 5725  | 784CIP2B_40   | 924  |
| 368  | 2154   | 3940  | 5726  | 784CIP2B_41   | 932  |
| 369  | 2155   | 3941  | 5727  | 784CIP2B_42   | 942  |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/408,725 |
|--|--|---|---|---|--|
| 370  | 2156   | 3942  | 5728  | 784CIP2B_43   | 958  |
| 371  | 2157   | 3943  | 5729  | 784CIP2B_44   | 968  |
| 372  | 2158   | 3944  | 5730  | 784CIP2B_45   | 992  |
| 373  | 2159   | 3945  | 5731  | 784CIP2B_46   | 1025                                       |
| 374  | 2160   | 3946  | 5732  | 784CIP2B_47   | 1074                                       |
| 375  | 2161   | 3947  | 5733  | 784CIP2B_48   | 1104                                       |
| 376  | 2162   | 3948  | 5734  | 784CIP2B_49   | 1114                                       |
| 377  | 2163   | 3949  | 5735  | 784CIP2B_50   | 1144                                       |
| 378  | 2164   | 3950  | 5736  | 784CIP2B_51   | 1262                                       |
| 379  | 2165   | 3951  | 5737  | 784CIP2B_52   | 1318                                       |
| 380  | 2166   | 3952  | 5738  | 784CIP2B_53   | 1319                                       |
| 381  | 2167   | 3953  | 5739  | 784CIP2B_54   | 1328                                       |
| 382  | 2168   | 3954  | 5740  | 784CIP2B_55   | 1436                                       |
| 383  | 2169   | 3955  | 5741  | 784CIP2B_56   | 1464                                       |
| 384  | 2170   | 3956  | 5742  | 784CIP2B_57   | 1584                                       |
| 385  | 2171   | 3957  | 5743  | 784CIP2B_58   | 1617                                       |
| 386  | 2172   | 3958  | 5744  | 784CIP2B_59   | 1724                                       |
| 387  | 2173   | 3959  | 5745  | 784CIP2B_60   | 1728                                       |
| 388  | 2174   | 3960  | 5746  | 784CIP2B_61   | 1772                                       |
| 389  | 2175   | 3961  | 5747  | 784CIP2B_62   | 1809                                       |
| 390  | 2176   | 3962  | 5748  | 784CIP2B_63   | 1868                                       |
| 391  | 2177   | 3963  | 5749  | 784CIP2B_64   | 1898                                       |
| 392  | 2178   | 3964  | 5750  | 784CIP2B_65   | 1926                                       |
| 393  | 2179   | 3965  | 5751  | 784CIP2B_66   | 1965                                       |
| 394  | 2180   | 3966  | 5752  | 784CIP2B_67   | 1967                                       |
| 395  | 2181   | 3967  | 5753  | 784CIP2B_68   | 1995                                       |
| 396  | 2182   | 3968  | 5754  | 784CIP2B_69   | 2005                                       |
| 397  | 2183   | 3969  | 5755  | 784CIP2B_70   | 2027                                       |
| 398  | 2184   | 3970  | 5756  | 784CIP2B_71   | 2055                                       |
| 399  | 2185   | 3971  | 5757  | 784CIP2B_72   | 2103                                       |
| 400  | 2186   | 3972  | 5758  | 784CIP2B_73   | 2106                                       |
| 401  | 2187   | 3973  | 5759  | 784CIP2B_74   | 2166                                       |
| 402  | 2188   | 3974  | 5760  | 784CIP2B_75   | 2175                                       |
| 403  | 2189   | 3975  | 5761  | 784CIP2B_76   | 2176                                       |
| 404  | 2190   | 3976  | 5762  | 784CIP2B_78   | 2236                                       |
| 405  | 2191   | 3977  | 5763  | 784CIP2B_79   | 2250                                       |
| 406  | 2192   | 3978  | 5764  | 784CIP2B_80   | 2300                                       |
| 407  | 2193   | 3979  | 5765  | 784CIP2B_81   | 2323                                       |
| 408  | 2194   | 3980  | 5766  | 784CIP2B_82   | 2340                                       |
| 409  | 2195   | 3981  | 5767  | 784CIP2B_83   | 2371                                       |
| 410  | 2196   | 3982  | 5768  | 784CIP2B_84   | 2399                                       |
| 411  | 2197   | 3983  | 5769  | 784CIP2B_85   | 2411                                       |
| 412  | 2198   | 3984  | 5770  | 784CIP2B_86   | 2428                                       |
| 413  | 2199   | 3985  | 5771  | 784CIP2B_87   | 2430                                       |
| 414  | 2200   | 3986  | 5772  | 784CIP2B_88   | 2439                                       |
| 415  | 2201   | 3987  | 5773  | 784CIP2B_89   | 2447                                       |
| 416  | 2202   | 3988  | 5774  | 784CIP2B_90   | 2461                                       |
| 417  | 2203   | 3989  | 5775  | 784CIP2B_91   | 2487                                       |
| 418  | 2204   | 3990  | 5776  | 784CIP2B_92   | 2492                                       |
| 419  | 2205   | 3991  | 5777  | 784CIP2B_93   | 2512                                       |
| 420  | 2206   | 3992  | 5778  | 784CIP2B_94   | 2564                                       |
| 421  | 2207   | 3993  | 5779  | 784CIP2B_95   | 2678                                       |
| 422  | 2208   | 3994  | 5780  | 784CIP2B_96   | 2816                                       |
| 423  | 2209   | 3995  | 5781  | 784CIP2B_97   | 2818                                       |
| 424  | 2210   | 3996  | 5782  | 784CIP2B_98   | 2819                                       |
| 425  | 2211   | 3997  | 5783  | 784CIP2B_99   | 2943                                       |
| 426  | 2212   | 3998  | 5784  | 784CIP2B_100  | 3137                                       |
| 427  | 2213   | 3999  | 5785  | 784CIP2B_101  | 3137                                       |
| 428  | 2214   | 4000  | 5786  | 784CIP2B_102  | 3160                                       |
| 429  | 2215   | 4001  | 5787  | 784CIP2B_103  | 3323                                       |
| 430  | 2216   | 4002  | 5788  | 784CIP2B_104  | 3360                                       |
| 431  | 2217   | 4003  | 5789  | 784CIP2B_105  | 3362                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 432  | 2218   | 4004  | 5790  | 784CIP2B_106  | 3417                                       |
| 433  | 2219   | 4005  | 5791  | 784CIP2B_107  | 3418                                       |
| 434  | 2220   | 4006  | 5792  | 784CIP2B_108  | 3442                                       |
| 435  | 2221   | 4007  | 5793  | 784CIP2B_109  | 3442                                       |
| 436  | 2222   | 4008  | 5794  | 784CIP2B_110  | 3444                                       |
| 437  | 2223   | 4009  | 5795  | 784CIP2B_111  | 3855                                       |
| 438  | 2224   | 4010  | 5796  | 784CIP2B_112  | 3863                                       |
| 439  | 2225   | 4011  | 5797  | 784CIP2B_113  | 4090                                       |
| 440  | 2226   | 4012  | 5798  | 784CIP2B_114  | 4105                                       |
| 441  | 2227   | 4013  | 5799  | 784CIP2B_115  | 4142                                       |
| 442  | 2228   | 4014  | 5800  | 784CIP2B_116  | 4142                                       |
| 443  | 2229   | 4015  | 5801  | 784CIP2B_117  | 4149                                       |
| 444  | 2230   | 4016  | 5802  | 784CIP2B_118  | 4196                                       |
| 445  | 2231   | 4017  | 5803  | 784CIP2B_119  | 4202                                       |
| 446  | 2232   | 4018  | 5804  | 784CIP2B_120  | 4274                                       |
| 447  | 2233   | 4019  | 5805  | 784CIP2B_121  | 4304                                       |
| 448  | 2234   | 4020  | 5806  | 784CIP2B_122  | 4306                                       |
| 449  | 2235   | 4021  | 5807  | 784CIP2B_123  | 4311                                       |
| 450  | 2236   | 4022  | 5808  | 784CIP2B_124  | 4321                                       |
| 451  | 2237   | 4023  | 5809  | 784CIP2B_125  | 4323                                       |
| 452  | 2238   | 4024  | 5810  | 784CIP2B_126  | 4332                                       |
| 453  | 2239   | 4025  | 5811  | 784CIP2B_127  | 4488                                       |
| 454  | 2240   | 4026  | 5812  | 784CIP2B_128  | 4588                                       |
| 455  | 2241   | 4027  | 5813  | 784CIP2B_129  | 5569                                       |
| 456  | 2242   | 4028  | 5814  | 784CIP2B_130  | 5573                                       |
| 457  | 2243   | 4029  | 5815  | 784CIP2B_131  | 5577                                       |
| 458  | 2244   | 4030  | 5816  | 784CIP2B_132  | 5579                                       |
| 459  | 2245   | 4031  | 5817  | 784CIP2B_133  | 5582                                       |
| 460  | 2246   | 4032  | 5818  | 784CIP2B_134  | 5583                                       |
| 461  | 2247   | 4033  | 5819  | 784CIP2B_135  | 5584                                       |
| 462  | 2248   | 4034  | 5820  | 784CIP2B_136  | 5585                                       |
| 463  | 2249   | 4035  | 5821  | 784CIP2B_137  | 5591                                       |
| 464  | 2250   | 4036  | 5822  | 784CIP2B_138  | 5593                                       |
| 465  | 2251   | 4037  | 5823  | 784CIP2B_139  | 5594                                       |
| 466  | 2252   | 4038  | 5824  | 784CIP2B_140  | 5594                                       |
| 467  | 2253   | 4039  | 5825  | 784CIP2B_141  | 5598                                       |
| 468  | 2254   | 4040  | 5826  | 784CIP2B_142  | 5602                                       |
| 469  | 2255   | 4041  | 5827  | 784CIP2B_143  | 5605                                       |
| 470  | 2256   | 4042  | 5828  | 784CIP2B_144  | 5608                                       |
| 471  | 2257   | 4043  | 5829  | 784CIP2B_145  | 5617                                       |
| 472  | 2258   | 4044  | 5830  | 784CIP2B_146  | 5620                                       |
| 473  | 2259   | 4045  | 5831  | 784CIP2B_147  | 5622                                       |
| 474  | 2260   | 4046  | 5832  | 784CIP2B_148  | 5623                                       |
| 475  | 2261   | 4047  | 5833  | 784CIP2B_149  | 5624                                       |
| 476  | 2262   | 4048  | 5834  | 784CIP2B_150  | 5625                                       |
| 477  | 2263   | 4049  | 5835  | 784CIP2B_151  | 5627                                       |
| 478  | 2264   | 4050  | 5836  | 784CIP2B_152  | 5628                                       |
| 479  | 2265   | 4051  | 5837  | 784CIP2B_153  | 5630                                       |
| 480  | 2266   | 4052  | 5838  | 784CIP2B_154  | 5632                                       |
| 481  | 2267   | 4053  | 5839  | 784CIP2B_155  | 5640                                       |
| 482  | 2268   | 4054  | 5840  | 784CIP2B_156  | 5641                                       |
| 483  | 2269   | 4055  | 5841  | 784CIP2B_157  | 5643                                       |
| 484  | 2270   | 4056  | 5842  | 784CIP2B_158  | 5647                                       |
| 485  | 2271   | 4057  | 5843  | 784CIP2B_159  | 5649                                       |
| 486  | 2272   | 4058  | 5844  | 784CIP2B_160  | 5658                                       |
| 487  | 2273   | 4059  | 5845  | 784CIP2B_161  | 5659                                       |
| 488  | 2274   | 4060  | 5846  | 784CIP2B_162  | 5667                                       |
| 489  | 2275   | 4061  | 5847  | 784CIP2B_163  | 5672                                       |
| 490  | 2276   | 4062  | 5848  | 784CIP2B_164  | 5674                                       |
| 491  | 2277   | 4063  | 5849  | 784CIP2B_165  | 5678                                       |
| 492  | 2278   | 4064  | 5850  | 784CIP2B_166  | 5680                                       |
| 493  | 2279   | 4065  | 5851  | 784CIP2B_167  | 5684                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 494  | 2280   | 4066  | 5852  | 784CIP2B_168  | 5686                                       |
| 495  | 2281   | 4067  | 5853  | 784CIP2B_169  | 5694                                       |
| 496  | 2282   | 4068  | 5854  | 784CIP2B_170  | 5698                                       |
| 497  | 2283   | 4069  | 5855  | 784CIP2B_171  | 5699                                       |
| 498  | 2284   | 4070  | 5856  | 784CIP2B_172  | 5712                                       |
| 499  | 2285   | 4071  | 5857  | 784CIP2B_173  | 5719                                       |
| 500  | 2286   | 4072  | 5858  | 784CIP2B_174  | 5720                                       |
| 501  | 2287   | 4073  | 5859  | 784CIP2B_175  | 5727                                       |
| 502  | 2288   | 4074  | 5860  | 784CIP2B_176  | 5730                                       |
| 503  | 2289   | 4075  | 5861  | 784CIP2B_177  | 5734                                       |
| 504  | 2290   | 4076  | 5862  | 784CIP2B_178  | 5738                                       |
| 505  | 2291   | 4077  | 5863  | 784CIP2B_179  | 5739                                       |
| 506  | 2292   | 4078  | 5864  | 784CIP2B_180  | 5740                                       |
| 507  | 2293   | 4079  | 5865  | 784CIP2B_181  | 5744                                       |
| 508  | 2294   | 4080  | 5866  | 784CIP2B_182  | 5748                                       |
| 509  | 2295   | 4081  | 5867  | 784CIP2B_183  | 5749                                       |
| 510  | 2296   | 4082  | 5868  | 784CIP2B_184  | 5750                                       |
| 511  | 2297   | 4083  | 5869  | 784CIP2B_185  | 5750                                       |
| 512  | 2298   | 4084  | 5870  | 784CIP2B_186  | 5750                                       |
| 513  | 2299   | 4085  | 5871  | 784CIP2B_187  | 5761                                       |
| 514  | 2300   | 4086  | 5872  | 784CIP2B_188  | 5762                                       |
| 515  | 2301   | 4087  | 5873  | 784CIP2B_189  | 5767                                       |
| 516  | 2302   | 4088  | 5874  | 784CIP2B_190  | 5773                                       |
| 517  | 2303   | 4089  | 5875  | 784CIP2B_191  | 5783                                       |
| 518  | 2304   | 4090  | 5876  | 784CIP2B_192  | 5784                                       |
| 519  | 2305   | 4091  | 5877  | 784CIP2B_193  | 5788                                       |
| 520  | 2306   | 4092  | 5878  | 784CIP2B_194  | 5798                                       |
| 521  | 2307   | 4093  | 5879  | 784CIP2B_196  | 5807                                       |
| 522  | 2308   | 4094  | 5880  | 784CIP2B_197  | 5818                                       |
| 523  | 2309   | 4095  | 5881  | 784CIP2B_198  | 5819                                       |
| 524  | 2310   | 4096  | 5882  | 784CIP2B_199  | 5827                                       |
| 525  | 2311   | 4097  | 5883  | 784CIP2B_200  | 5828                                       |
| 526  | 2312   | 4098  | 5884  | 784CIP2B_201  | 5842                                       |
| 527  | 2313   | 4099  | 5885  | 784CIP2B_202  | 5853                                       |
| 528  | 2314   | 4100  | 5886  | 784CIP2B_203  | 5861                                       |
| 529  | 2315   | 4101  | 5887  | 784CIP2B_204  | 5864                                       |
| 530  | 2316   | 4102  | 5888  | 784CIP2B_205  | 5865                                       |
| 531  | 2317   | 4103  | 5889  | 784CIP2B_206  | 5871                                       |
| 532  | 2318   | 4104  | 5890  | 784CIP2B_207  | 5873                                       |
| 533  | 2319   | 4105  | 5891  | 784CIP2B_208  | 5873                                       |
| 534  | 2320   | 4106  | 5892  | 784CIP2B_209  | 5875                                       |
| 535  | 2321   | 4107  | 5893  | 784CIP2B_210  | 5878                                       |
| 536  | 2322   | 4108  | 5894  | 784CIP2B_211  | 5879                                       |
| 537  | 2323   | 4109  | 5895  | 784CIP2B_212  | 5880                                       |
| 538  | 2324   | 4110  | 5896  | 784CIP2B_213  | 5880                                       |
| 539  | 2325   | 4111  | 5897  | 784CIP2B_214  | 5880                                       |
| 540  | 2326   | 4112  | 5898  | 784CIP2B_215  | 5880                                       |
| 541  | 2327   | 4113  | 5899  | 784CIP2B_216  | 5885                                       |
| 542  | 2328   | 4114  | 5900  | 784CIP2B_217  | 5895                                       |
| 543  | 2329   | 4115  | 5901  | 784CIP2B_218  | 5898                                       |
| 544  | 2330   | 4116  | 5902  | 784CIP2B_219  | 5902                                       |
| 545  | 2331   | 4117  | 5903  | 784CIP2B_220  | 5904                                       |
| 546  | 2332   | 4118  | 5904  | 784CIP2B_221  | 5918                                       |
| 547  | 2333   | 4119  | 5905  | 784CIP2B_222  | 5921                                       |
| 548  | 2334   | 4120  | 5906  | 784CIP2B_223  | 5927                                       |
| 549  | 2335   | 4121  | 5907  | 784CIP2B_224  | 5932                                       |
| 550  | 2336   | 4122  | 5908  | 784CIP2B_225  | 5939                                       |
| 551  | 2337   | 4123  | 5909  | 784CIP2B_226  | 5945                                       |
| 552  | 2338   | 4124  | 5910  | 784CIP2B_227  | 5946                                       |
| 553  | 2339   | 4125  | 5911  | 784CIP2B_228  | 5947                                       |
| 554  | 2340   | 4126  | 5912  | 784CIP2B_229  | 5956                                       |
| 555  | 2341   | 4127  | 5913  | 784CIP2B_230  | 5967                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 556  | 2342   | 4128  | 5914  | 784CIP2B_232  | 5975                                       |
| 557  | 2343   | 4129  | 5915  | 784CIP2B_233  | 5977                                       |
| 558  | 2344   | 4130  | 5916  | 784CIP2B_234  | 5978                                       |
| 559  | 2345   | 4131  | 5917  | 784CIP2B_235  | 5979                                       |
| 560  | 2346   | 4132  | 5918  | 784CIP2B_236  | 5980                                       |
| 561  | 2347   | 4133  | 5919  | 784CIP2B_237  | 5988                                       |
| 562  | 2348   | 4134  | 5920  | 784CIP2B_238  | 5989                                       |
| 563  | 2349   | 4135  | 5921  | 784CIP2B_239  | 5991                                       |
| 564  | 2350   | 4136  | 5922  | 784CIP2B_240  | 5997                                       |
| 565  | 2351   | 4137  | 5923  | 784CIP2B_241  | 5998                                       |
| 566  | 2352   | 4138  | 5924  | 784CIP2B_242  | 6003                                       |
| 567  | 2353   | 4139  | 5925  | 784CIP2B_243  | 6004                                       |
| 568  | 2354   | 4140  | 5926  | 784CIP2B_244  | 6013                                       |
| 569  | 2355   | 4141  | 5927  | 784CIP2B_245  | 6028                                       |
| 570  | 2356   | 4142  | 5928  | 784CIP2B_246  | 6028                                       |
| 571  | 2357   | 4143  | 5929  | 784CIP2B_247  | 6029                                       |
| 572  | 2358   | 4144  | 5930  | 784CIP2B_248  | 6031                                       |
| 573  | 2359   | 4145  | 5931  | 784CIP2B_249  | 6031                                       |
| 574  | 2360   | 4146  | 5932  | 784CIP2B_250  | 6032                                       |
| 575  | 2361   | 4147  | 5933  | 784CIP2B_251  | 6037                                       |
| 576  | 2362   | 4148  | 5934  | 784CIP2B_252  | 6037                                       |
| 577  | 2363   | 4149  | 5935  | 784CIP2B_253  | 6043                                       |
| 578  | 2364   | 4150  | 5936  | 784CIP2B_254  | 6044                                       |
| 579  | 2365   | 4151  | 5937  | 784CIP2B_255  | 6046                                       |
| 580  | 2366   | 4152  | 5938  | 784CIP2B_256  | 6048                                       |
| 581  | 2367   | 4153  | 5939  | 784CIP2B_257  | 6049                                       |
| 582  | 2368   | 4154  | 5940  | 784CIP2B_258  | 6051                                       |
| 583  | 2369   | 4155  | 5941  | 784CIP2B_259  | 6053                                       |
| 584  | 2370   | 4156  | 5942  | 784CIP2B_260  | 6060                                       |
| 585  | 2371   | 4157  | 5943  | 784CIP2B_261  | 6063                                       |
| 586  | 2372   | 4158  | 5944  | 784CIP2B_262  | 6066                                       |
| 587  | 2373   | 4159  | 5945  | 784CIP2B_263  | 6067                                       |
| 588  | 2374   | 4160  | 5946  | 784CIP2B_264  | 6068                                       |
| 589  | 2375   | 4161  | 5947  | 784CIP2B_265  | 6073                                       |
| 590  | 2376   | 4162  | 5948  | 784CIP2B_266  | 6076                                       |
| 591  | 2377   | 4163  | 5949  | 784CIP2B_267  | 6076                                       |
| 592  | 2378   | 4164  | 5950  | 784CIP2B_268  | 6077                                       |
| 593  | 2379   | 4165  | 5951  | 784CIP2B_269  | 6079                                       |
| 594  | 2380   | 4166  | 5952  | 784CIP2B_270  | 6082                                       |
| 595  | 2381   | 4167  | 5953  | 784CIP2B_272  | 6088                                       |
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| 603  | 2389   | 4175  | 5961  | 784CIP2B_280  | 6121                                       |
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| 605  | 2391   | 4177  | 5963  | 784CIP2B_282  | 6126                                       |
| 606  | 2392   | 4178  | 5964  | 784CIP2B_283  | 6128                                       |
| 607  | 2393   | 4179  | 5965  | 784CIP2B_284  | 6129                                       |
| 608  | 2394   | 4180  | 5966  | 784CIP2B_285  | 6133                                       |
| 609  | 2395   | 4181  | 5967  | 784CIP2B_286  | 6133                                       |
| 610  | 2396   | 4182  | 5968  | 784CIP2B_287  | 6135                                       |
| 611  | 2397   | 4183  | 5969  | 784CIP2B_288  | 6139                                       |
| 612  | 2398   | 4184  | 5970  | 784CIP2B_289  | 6141                                       |
| 613  | 2399   | 4185  | 5971  | 784CIP2B_290  | 6145                                       |
| 614  | 2400   | 4186  | 5972  | 784CIP2B_291  | 6146                                       |
| 615  | 2401   | 4187  | 5973  | 784CIP2B_292  | 6148                                       |
| 616  | 2402   | 4188  | 5974  | 784CIP2B_293  | 6149                                       |
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| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
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| 618  | 2404   | 4190  | 5976  | 784CIP2B_295   | 6153                                       |
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| 621  | 2407   | 4193  | 5979  | 784CIP2B_298   | 6167                                       |
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| 625  | 2411   | 4197  | 5983  | 784CIP2B_302   | 6194                                       |
| 626  | 2412   | 4198  | 5984  | 784CIP2B_303   | 6196                                       |
| 627  | 2413   | 4199  | 5985  | 784CIP2B_304   | 6197                                       |
| 628  | 2414   | 4200  | 5986  | 784CIP2B_305   | 6198                                       |
| 629  | 2415   | 4201  | 5987  | 784CIP2B_306   | 6198                                       |
| 630  | 2416   | 4202  | 5988  | 784CIP2B_308   | 6214                                       |
| 631  | 2417   | 4203  | 5989  | 784CIP2B_309   | 6215                                       |
| 632  | 2418   | 4204  | 5990  | 784CIP2B_310   | 6219                                       |
| 633  | 2419   | 4205  | 5991  | 784CIP2B_311   | 6226                                       |
| 634  | 2420   | 4206  | 5992  | 784CIP2B_312   | 6229                                       |
| 635  | 2421   | 4207  | 5993  | 784CIP2B_313   | 6234                                       |
| 636  | 2422   | 4208  | 5994  | 784CIP2B_314   | 6237                                       |
| 637  | 2423   | 4209  | 5995  | 784CIP2B_315   | 6238                                       |
| 638  | 2424   | 4210  | 5996  | 784CIP2B_316   | 6239                                       |
| 639  | 2425   | 4211  | 5997  | 784CIP2B_317   | 6239                                       |
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| 644  | 2430   | 4216  | 6002  | 784CIP2B_322   | 6250                                       |
| 645  | 2431   | 4217  | 6003  | 784CIP2B_323   | 6252                                       |
| 646  | 2432   | 4218  | 6004  | 784CIP2B_324   | 6252                                       |
| 647  | 2433   | 4219  | 6005  | 784CIP2B_325   | 6256                                       |
| 648  | 2434   | 4220  | 6006  | 784CIP2B_326   | 6260                                       |
| 649  | 2435   | 4221  | 6007  | 784CIP2B_327   | 6261                                       |
| 650  | 2436   | 4222  | 6008  | 784CIP2B_328   | 6264                                       |
| 651  | 2437   | 4223  | 6009  | 784CIP2B_329   | 6265                                       |
| 652  | 2438   | 4224  | 6010  | 784CIP2B_330   | 6266                                       |
| 653  | 2439   | 4225  | 6011  | 784CIP2B_331   | 6270                                       |
| 654  | 2440   | 4226  | 6012  | 784CIP2B_332   | 6271                                       |
| 655  | 2441   | 4227  | 6013  | 784CIP2B_334   | 6274                                       |
| 656  | 2442   | 4228  | 6014  | 784CIP2B_335   | 6276                                       |
| 657  | 2443   | 4229  | 6015  | 784CIP2B_336   | 6281                                       |
| 658  | 2444   | 4230  | 6016  | 784CIP2B_337   | 6281                                       |
| 659  | 2445   | 4231  | 6017  | 784CIP2B_338   | 6288                                       |
| 660  | 2446   | 4232  | 6018  | 784CIP2B_339   | 6292                                       |
| 661  | 2447   | 4233  | 6019  | 784CIP2B_340   | 6294                                       |
| 662  | 2448   | 4234  | 6020  | 784CIP2B_343   | 6312                                       |
| 663  | 2449   | 4235  | 6021  | 784CIP2B_344   | 6312                                       |
| 664  | 2450   | 4236  | 6022  | 784CIP2B_345   | 6312                                       |
| 665  | 2451   | 4237  | 6023  | 784CIP2B_346   | 6322                                       |
| 666  | 2452   | 4238  | 6024  | 784CIP2B_347   | 6324                                       |
| 667  | 2453   | 4239  | 6025  | 784CIP2B_349   | 6329                                       |
| 668  | 2454   | 4240  | 6026  | 784CIP2B_350   | 6331                                       |
| 669  | 2455   | 4241  | 6027  | 784CIP2B_351   | 6333                                       |
| 670  | 2456   | 4242  | 6028  | 784CIP2B_352   | 6334                                       |
| 671  | 2457   | 4243  | 6029  | 784CIP2B_353   | 6337                                       |
| 672  | 2458   | 4244  | 6030  | 784CIP2B_354   | 6339                                       |
| 673  | 2459   | 4245  | 6031  | 784CIP2B_355   | 6346                                       |
| 674  | 2460   | 4246  | 6032  | 784CIP2B_356   | 6348                                       |
| 675  | 2461   | 4247  | 6033  | 784CIP2B_357   | 6348                                       |
| 676  | 2462   | 4248  | 6034  | 784CIP2B_358   | 6350                                       |
| 677  | 2463   | 4249  | 6035  | 784CIP2B_359   | 6351                                       |
| 678  | 2464   | 4250  | 6036  | 784CIP2B_360   | 6355                                       |
| 679  | 2465   | 4251  | 6037  | 784CIP2B_361   | 6362                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 680  | 2466   | 4252  | 6038  | 784CIP2B_362  | 6368                                       |
| 681  | 2467   | 4253  | 6039  | 784CIP2B_363  | 6369                                       |
| 682  | 2468   | 4254  | 6040  | 784CIP2B_364  | 6371                                       |
| 683  | 2469   | 4255  | 6041  | 784CIP2B_365  | 6376                                       |
| 684  | 2470   | 4256  | 6042  | 784CIP2B_366  | 6379                                       |
| 685  | 2471   | 4257  | 6043  | 784CIP2B_367  | 6380                                       |
| 686  | 2472   | 4258  | 6044  | 784CIP2B_368  | 6381                                       |
| 687  | 2473   | 4259  | 6045  | 784CIP2B_369  | 6392                                       |
| 688  | 2474   | 4260  | 6046  | 784CIP2B_370  | 6395                                       |
| 689  | 2475   | 4261  | 6047  | 784CIP2B_371  | 6397                                       |
| 690  | 2476   | 4262  | 6048  | 784CIP2B_372  | 6400                                       |
| 691  | 2477   | 4263  | 6049  | 784CIP2B_373  | 6401                                       |
| 692  | 2478   | 4264  | 6050  | 784CIP2B_374  | 6411                                       |
| 693  | 2479   | 4265  | 6051  | 784CIP2B_375  | 6411                                       |
| 694  | 2480   | 4266  | 6052  | 784CIP2B_376  | 6411                                       |
| 695  | 2481   | 4267  | 6053  | 784CIP2B_377  | 6416                                       |
| 696  | 2482   | 4268  | 6054  | 784CIP2B_378  | 6418                                       |
| 697  | 2483   | 4269  | 6055  | 784CIP2B_379  | 6422                                       |
| 698  | 2484   | 4270  | 6056  | 784CIP2B_380  | 6423                                       |
| 699  | 2485   | 4271  | 6057  | 784CIP2B_381  | 6426                                       |
| 700  | 2486   | 4272  | 6058  | 784CIP2B_382  | 6427                                       |
| 701  | 2487   | 4273  | 6059  | 784CIP2B_383  | 6428                                       |
| 702  | 2488   | 4274  | 6060  | 784CIP2B_384  | 6429                                       |
| 703  | 2489   | 4275  | 6061  | 784CIP2B_385  | 6430                                       |
| 704  | 2490   | 4276  | 6062  | 784CIP2B_386  | 6432                                       |
| 705  | 2491   | 4277  | 6063  | 784CIP2B_387  | 6432                                       |
| 706  | 2492   | 4278  | 6064  | 784CIP2B_388  | 6438                                       |
| 707  | 2493   | 4279  | 6065  | 784CIP2B_389  | 6441                                       |
| 708  | 2494   | 4280  | 6066  | 784CIP2B_390  | 6446                                       |
| 709  | 2495   | 4281  | 6067  | 784CIP2B_391  | 6454                                       |
| 710  | 2496   | 4282  | 6068  | 784CIP2B_392  | 6459                                       |
| 711  | 2497   | 4283  | 6069  | 784CIP2B_394  | 6461                                       |
| 712  | 2498   | 4284  | 6070  | 784CIP2B_395  | 6467                                       |
| 713  | 2499   | 4285  | 6071  | 784CIP2B_396  | 6468                                       |
| 714  | 2500   | 4286  | 6072  | 784CIP2B_397  | 6487                                       |
| 715  | 2501   | 4287  | 6073  | 784CIP2B_398  | 6491                                       |
| 716  | 2502   | 4288  | 6074  | 784CIP2B_399  | 6506                                       |
| 717  | 2503   | 4289  | 6075  | 784CIP2B_401  | 6514                                       |
| 718  | 2504   | 4290  | 6076  | 784CIP2B_402  | 6519                                       |
| 719  | 2505   | 4291  | 6077  | 784CIP2B_403  | 6521                                       |
| 720  | 2506   | 4292  | 6078  | 784CIP2B_404  | 6532                                       |
| 721  | 2507   | 4293  | 6079  | 784CIP2B_405  | 6536                                       |
| 722  | 2508   | 4294  | 6080  | 784CIP2B_406  | 6543                                       |
| 723  | 2509   | 4295  | 6081  | 784CIP2B_407  | 6544                                       |
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| 725  | 2511   | 4297  | 6083  | 784CIP2B_409  | 6551                                       |
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| 727  | 2513   | 4299  | 6085  | 784CIP2B_411  | 6552                                       |
| 728  | 2514   | 4300  | 6086  | 784CIP2B_412  | 6554                                       |
| 729  | 2515   | 4301  | 6087  | 784CIP2B_413  | 6556                                       |
| 730  | 2516   | 4302  | 6088  | 784CIP2B_414  | 6560                                       |
| 731  | 2517   | 4303  | 6089  | 784CIP2B_415  | 6563                                       |
| 732  | 2518   | 4304  | 6090  | 784CIP2B_416  | 6564                                       |
| 733  | 2519   | 4305  | 6091  | 784CIP2B_417  | 6567                                       |
| 734  | 2520   | 4306  | 6092  | 784CIP2B_418  | 6573                                       |
| 735  | 2521   | 4307  | 6093  | 784CIP2B_419  | 6575                                       |
| 736  | 2522   | 4308  | 6094  | 784CIP2B_420  | 6577                                       |
| 737  | 2523   | 4309  | 6095  | 784CIP2B_421  | 6593                                       |
| 738  | 2524   | 4310  | 6096  | 784CIP2B_422  | 6595                                       |
| 739  | 2525   | 4311  | 6097  | 784CIP2B_423  | 6599                                       |
| 740  | 2526   | 4312  | 6098  | 784CIP2B_424  | 6625                                       |
| 741  | 2527   | 4313  | 6099  | 784CIP2B_425  | 6625                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 742  | 2528   | 4314  | 6100  | 784CIP2B_426  | 6626                                       |
| 743  | 2529   | 4315  | 6101  | 784CIP2B_427  | 6630                                       |
| 744  | 2530   | 4316  | 6102  | 784CIP2B_428  | 6631                                       |
| 745  | 2531   | 4317  | 6103  | 784CIP2B_429  | 6632                                       |
| 746  | 2532   | 4318  | 6104  | 784CIP2B_430  | 6633                                       |
| 747  | 2533   | 4319  | 6105  | 784CIP2B_431  | 6634                                       |
| 748  | 2534   | 4320  | 6106  | 784CIP2B_432  | 6638                                       |
| 749  | 2535   | 4321  | 6107  | 784CIP2B_433  | 6641                                       |
| 750  | 2536   | 4322  | 6108  | 784CIP2B_434  | 6644                                       |
| 751  | 2537   | 4323  | 6109  | 784CIP2B_435  | 6646                                       |
| 752  | 2538   | 4324  | 6110  | 784CIP2B_436  | 6648                                       |
| 753  | 2539   | 4325  | 6111  | 784CIP2B_437  | 6652                                       |
| 754  | 2540   | 4326  | 6112  | 784CIP2B_438  | 6654                                       |
| 755  | 2541   | 4327  | 6113  | 784CIP2B_439  | 6657                                       |
| 756  | 2542   | 4328  | 6114  | 784CIP2B_440  | 6658                                       |
| 757  | 2543   | 4329  | 6115  | 784CIP2B_441  | 6663                                       |
| 758  | 2544   | 4330  | 6116  | 784CIP2B_442  | 6664                                       |
| 759  | 2545   | 4331  | 6117  | 784CIP2B_443  | 6668                                       |
| 760  | 2546   | 4332  | 6118  | 784CIP2B_444  | 6669                                       |
| 761  | 2547   | 4333  | 6119  | 784CIP2B_445  | 6673                                       |
| 762  | 2548   | 4334  | 6120  | 784CIP2B_446  | 6685                                       |
| 763  | 2549   | 4335  | 6121  | 784CIP2B_447  | 6687                                       |
| 764  | 2550   | 4336  | 6122  | 784CIP2B_448  | 6689                                       |
| 765  | 2551   | 4337  | 6123  | 784CIP2B_449  | 6693                                       |
| 766  | 2552   | 4338  | 6124  | 784CIP2B_450  | 6698                                       |
| 767  | 2553   | 4339  | 6125  | 784CIP2B_451  | 6699                                       |
| 768  | 2554   | 4340  | 6126  | 784CIP2B_452  | 6705                                       |
| 769  | 2555   | 4341  | 6127  | 784CIP2B_453  | 6711                                       |
| 770  | 2556   | 4342  | 6128  | 784CIP2B_454  | 6713                                       |
| 771  | 2557   | 4343  | 6129  | 784CIP2B_455  | 6716                                       |
| 772  | 2558   | 4344  | 6130  | 784CIP2B_456  | 6725                                       |
| 773  | 2559   | 4345  | 6131  | 784CIP2B_457  | 6726                                       |
| 774  | 2560   | 4346  | 6132  | 784CIP2B_458  | 6727                                       |
| 775  | 2561   | 4347  | 6133  | 784CIP2B_459  | 6730                                       |
| 776  | 2562   | 4348  | 6134  | 784CIP2B_460  | 6730                                       |
| 777  | 2563   | 4349  | 6135  | 784CIP2B_461  | 6730                                       |
| 778  | 2564   | 4350  | 6136  | 784CIP2B_462  | 6732                                       |
| 779  | 2565   | 4351  | 6137  | 784CIP2B_463  | 6733                                       |
| 780  | 2566   | 4352  | 6138  | 784CIP2B_464  | 6737                                       |
| 781  | 2567   | 4353  | 6139  | 784CIP2B_465  | 6745                                       |
| 782  | 2568   | 4354  | 6140  | 784CIP2B_466  | 6751                                       |
| 783  | 2569   | 4355  | 6141  | 784CIP2B_467  | 6754                                       |
| 784  | 2570   | 4356  | 6142  | 784CIP2B_468  | 6758                                       |
| 785  | 2571   | 4357  | 6143  | 784CIP2B_469  | 6761                                       |
| 786  | 2572   | 4358  | 6144  | 784CIP2B_470  | 6765                                       |
| 787  | 2573   | 4359  | 6145  | 784CIP2B_471  | 6768                                       |
| 788  | 2574   | 4360  | 6146  | 784CIP2B_472  | 6773                                       |
| 789  | 2575   | 4361  | 6147  | 784CIP2B_473  | 6776                                       |
| 790  | 2576   | 4362  | 6148  | 784CIP2B_474  | 6796                                       |
| 791  | 2577   | 4363  | 6149  | 784CIP2B_475  | 6798                                       |
| 792  | 2578   | 4364  | 6150  | 784CIP2B_476  | 6823                                       |
| 793  | 2579   | 4365  | 6151  | 784CIP2B_477  | 6825                                       |
| 794  | 2580   | 4366  | 6152  | 784CIP2B_478  | 6826                                       |
| 795  | 2581   | 4367  | 6153  | 784CIP2B_479  | 6839                                       |
| 796  | 2582   | 4368  | 6154  | 784CIP2B_480  | 6844                                       |
| 797  | 2583   | 4369  | 6155  | 784CIP2B_482  | 6849                                       |
| 798  | 2584   | 4370  | 6156  | 784CIP2B_483  | 6854                                       |
| 799  | 2585   | 4371  | 6157  | 784CIP2B_484  | 6857                                       |
| 800  | 2586   | 4372  | 6158  | 784CIP2B_485  | 6861                                       |
| 801  | 2587   | 4373  | 6159  | 784CIP2B_486  | 6873                                       |
| 802  | 2588   | 4374  | 6160  | 784CIP2B_487  | 6875                                       |
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| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
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| 808  | 2594   | 4380  | 6166  | 784CIP2B_493   | 6894                                       |
| 809  | 2595   | 4381  | 6167  | 784CIP2B_494   | 6901                                       |
| 810  | 2596   | 4382  | 6168  | 784CIP2B_495   | 6904                                       |
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| 813  | 2599   | 4385  | 6171  | 784CIP2B_498   | 6917                                       |
| 814  | 2600   | 4386  | 6172  | 784CIP2B_499   | 6923                                       |
| 815  | 2601   | 4387  | 6173  | 784CIP2B_500   | 6929                                       |
| 816  | 2602   | 4388  | 6174  | 784CIP2B_501   | 6931                                       |
| 817  | 2603   | 4389  | 6175  | 784CIP2B_502   | 6935                                       |
| 818  | 2604   | 4390  | 6176  | 784CIP2B_503   | 6940                                       |
| 819  | 2605   | 4391  | 6177  | 784CIP2B_504   | 6945                                       |
| 820  | 2606   | 4392  | 6178  | 784CIP2B_505   | 6946                                       |
| 821  | 2607   | 4393  | 6179  | 784CIP2B_506   | 6947                                       |
| 822  | 2608   | 4394  | 6180  | 784CIP2B_507   | 6949                                       |
| 823  | 2609   | 4395  | 6181  | 784CIP2B_508   | 6959                                       |
| 824  | 2610   | 4396  | 6182  | 784CIP2B_509   | 6960                                       |
| 825  | 2611   | 4397  | 6183  | 784CIP2B_510   | 6962                                       |
| 826  | 2612   | 4398  | 6184  | 784CIP2B_511   | 6963                                       |
| 827  | 2613   | 4399  | 6185  | 784CIP2B_512   | 6967                                       |
| 828  | 2614   | 4400  | 6186  | 784CIP2B_513   | 6983                                       |
| 829  | 2615   | 4401  | 6187  | 784CIP2B_514   | 6988                                       |
| 830  | 2616   | 4402  | 6188  | 784CIP2B_515   | 6996                                       |
| 831  | 2617   | 4403  | 6189  | 784CIP2B_516   | 7003                                       |
| 832  | 2618   | 4404  | 6190  | 784CIP2B_517   | 7016                                       |
| 833  | 2619   | 4405  | 6191  | 784CIP2B_518   | 7017                                       |
| 834  | 2620   | 4406  | 6192  | 784CIP2B_519   | 7025                                       |
| 835  | 2621   | 4407  | 6193  | 784CIP2B_520   | 7025                                       |
| 836  | 2622   | 4408  | 6194  | 784CIP2B_521   | 7025                                       |
| 837  | 2623   | 4409  | 6195  | 784CIP2B_522   | 7050                                       |
| 838  | 2624   | 4410  | 6196  | 784CIP2B_523   | 7051                                       |
| 839  | 2625   | 4411  | 6197  | 784CIP2B_524   | 7055                                       |
| 840  | 2626   | 4412  | 6198  | 784CIP2B_525   | 7060                                       |
| 841  | 2627   | 4413  | 6199  | 784CIP2B_526   | 7064                                       |
| 842  | 2628   | 4414  | 6200  | 784CIP2B_527   | 7067                                       |
| 843  | 2629   | 4415  | 6201  | 784CIP2B_528   | 7071                                       |
| 844  | 2630   | 4416  | 6202  | 784CIP2B_529   | 7072                                       |
| 845  | 2631   | 4417  | 6203  | 784CIP2B_530   | 7073                                       |
| 846  | 2632   | 4418  | 6204  | 784CIP2B_531   | 7076                                       |
| 847  | 2633   | 4419  | 6205  | 784CIP2B_532   | 7088                                       |
| 848  | 2634   | 4420  | 6206  | 784CIP2B_533   | 7089                                       |
| 849  | 2635   | 4421  | 6207  | 784CIP2B_534   | 7091                                       |
| 850  | 2636   | 4422  | 6208  | 784CIP2B_535   | 7091                                       |
| 851  | 2637   | 4423  | 6209  | 784CIP2B_536   | 7104                                       |
| 852  | 2638   | 4424  | 6210  | 784CIP2B_537   | 7105                                       |
| 853  | 2639   | 4425  | 6211  | 784CIP2B_538   | 7105                                       |
| 854  | 2640   | 4426  | 6212  | 784CIP2B_539   | 7109                                       |
| 855  | 2641   | 4427  | 6213  | 784CIP2B_540   | 7109                                       |
| 856  | 2642   | 4428  | 6214  | 784CIP2B_541   | 7119                                       |
| 857  | 2643   | 4429  | 6215  | 784CIP2B_542   | 7120                                       |
| 858  | 2644   | 4430  | 6216  | 784CIP2B_543   | 7121                                       |
| 859  | 2645   | 4431  | 6217  | 784CIP2B_544   | 7126                                       |
| 860  | 2646   | 4432  | 6218  | 784CIP2B_545   | 7127                                       |
| 861  | 2647   | 4433  | 6219  | 784CIP2B_546   | 7130                                       |
| 862  | 2648   | 4434  | 6220  | 784CIP2B_547   | 7131                                       |
| 863  | 2649   | 4435  | 6221  | 784CIP2B_548   | 7144                                       |
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| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
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| 869  | 2655   | 4441  | 6227  | 784CIP2B_554  | 7190                                       |
| 870  | 2656   | 4442  | 6228  | 784CIP2B_555  | 7191                                       |
| 871  | 2657   | 4443  | 6229  | 784CIP2B_556  | 7203                                       |
| 872  | 2658   | 4444  | 6230  | 784CIP2B_557  | 7204                                       |
| 873  | 2659   | 4445  | 6231  | 784CIP2B_558  | 7208                                       |
| 874  | 2660   | 4446  | 6232  | 784CIP2B_559  | 7209                                       |
| 875  | 2661   | 4447  | 6233  | 784CIP2B_560  | 7210                                       |
| 876  | 2662   | 4448  | 6234  | 784CIP2B_561  | 7216                                       |
| 877  | 2663   | 4449  | 6235  | 784CIP2B_562  | 7221                                       |
| 878  | 2664   | 4450  | 6236  | 784CIP2B_563  | 7230                                       |
| 879  | 2665   | 4451  | 6237  | 784CIP2B_564  | 7237                                       |
| 880  | 2666   | 4452  | 6238  | 784CIP2B_565  | 7240                                       |
| 881  | 2667   | 4453  | 6239  | 784CIP2B_566  | 7245                                       |
| 882  | 2668   | 4454  | 6240  | 784CIP2B_567  | 7250                                       |
| 883  | 2669   | 4455  | 6241  | 784CIP2B_568  | 7251                                       |
| 884  | 2670   | 4456  | 6242  | 784CIP2B_569  | 7255                                       |
| 885  | 2671   | 4457  | 6243  | 784CIP2B_570  | 7260                                       |
| 886  | 2672   | 4458  | 6244  | 784CIP2B_571  | 7265                                       |
| 887  | 2673   | 4459  | 6245  | 784CIP2B_572  | 7268                                       |
| 888  | 2674   | 4460  | 6246  | 784CIP2B_573  | 7275                                       |
| 889  | 2675   | 4461  | 6247  | 784CIP2B_574  | 7279                                       |
| 890  | 2676   | 4462  | 6248  | 784CIP2B_575  | 7283                                       |
| 891  | 2677   | 4463  | 6249  | 784CIP2B_576  | 7283                                       |
| 892  | 2678   | 4464  | 6250  | 784CIP2B_577  | 7287                                       |
| 893  | 2679   | 4465  | 6251  | 784CIP2B_578  | 7301                                       |
| 894  | 2680   | 4466  | 6252  | 784CIP2B_579  | 7308                                       |
| 895  | 2681   | 4467  | 6253  | 784CIP2B_580  | 7308                                       |
| 896  | 2682   | 4468  | 6254  | 784CIP2B_581  | 7309                                       |
| 897  | 2683   | 4469  | 6255  | 784CIP2B_582  | 7319                                       |
| 898  | 2684   | 4470  | 6256  | 784CIP2B_583  | 7320                                       |
| 899  | 2685   | 4471  | 6257  | 784CIP2B_584  | 7326                                       |
| 900  | 2686   | 4472  | 6258  | 784CIP2B_585  | 7326                                       |
| 901  | 2687   | 4473  | 6259  | 784CIP2B_586  | 7334                                       |
| 902  | 2688   | 4474  | 6260  | 784CIP2B_587  | 7337                                       |
| 903  | 2689   | 4475  | 6261  | 784CIP2B_588  | 7339                                       |
| 904  | 2690   | 4476  | 6262  | 784CIP2B_589  | 7344                                       |
| 905  | 2691   | 4477  | 6263  | 784CIP2B_590  | 7355                                       |
| 906  | 2692   | 4478  | 6264  | 784CIP2B_591  | 7363                                       |
| 907  | 2693   | 4479  | 6265  | 784CIP2B_592  | 7363                                       |
| 908  | 2694   | 4480  | 6266  | 784CIP2B_593  | 7365                                       |
| 909  | 2695   | 4481  | 6267  | 784CIP2B_594  | 7368                                       |
| 910  | 2696   | 4482  | 6268  | 784CIP2B_595  | 7369                                       |
| 911  | 2697   | 4483  | 6269  | 784CIP2B_596  | 7372                                       |
| 912  | 2698   | 4484  | 6270  | 784CIP2B_599  | 7375                                       |
| 913  | 2699   | 4485  | 6271  | 784CIP2B_600  | 7381                                       |
| 914  | 2700   | 4486  | 6272  | 784CIP2B_601  | 7383                                       |
| 915  | 2701   | 4487  | 6273  | 784CIP2B_602  | 7387                                       |
| 916  | 2702   | 4488  | 6274  | 784CIP2B_603  | 7391                                       |
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| 918  | 2704   | 4490  | 6276  | 784CIP2B_605  | 7395                                       |
| 919  | 2705   | 4491  | 6277  | 784CIP2B_606  | 7397                                       |
| 920  | 2706   | 4492  | 6278  | 784CIP2B_607  | 7399                                       |
| 921  | 2707   | 4493  | 6279  | 784CIP2B_608  | 7405                                       |
| 922  | 2708   | 4494  | 6280  | 784CIP2B_609  | 7406                                       |
| 923  | 2709   | 4495  | 6281  | 784CIP2B_610  | 7406                                       |
| 924  | 2710   | 4496  | 6282  | 784CIP2B_611  | 7409                                       |
| 925  | 2711   | 4497  | 6283  | 784CIP2B_612  | 7410                                       |
| 926  | 2712   | 4498  | 6284  | 784CIP2B_613  | 7411                                       |
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| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
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| 928  | 2714   | 4500  | 6286  | 784CIP2B_615   | 7418                                       |
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| 939  | 2725   | 4511  | 6297  | 784CIP2B_626   | 7437                                       |
| 940  | 2726   | 4512  | 6298  | 784CIP2B_627   | 7439                                       |
| 941  | 2727   | 4513  | 6299  | 784CIP2B_628   | 7440                                       |
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| 943  | 2729   | 4515  | 6301  | 784CIP2B_630   | 7450                                       |
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| 945  | 2731   | 4517  | 6303  | 784CIP2B_632   | 7452                                       |
| 946  | 2732   | 4518  | 6304  | 784CIP2B_633   | 7454                                       |
| 947  | 2733   | 4519  | 6305  | 784CIP2B_634   | 7457                                       |
| 948  | 2734   | 4520  | 6306  | 784CIP2B_635   | 7459                                       |
| 949  | 2735   | 4521  | 6307  | 784CIP2B_636   | 7461                                       |
| 950  | 2736   | 4522  | 6308  | 784CIP2B_637   | 7463                                       |
| 951  | 2737   | 4523  | 6309  | 784CIP2B_638   | 7466                                       |
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| 953  | 2739   | 4525  | 6311  | 784CIP2B_640   | 7473                                       |
| 954  | 2740   | 4526  | 6312  | 784CIP2B_641   | 7481                                       |
| 955  | 2741   | 4527  | 6313  | 784CIP2B_642   | 7482                                       |
| 956  | 2742   | 4528  | 6314  | 784CIP2B_643   | 7482                                       |
| 957  | 2743   | 4529  | 6315  | 784CIP2B_644   | 7483                                       |
| 958  | 2744   | 4530  | 6316  | 784CIP2B_645   | 7485                                       |
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| 960  | 2746   | 4532  | 6318  | 784CIP2B_647   | 7487                                       |
| 961  | 2747   | 4533  | 6319  | 784CIP2B_648   | 7491                                       |
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| 965  | 2751   | 4537  | 6323  | 784CIP2B_652   | 7504                                       |
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| 967  | 2753   | 4539  | 6325  | 784CIP2B_654   | 7516                                       |
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| 969  | 2755   | 4541  | 6327  | 784CIP2B_656   | 7519                                       |
| 970  | 2756   | 4542  | 6328  | 784CIP2B_657   | 7521                                       |
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| 972  | 2758   | 4544  | 6330  | 784CIP2B_659   | 7532                                       |
| 973  | 2759   | 4545  | 6331  | 784CIP2B_660   | 7533                                       |
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| 977  | 2763   | 4549  | 6335  | 784CIP2B_664   | 7552                                       |
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| 979  | 2765   | 4551  | 6337  | 784CIP2B_666   | 7567                                       |
| 980  | 2766   | 4552  | 6338  | 784CIP2B_667   | 7569                                       |
| 981  | 2767   | 4553  | 6339  | 784CIP2B_668   | 7575                                       |
| 982  | 2768   | 4554  | 6340  | 784CIP2B_669   | 7576                                       |
| 983  | 2769   | 4555  | 6341  | 784CIP2B_670   | 7577                                       |
| 984  | 2770   | 4556  | 6342  | 784CIP2B_671   | 7579                                       |
| 985  | 2771   | 4557  | 6343  | 784CIP2B_672   | 7582                                       |
| 986  | 2772   | 4558  | 6344  | 784CIP2B_673   | 7587                                       |
| 987  | 2773   | 4559  | 6345  | 784CIP2B_674   | 7589                                       |
| 988  | 2774   | 4560  | 6346  | 784CIP2B_675   | 7597                                       |
| 989  | 2775   | 4561  | 6347  | 784CIP2B_676   | 7597                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
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| 991  | 2777   | 4563  | 6349  | 784CIP2B_678  | 7609                                       |
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| 993  | 2779   | 4565  | 6351  | 784CIP2B_680  | 7613                                       |
| 994  | 2780   | 4566  | 6352  | 784CIP2B_681  | 7623                                       |
| 995  | 2781   | 4567  | 6353  | 784CIP2B_682  | 7629                                       |
| 996  | 2782   | 4568  | 6354  | 784CIP2B_683  | 7630                                       |
| 997  | 2783   | 4569  | 6355  | 784CIP2B_684  | 7633                                       |
| 998  | 2784   | 4570  | 6356  | 784CIP2B_685  | 7635                                       |
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| 1000   | 2786   | 4572  | 6358  | 784CIP2B_687  | 7639                                       |
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| 1002   | 2788   | 4574  | 6360  | 784CIP2B_689  | 7647                                       |
| 1003   | 2789   | 4575  | 6361  | 784CIP2B_690  | 7648                                       |
| 1004   | 2790   | 4576  | 6362  | 784CIP2B_691  | 7658                                       |
| 1005   | 2791   | 4577  | 6363  | 784CIP2B_692  | 7664                                       |
| 1006   | 2792   | 4578  | 6364  | 784CIP2B_693  | 7664                                       |
| 1007   | 2793   | 4579  | 6365  | 784CIP2B_695  | 7674                                       |
| 1008   | 2794   | 4580  | 6366  | 784CIP2B_696  | 7675                                       |
| 1009   | 2795   | 4581  | 6367  | 784CIP2B_697  | 7676                                       |
| 1010   | 2796   | 4582  | 6368  | 784CIP2B_698  | 7681                                       |
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| 1015   | 2801   | 4587  | 6373  | 784CIP2B_703  | 7716                                       |
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| 1017   | 2803   | 4589  | 6375  | 784CIP2B_705  | 7721                                       |
| 1018   | 2804   | 4590  | 6376  | 784CIP2B_706  | 7723                                       |
| 1019   | 2805   | 4591  | 6377  | 784CIP2B_707  | 7729                                       |
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| 1021   | 2807   | 4593  | 6379  | 784CIP2B_709  | 7735                                       |
| 1022   | 2808   | 4594  | 6380  | 784CIP2B_710  | 7741                                       |
| 1023   | 2809   | 4595  | 6381  | 784CIP2B_711  | 7743                                       |
| 1024   | 2810   | 4596  | 6382  | 784CIP2B_712  | 7748                                       |
| 1025   | 2811   | 4597  | 6383  | 784CIP2B_713  | 7749                                       |
| 1026   | 2812   | 4598  | 6384  | 784CIP2B_714  | 7750                                       |
| 1027   | 2813   | 4599  | 6385  | 784CIP2B_715  | 7757                                       |
| 1028   | 2814   | 4600  | 6386  | 784CIP2B_716  | 7759                                       |
| 1029   | 2815   | 4601  | 6387  | 784CIP2B_717  | 7760                                       |
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| 1036   | 2822   | 4608  | 6394  | 784CIP2B_724  | 7770                                       |
| 1037   | 2823   | 4609  | 6395  | 784CIP2B_725  | 7774                                       |
| 1038   | 2824   | 4610  | 6396  | 784CIP2B_726  | 7779                                       |
| 1039   | 2825   | 4611  | 6397  | 784CIP2B_727  | 7781                                       |
| 1040   | 2826   | 4612  | 6398  | 784CIP2B_728  | 7782                                       |
| 1041   | 2827   | 4613  | 6399  | 784CIP2B_729  | 7783                                       |
| 1042   | 2828   | 4614  | 6400  | 784CIP2B_730  | 7787                                       |
| 1043   | 2829   | 4615  | 6401  | 784CIP2B_731  | 7792                                       |
| 1044   | 2830   | 4616  | 6402  | 784CIP2B_732  | 7795                                       |
| 1045   | 2831   | 4617  | 6403  | 784CIP2B_733  | 7801                                       |
| 1046   | 2832   | 4618  | 6404  | 784CIP2B_734  | 7807                                       |
| 1047   | 2833   | 4619  | 6405  | 784CIP2B_735  | 7808                                       |
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| 1049   | 2835   | 4621  | 6407  | 784CIP2B_737  | 7824                                       |
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| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide.<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
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| 1054   | 2840  | 4626  | 6412  | 784CIP2B_743  | 7847                                       |
| 1055   | 2841  | 4627  | 6413  | 784CIP2B_744  | 7848                                       |
| 1056   | 2842  | 4628  | 6414  | 784CIP2B_745  | 7853                                       |
| 1057   | 2843  | 4629  | 6415  | 784CIP2B_746  | 7854                                       |
| 1058   | 2844  | 4630  | 6416  | 784CIP2B_747  | 7856                                       |
| 1059   | 2845  | 4631  | 6417  | 784CIP2B_748  | 7862                                       |
| 1060   | 2846  | 4632  | 6418  | 784CIP2B_749  | 7865                                       |
| 1061   | 2847  | 4633  | 6419  | 784CIP2B_750  | 7874                                       |
| 1062   | 2848  | 4634  | 6420  | 784CIP2B_751  | 7877                                       |
| 1063   | 2849  | 4635  | 6421  | 784CIP2B_752  | 7880                                       |
| 1064   | 2850  | 4636  | 6422  | 784CIP2B_753  | 7882                                       |
| 1065   | 2851  | 4637  | 6423  | 784CIP2B_754  | 7884                                       |
| 1066   | 2852  | 4638  | 6424  | 784CIP2B_755  | 7886                                       |
| 1067   | 2853  | 4639  | 6425  | 784CIP2B_756  | 7888                                       |
| 1068   | 2854  | 4640  | 6426  | 784CIP2B_757  | 7889                                       |
| 1069   | 2855  | 4641  | 6427  | 784CIP2B_758  | 7901                                       |
| 1070   | 2856  | 4642  | 6428  | 784CIP2B_759  | 7910                                       |
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| 1077   | 2863  | 4649  | 6435  | 784CIP2B_766  | 7929                                       |
| 1078   | 2864  | 4650  | 6436  | 784CIP2B_767  | 7930                                       |
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| 1081   | 2867  | 4653  | 6439  | 784CIP2B_770  | 7942                                       |
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| 1085   | 2871  | 4657  | 6443  | 784CIP2B_774  | 7951                                       |
| 1086   | 2872  | 4658  | 6444  | 784CIP2B_775  | 7952                                       |
| 1087   | 2873  | 4659  | 6445  | 784CIP2B_776  | 7953                                       |
| 1088   | 2874  | 4660  | 6446  | 784CIP2B_777  | 7954                                       |
| 1089   | 2875  | 4661  | 6447  | 784CIP2B_778  | 7957                                       |
| 1090   | 2876  | 4662  | 6448  | 784CIP2B_779  | 7958                                       |
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| 1101   | 2887  | 4673  | 6459  | 784CIP2B_790  | 7992                                       |
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| 1104   | 2890  | 4676  | 6462  | 784CIP2B_793  | 8014                                       |
| 1105   | 2891  | 4677  | 6463  | 784CIP2B_794  | 8015                                       |
| 1106   | 2892  | 4678  | 6464  | 784CIP2B_795  | 8016                                       |
| 1107   | 2893  | 4679  | 6465  | 784CIP2B_796  | 8017                                       |
| 1108   | 2894  | 4680  | 6466  | 784CIP2B_797  | 8019                                       |
| 1109   | 2895  | 4681  | 6467  | 784CIP2B_798  | 8020                                       |
| 1110   | 2896  | 4682  | 6468  | 784CIP2B_799  | 8022                                       |
| 1111   | 2897  | 4683  | 6469  | 784CIP2B_800  | 8022                                       |
| 1112   | 2898  | 4684  | 6470  | 784CIP2B_801  | 8028                                       |
| 1113   | 2899  | 4685  | 6471  | 784CIP2B_802  | 8030                                       |



| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 1114   | 2900   | 4686  | 6472  | 784CIP2B_803  | 8038                                       |
| 1115   | 2901   | 4687  | 6473  | 784CIP2B_804  | 8042                                       |
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| 1117   | 2903   | 4689  | 6475  | 784CIP2B_806  | 8045                                       |
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| 1125   | 2911   | 4697  | 6483  | 784CIP2B_814  | 8077                                       |
| 1126   | 2912   | 4698  | 6484  | 784CIP2B_815  | 8078                                       |
| 1127   | 2913   | 4699  | 6485  | 784CIP2B_816  | 8079                                       |
| 1128   | 2914   | 4700  | 6486  | 784CIP2B_817  | 8084                                       |
| 1129   | 2915   | 4701  | 6487  | 784CIP2B_818  | 8088                                       |
| 1130   | 2916   | 4702  | 6488  | 784CIP2B_819  | 8090                                       |
| 1131   | 2917   | 4703  | 6489  | 784CIP2B_820  | 8091                                       |
| 1132   | 2918   | 4704  | 6490  | 784CIP2B_821  | 8099                                       |
| 1133   | 2919   | 4705  | 6491  | 784CIP2B_822  | 8099                                       |
| 1134   | 2920   | 4706  | 6492  | 784CIP2B_823  | 8100                                       |
| 1135   | 2921   | 4707  | 6493  | 784CIP2B_824  | 8102                                       |
| 1136   | 2922   | 4708  | 6494  | 784CIP2B_825  | 8103                                       |
| 1137   | 2923   | 4709  | 6495  | 784CIP2B_826  | 8103                                       |
| 1138   | 2924   | 4710  | 6496  | 784CIP2B_827  | 8104                                       |
| 1139   | 2925   | 4711  | 6497  | 784CIP2B_828  | 8108                                       |
| 1140   | 2926   | 4712  | 6498  | 784CIP2B_829  | 8110                                       |
| 1141   | 2927   | 4713  | 6499  | 784CIP2B_830  | 8116                                       |
| 1142   | 2928   | 4714  | 6500  | 784CIP2B_831  | 8117                                       |
| 1143   | 2929   | 4715  | 6501  | 784CIP2B_832  | 8123                                       |
| 1144   | 2930   | 4716  | 6502  | 784CIP2B_833  | 8130                                       |
| 1145   | 2931   | 4717  | 6503  | 784CIP2B_834  | 8130                                       |
| 1146   | 2932   | 4718  | 6504  | 784CIP2B_835  | 8143                                       |
| 1147   | 2933   | 4719  | 6505  | 784CIP2B_836  | 8143                                       |
| 1148   | 2934   | 4720  | 6506  | 784CIP2B_837  | 8154                                       |
| 1149   | 2935   | 4721  | 6507  | 784CIP2B_838  | 8155                                       |
| 1150   | 2936   | 4722  | 6508  | 784CIP2B_839  | 8162                                       |
| 1151   | 2937   | 4723  | 6509  | 784CIP2B_840  | 8163                                       |
| 1152   | 2938   | 4724  | 6510  | 784CIP2B_841  | 8172                                       |
| 1153   | 2939   | 4725  | 6511  | 784CIP2B_842  | 8173                                       |
| 1154   | 2940   | 4726  | 6512  | 784CIP2B_843  | 8179                                       |
| 1155   | 2941   | 4727  | 6513  | 784CIP2B_844  | 8182                                       |
| 1156   | 2942   | 4728  | 6514  | 784CIP2B_845  | 8183                                       |
| 1157   | 2943   | 4729  | 6515  | 784CIP2B_846  | 8184                                       |
| 1158   | 2944   | 4730  | 6516  | 784CIP2B_847  | 8185                                       |
| 1159   | 2945   | 4731  | 6517  | 784CIP2B_848  | 8187                                       |
| 1160   | 2946   | 4732  | 6518  | 784CIP2B_849  | 8188                                       |
| 1161   | 2947   | 4733  | 6519  | 784CIP2B_850  | 8190                                       |
| 1162   | 2948   | 4734  | 6520  | 784CIP2B_851  | 8190                                       |
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| 1164   | 2950   | 4736  | 6522  | 784CIP2B_853  | 8193                                       |
| 1165   | 2951   | 4737  | 6523  | 784CIP2B_854  | 8197                                       |
| 1166   | 2952   | 4738  | 6524  | 784CIP2B_855  | 8197                                       |
| 1167   | 2953   | 4739  | 6525  | 784CIP2B_856  | 8199                                       |
| 1168   | 2954   | 4740  | 6526  | 784CIP2B_857  | 8202                                       |
| 1169   | 2955   | 4741  | 6527  | 784CIP2B_858  | 8203                                       |
| 1170   | 2956   | 4742  | 6528  | 784CIP2B_859  | 8208                                       |
| 1171   | 2957   | 4743  | 6529  | 784CIP2B_860  | 8209                                       |
| 1172   | 2958   | 4744  | 6530  | 784CIP2B_861  | 8211                                       |
| 1173   | 2959   | 4745  | 6531  | 784CIP2B_862  | 8214                                       |
| 1174   | 2960   | 4746  | 6532  | 784CIP2B_863  | 8217                                       |
| 1175   | 2961   | 4747  | 6533  | 784CIP2B_864  | 8223                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|--|--|
| 1176   | 2962   | 4748  | 6534  | 784CIP2B_865   | 8224                                       |
| 1177   | 2963   | 4749  | 6535  | 784CIP2B_866   | 8226                                       |
| 1178   | 2964   | 4750  | 6536  | 784CIP2B_867   | 8227                                       |
| 1179   | 2965   | 4751  | 6537  | 784CIP2B_868   | 8229                                       |
| 1180   | 2966   | 4752  | 6538  | 784CIP2B_869   | 8232                                       |
| 1181   | 2967   | 4753  | 6539  | 784CIP2B_870   | 8236                                       |
| 1182   | 2968   | 4754  | 6540  | 784CIP2B_871   | 8239                                       |
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| 1186   | 2972   | 4758  | 6544  | 784CIP2B_875   | 8251                                       |
| 1187   | 2973   | 4759  | 6545  | 784CIP2B_876   | 8253                                       |
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| 1189   | 2975   | 4761  | 6547  | 784CIP2B_878   | 8262                                       |
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| 1191   | 2977   | 4763  | 6549  | 784CIP2B_880   | 8270                                       |
| 1192   | 2978   | 4764  | 6550  | 784CIP2B_881   | 8272                                       |
| 1193   | 2979   | 4765  | 6551  | 784CIP2B_882   | 8274                                       |
| 1194   | 2980   | 4766  | 6552  | 784CIP2B_883   | 8274                                       |
| 1195   | 2981   | 4767  | 6553  | 784CIP2B_884   | 8275                                       |
| 1196   | 2982   | 4768  | 6554  | 784CIP2B_885   | 8277                                       |
| 1197   | 2983   | 4769  | 6555  | 784CIP2B_886   | 8281                                       |
| 1198   | 2984   | 4770  | 6556  | 784CIP2B_887   | 8283                                       |
| 1199   | 2985   | 4771  | 6557  | 784CIP2B_888   | 8289                                       |
| 1200   | 2986   | 4772  | 6558  | 784CIP2B_889   | 8295                                       |
| 1201   | 2987   | 4773  | 6559  | 784CIP2B_890   | 8300                                       |
| 1202   | 2988   | 4774  | 6560  | 784CIP2B_891   | 8303                                       |
| 1203   | 2989   | 4775  | 6561  | 784CIP2B_892   | 8304                                       |
| 1204   | 2990   | 4776  | 6562  | 784CIP2B_893   | 8305                                       |
| 1205   | 2991   | 4777  | 6563  | 784CIP2B_894   | 8309                                       |
| 1206   | 2992   | 4778  | 6564  | 784CIP2B_895   | 8318                                       |
| 1207   | 2993   | 4779  | 6565  | 784CIP2B_896   | 8319                                       |
| 1208   | 2994   | 4780  | 6566  | 784CIP2B_897   | 8321                                       |
| 1209   | 2995   | 4781  | 6567  | 784CIP2B_898   | 8322                                       |
| 1210   | 2996   | 4782  | 6568  | 784CIP2B_899   | 8323                                       |
| 1211   | 2997   | 4783  | 6569  | 784CIP2B_900   | 8325                                       |
| 1212   | 2998   | 4784  | 6570  | 784CIP2B_901   | 8331                                       |
| 1213   | 2999   | 4785  | 6571  | 784CIP2B_902   | 8332                                       |
| 1214   | 3000   | 4786  | 6572  | 784CIP2B_903   | 8333                                       |
| 1215   | 3001   | 4787  | 6573  | 784CIP2B_904   | 8335                                       |
| 1216   | 3002   | 4788  | 6574  | 784CIP2B_905   | 8336                                       |
| 1217   | 3003   | 4789  | 6575  | 784CIP2B_906   | 8337                                       |
| 1218   | 3004   | 4790  | 6576  | 784CIP2B_907   | 8340                                       |
| 1219   | 3005   | 4791  | 6577  | 784CIP2B_908   | 8343                                       |
| 1220   | 3006   | 4792  | 6578  | 784CIP2B_909   | 8347                                       |
| 1221   | 3007   | 4793  | 6579  | 784CIP2B_910   | 8349                                       |
| 1222   | 3008   | 4794  | 6580  | 784CIP2B_911   | 8351                                       |
| 1223   | 3009   | 4795  | 6581  | 784CIP2B_912   | 8353                                       |
| 1224   | 3010   | 4796  | 6582  | 784CIP2B_913   | 8355                                       |
| 1225   | 3011   | 4797  | 6583  | 784CIP2B_914   | 8361                                       |
| 1226   | 3012   | 4798  | 6584  | 784CIP2B_915   | 8365                                       |
| 1227   | 3013   | 4799  | 6585  | 784CIP2B_916   | 8367                                       |
| 1228   | 3014   | 4800  | 6586  | 784CIP2B_917   | 8369                                       |
| 1229   | 3015   | 4801  | 6587  | 784CIP2B_919   | 8375                                       |
| 1230   | 3016   | 4802  | 6588  | 784CIP2B_920   | 8387                                       |
| 1231   | 3017   | 4803  | 6589  | 784CIP2B_921   | 8391                                       |
| 1232   | 3018   | 4804  | 6590  | 784CIP2B_922   | 8393                                       |
| 1233   | 3019   | 4805  | 6591  | 784CIP2B_923   | 8393                                       |
| 1234   | 3020   | 4806  | 6592  | 784CIP2B_924   | 8394                                       |
| 1235   | 3021   | 4807  | 6593  | 784CIP2B_925   | 8395                                       |
| 1236   | 3022   | 4808  | 6594  | 784CIP2B_926   | 8396                                       |
| 1237   | 3023   | 4809  | 6595  | 784CIP2B_927   | 8398                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number,<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
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| 1239   | 3025   | 4811  | 6597  | 784CIP2B_929  | 8402                                       |
| 1240   | 3026   | 4812  | 6598  | 784CIP2B_930  | 8405                                       |
| 1241   | 3027   | 4813  | 6599  | 784CIP2B_931  | 8406                                       |
| 1242   | 3028   | 4814  | 6600  | 784CIP2B_932  | 8409                                       |
| 1243   | 3029   | 4815  | 6601  | 784CIP2B_933  | 8410                                       |
| 1244   | 3030   | 4816  | 6602  | 784CIP2B_934  | 8414                                       |
| 1245   | 3031   | 4817  | 6603  | 784CIP2B_935  | 8415                                       |
| 1246   | 3032   | 4818  | 6604  | 784CIP2B_936  | 8419                                       |
| 1247   | 3033   | 4819  | 6605  | 784CIP2B_937  | 8426                                       |
| 1248   | 3034   | 4820  | 6606  | 784CIP2B_938  | 8430                                       |
| 1249   | 3035   | 4821  | 6607  | 784CIP2B_939  | 8431                                       |
| 1250   | 3036   | 4822  | 6608  | 784CIP2B_940  | 8432                                       |
| 1251   | 3037   | 4823  | 6609  | 784CIP2B_941  | 8433                                       |
| 1252   | 3038   | 4824  | 6610  | 784CIP2B_942  | 8434                                       |
| 1253   | 3039   | 4825  | 6611  | 784CIP2B_943  | 8438                                       |
| 1254   | 3040   | 4826  | 6612  | 784CIP2B_944  | 8439                                       |
| 1255   | 3041   | 4827  | 6613  | 784CIP2B_945  | 8441                                       |
| 1256   | 3042   | 4828  | 6614  | 784CIP2B_946  | 8450                                       |
| 1257   | 3043   | 4829  | 6615  | 784CIP2B_947  | 8451                                       |
| 1258   | 3044   | 4830  | 6616  | 784CIP2B_948  | 8452                                       |
| 1259   | 3045   | 4831  | 6617  | 784CIP2B_949  | 8460                                       |
| 1260   | 3046   | 4832  | 6618  | 784CIP2B_950  | 8461                                       |
| 1261   | 3047   | 4833  | 6619  | 784CIP2B_951  | 8462                                       |
| 1262   | 3048   | 4834  | 6620  | 784CIP2B_952  | 8464                                       |
| 1263   | 3049   | 4835  | 6621  | 784CIP2B_953  | 8465                                       |
| 1264   | 3050   | 4836  | 6622  | 784CIP2B_954  | 8467                                       |
| 1265   | 3051   | 4837  | 6623  | 784CIP2B_955  | 8470                                       |
| 1266   | 3052   | 4838  | 6624  | 784CIP2B_956  | 8471                                       |
| 1267   | 3053   | 4839  | 6625  | 784CIP2B_957  | 8473                                       |
| 1268   | 3054   | 4840  | 6626  | 784CIP2B_958  | 8474                                       |
| 1269   | 3055   | 4841  | 6627  | 784CIP2B_959  | 8475                                       |
| 1270   | 3056   | 4842  | 6628  | 784CIP2B_960  | 8476                                       |
| 1271   | 3057   | 4843  | 6629  | 784CIP2B_961  | 8480                                       |
| 1272   | 3058   | 4844  | 6630  | 784CIP2B_962  | 8482                                       |
| 1273   | 3059   | 4845  | 6631  | 784CIP2B_963  | 8482                                       |
| 1274   | 3060   | 4846  | 6632  | 784CIP2B_964  | 8486                                       |
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| 1276   | 3062   | 4848  | 6634  | 784CIP2B_966  | 8492                                       |
| 1277   | 3063   | 4849  | 6635  | 784CIP2B_967  | 8494                                       |
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| 1285   | 3071   | 4857  | 6643  | 784CIP2B_975  | 8533                                       |
| 1286   | 3072   | 4858  | 6644  | 784CIP2B_976  | 8542                                       |
| 1287   | 3073   | 4859  | 6645  | 784CIP2B_977  | 8544                                       |
| 1288   | 3074   | 4860  | 6646  | 784CIP2B_978  | 8565                                       |
| 1289   | 3075   | 4861  | 6647  | 784CIP2B_979  | 8565                                       |
| 1290   | 3076   | 4862  | 6648  | 784CIP2B_980  | 8572                                       |
| 1291   | 3077   | 4863  | 6649  | 784CIP2B_981  | 8576                                       |
| 1292   | 3078   | 4864  | 6650  | 784CIP2B_982  | 8578                                       |
| 1293   | 3079   | 4865  | 6651  | 784CIP2B_983  | 8584                                       |
| 1294   | 3080   | 4866  | 6652  | 784CIP2B_984  | 8598                                       |
| 1295   | 3081   | 4867  | 6653  | 784CIP2B_985  | 8602                                       |
| 1296   | 3082   | 4868  | 6654  | 784CIP2B_986  | 8604                                       |
| 1297   | 3083   | 4869  | 6655  | 784CIP2B_987  | 8609                                       |
| 1298   | 3084   | 4870  | 6656  | 784CIP2B_988  | 8612                                       |
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| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
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| 1303   | 3089   | 4875  | 6661  | 784CIP2B_993  | 8650                                       |
| 1304   | 3090   | 4876  | 6662  | 784CIP2B_994  | 8651                                       |
| 1305   | 3091   | 4877  | 6663  | 784CIP2B_995  | 8654                                       |
| 1306   | 3092   | 4878  | 6664  | 784CIP2B_996  | 8655                                       |
| 1307   | 3093   | 4879  | 6665  | 784CIP2B_997  | 8657                                       |
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| 1310   | 3096   | 4882  | 6668  | 784CIP2B_1000   | 8671                                       |
| 1311   | 3097   | 4883  | 6669  | 784CIP2B_1001   | 8672                                       |
| 1312   | 3098   | 4884  | 6670  | 784CIP2B_1002   | 8692                                       |
| 1313   | 3099   | 4885  | 6671  | 784CIP2B_1003   | 8706                                       |
| 1314   | 3100   | 4886  | 6672  | 784CIP2B_1004   | 8716                                       |
| 1315   | 3101   | 4887  | 6673  | 784CIP2B_1005   | 8719                                       |
| 1316   | 3102   | 4888  | 6674  | 784CIP2B_1006   | 8743                                       |
| 1317   | 3103   | 4889  | 6675  | 784CIP2B_1007   | 8764                                       |
| 1318   | 3104   | 4890  | 6676  | 784CIP2B_1008   | 8764                                       |
| 1319   | 3105   | 4891  | 6677  | 784CIP2B_1009   | 8764                                       |
| 1320   | 3106   | 4892  | 6678  | 784CIP2B_1010   | 8774                                       |
| 1321   | 3107   | 4893  | 6679  | 784CIP2B_1011   | 8782                                       |
| 1322   | 3108   | 4894  | 6680  | 784CIP2B_1012   | 8796                                       |
| 1323   | 3109   | 4895  | 6681  | 784CIP2B_1013   | 8827                                       |
| 1324   | 3110   | 4896  | 6682  | 784CIP2B_1014   | 8842                                       |
| 1325   | 3111   | 4897  | 6683  | 784CIP2B_1015   | 8842                                       |
| 1326   | 3112   | 4898  | 6684  | 784CIP2B_1016   | 8858                                       |
| 1327   | 3113   | 4899  | 6685  | 784CIP2B_1017   | 8871                                       |
| 1328   | 3114   | 4900  | 6686  | 784CIP2B_1018   | 8921                                       |
| 1329   | 3115   | 4901  | 6687  | 784CIP2B_1019   | 8927                                       |
| 1330   | 3116   | 4902  | 6688  | 784CIP2B_1020   | 8942                                       |
| 1331   | 3117   | 4903  | 6689  | 784CIP2B_1021   | 8994                                       |
| 1332   | 3118   | 4904  | 6690  | 784CIP2B_1022   | 9023                                       |
| 1333   | 3119   | 4905  | 6691  | 784CIP2B_1023   | 9028                                       |
| 1334   | 3120   | 4906  | 6692  | 784CIP2B_1024   | 9058                                       |
| 1335   | 3121   | 4907  | 6693  | 784CIP2B_1025   | 9058                                       |
| 1336   | 3122   | 4908  | 6694  | 784CIP2B_1026   | 9079                                       |
| 1337   | 3123   | 4909  | 6695  | 784CIP2B_1027   | 9079                                       |
| 1338   | 3124   | 4910  | 6696  | 784CIP2B_1028   | 9082                                       |
| 1339   | 3125   | 4911  | 6697  | 784CIP2B_1029   | 9084                                       |
| 1340   | 3126   | 4912  | 6698  | 784CIP2B_1030   | 9093                                       |
| 1341   | 3127   | 4913  | 6699  | 784CIP2B_1031   | 9101                                       |
| 1342   | 3128   | 4914  | 6700  | 784CIP2B_1032   | 9103                                       |
| 1343   | 3129   | 4915  | 6701  | 784CIP2B_1033   | 9105                                       |
| 1344   | 3130   | 4916  | 6702  | 784CIP2B_1034   | 9151                                       |
| 1345   | 3131   | 4917  | 6703  | 784CIP2B_1035   | 9161                                       |
| 1346   | 3132   | 4918  | 6704  | 784CIP2B_1036   | 9172                                       |
| 1347   | 3133   | 4919  | 6705  | 784CIP2B_1037   | 9174                                       |
| 1348   | 3134   | 4920  | 6706  | 784CIP2B_1038   | 9204                                       |
| 1349   | 3135   | 4921  | 6707  | 784CIP2B_1039   | 9234                                       |
| 1350   | 3136   | 4922  | 6708  | 784CIP2B_1040   | 9235                                       |
| 1351   | 3137   | 4923  | 6709  | 784CIP2B_1041   | 9239                                       |
| 1352   | 3138   | 4924  | 6710  | 784CIP2B_1042   | 9256                                       |
| 1353   | 3139   | 4925  | 6711  | 784CIP2B_1043   | 9276                                       |
| 1354   | 3140   | 4926  | 6712  | 784CIP2B_1044   | 9345                                       |
| 1355   | 3141   | 4927  | 6713  | 784CIP2B_1045   | 9379                                       |
| 1356   | 3142   | 4928  | 6714  | 784CIP2B_1046   | 9435                                       |
| 1357   | 3143   | 4929  | 6715  | 784CIP2B_1047   | 9437                                       |
| 1358   | 3144   | 4930  | 6716  | 784CIP2B_1048   | 9469                                       |
| 1359   | 3145   | 4931  | 6717  | 784CIP2B_1049   | 9500                                       |
| 1360   | 3146   | 4932  | 6718  | 784CIP2B_1050   | 9502                                       |
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| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|--|--|
| 1362   | 3148   | 4934  | 6720  | 784CIP2B_1052  | 9541                                       |
| 1363   | 3149   | 4935  | 6721  | 784CIP2B_1053  | 9541                                       |
| 1364   | 3150   | 4936  | 6722  | 784CIP2B_1054  | 9548                                       |
| 1365   | 3151   | 4937  | 6723  | 784CIP2B_1055  | 9556                                       |
| 1366   | 3152   | 4938  | 6724  | 784CIP2B_1056  | 9556                                       |
| 1367   | 3153   | 4939  | 6725  | 784CIP2B_1057  | 9575                                       |
| 1368   | 3154   | 4940  | 6726  | 784CIP2B_1058  | 9589                                       |
| 1369   | 3155   | 4941  | 6727  | 784CIP2B_1059  | 9599                                       |
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| 1371   | 3157   | 4943  | 6729  | 784CIP2B_1061  | 9606                                       |
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| 1373   | 3159   | 4945  | 6731  | 784CIP2B_1063  | 9623                                       |
| 1374   | 3160   | 4946  | 6732  | 784CIP2B_1064  | 9646                                       |
| 1375   | 3161   | 4947  | 6733  | 784CIP2B_1065  | 9747                                       |
| 1376   | 3162   | 4948  | 6734  | 784CIP2B_1066  | 9773                                       |
| 1377   | 3163   | 4949  | 6735  | 784CIP2B_1067  | 9785                                       |
| 1378   | 3164   | 4950  | 6736  | 784CIP2B_1068  | 9801                                       |
| 1379   | 3165   | 4951  | 6737  | 784CIP2B_1069  | 9811                                       |
| 1380   | 3166   | 4952  | 6738  | 784CIP2B_1070  | 9843                                       |
| 1381   | 3167   | 4953  | 6739  | 784CIP2B_1071  | 9854                                       |
| 1382   | 3168   | 4954  | 6740  | 784CIP2B_1072  | 9854                                       |
| 1383   | 3169   | 4955  | 6741  | 784CIP2B_1073  | 9864                                       |
| 1384   | 3170   | 4956  | 6742  | 784CIP2B_1074  | 9864                                       |
| 1385   | 3171   | 4957  | 6743  | 784CIP2B_1075  | 9871                                       |
| 1386   | 3172   | 4958  | 6744  | 784CIP2B_1076  | 9879                                       |
| 1387   | 3173   | 4959  | 6745  | 784CIP2B_1077  | 9881                                       |
| 1388   | 3174   | 4960  | 6746  | 784CIP2B_1078  | 9885                                       |
| 1389   | 3175   | 4961  | 6747  | 784CIP2B_1079  | 9901                                       |
| 1390   | 3176   | 4962  | 6748  | 784CIP2B_1080  | 9912                                       |
| 1391   | 3177   | 4963  | 6749  | 784CIP2B_1081  | 9916                                       |
| 1392   | 3178   | 4964  | 6750  | 784CIP2B_1082  | 9921                                       |
| 1393   | 3179   | 4965  | 6751  | 784CIP2B_1083  | 9925                                       |
| 1394   | 3180   | 4966  | 6752  | 784CIP2B_1084  | 9930                                       |
| 1395   | 3181   | 4967  | 6753  | 784CIP2B_1085  | 9949                                       |
| 1396   | 3182   | 4968  | 6754  | 784CIP2B_1086  | 9951                                       |
| 1397   | 3183   | 4969  | 6755  | 784CIP2B_1087  | 9959                                       |
| 1398   | 3184   | 4970  | 6756  | 784CIP2B_1088  | 9973                                       |
| 1399   | 3185   | 4971  | 6757  | 784CIP2B_1089  | 9982                                       |
| 1400   | 3186   | 4972  | 6758  | 784CIP2B_1090  | 9994                                       |
| 1401   | 3187   | 4973  | 6759  | 784CIP2B_1091  | 10021                                      |
| 1402   | 3188   | 4974  | 6760  | 784CIP2B_1092  | 10041                                      |
| 1403   | 3189   | 4975  | 6761  | 784CIP2B_1094  | 10067                                      |
| 1404   | 3190   | 4976  | 6762  | 784CIP2B_1095  | 10073                                      |
| 1405   | 3191   | 4977  | 6763  | 784CIP2B_1096  | 10112                                      |
| 1406   | 3192   | 4978  | 6764  | 784CIP2B_1097  | 10117                                      |
| 1407   | 3193   | 4979  | 6765  | 784CIP2B_1098  | 10132                                      |
| 1408   | 3194   | 4980  | 6766  | 784CIP2B_1099  | 10169                                      |
| 1409   | 3195   | 4981  | 6767  | 784CIP2B_1100  | 10217                                      |
| 1410   | 3196   | 4982  | 6768  | 784CIP2B_1101  | 10226                                      |
| 1411   | 3197   | 4983  | 6769  | 784CIP2B_1102  | 10232                                      |
| 1412   | 3198   | 4984  | 6770  | 784CIP2B_1103  | 10237                                      |
| 1413   | 3199   | 4985  | 6771  | 784CIP2B_1104  | 10279                                      |
| 1414   | 3200   | 4986  | 6772  | 784CIP2C_1   | 33   |
| 1415   | 3201   | 4987  | 6773  | 784CIP2C_2   | 271  |
| 1416   | 3202   | 4988  | 6774  | 784CIP2C_3   | 848  |
| 1417   | 3203   | 4989  | 6775  | 784CIP2C_4   | 849  |
| 1418   | 3204   | 4990  | 6776  | 784CIP2C_5   | 864  |
| 1419   | 3205   | 4991  | 6777  | 784CIP2C_6   | 953  |
| 1420   | 3206   | 4992  | 6778  | 784CIP2C_7   | 980  |
| 1421   | 3207   | 4993  | 6779  | 784CIP2C_8   | 1595                                       |
| 1422   | 3208   | 4994  | 6780  | 784CIP2C_9   | 1697                                       |
| 1423   | 3209   | 4995  | 6781  | 784CIP2C_10  | 1744                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 1424   | 3210   | 4996  | 6782  | 784CIP2C_11   | 1937                                       |
| 1425   | 3211   | 4997  | 6783  | 784CIP2C_12   | 1955                                       |
| 1426   | 3212   | 4998  | 6784  | 784CIP2C_13   | 1955                                       |
| 1427   | 3213   | 4999  | 6785  | 784CIP2C_14   | 2185                                       |
| 1428   | 3214   | 5000  | 6786  | 784CIP2C_15   | 2889                                       |
| 1429   | 3215   | 5001  | 6787  | 784CIP2C_16   | 2901                                       |
| 1430   | 3216   | 5002  | 6788  | 784CIP2C_17   | 2902                                       |
| 1431   | 3217   | 5003  | 6789  | 784CIP2C_18   | 2905                                       |
| 1432   | 3218   | 5004  | 6790  | 784CIP2C_19   | 2948                                       |
| 1433   | 3219   | 5005  | 6791  | 784CIP2C_20   | 2956                                       |
| 1434   | 3220   | 5006  | 6792  | 784CIP2C_21   | 2959                                       |
| 1435   | 3221   | 5007  | 6793  | 784CIP2C_22   | 2965                                       |
| 1436   | 3222   | 5008  | 6794  | 784CIP2C_23   | 2966                                       |
| 1437   | 3223   | 5009  | 6795  | 784CIP2C_24   | 2970                                       |
| 1438   | 3224   | 5010  | 6796  | 784CIP2C_25   | 2985                                       |
| 1439   | 3225   | 5011  | 6797  | 784CIP2C_26   | 2987                                       |
| 1440   | 3226   | 5012  | 6798  | 784CIP2C_27   | 2993                                       |
| 1441   | 3227   | 5013  | 6799  | 784CIP2C_28   | 2993                                       |
| 1442   | 3228   | 5014  | 6800  | 784CIP2C_29   | 3017                                       |
| 1443   | 3229   | 5015  | 6801  | 784CIP2C_30   | 3046                                       |
| 1444   | 3230   | 5016  | 6802  | 784CIP2C_31   | 3050                                       |
| 1445   | 3231   | 5017  | 6803  | 784CIP2C_32   | 3357                                       |
| 1446   | 3232   | 5018  | 6804  | 784CIP2C_33   | 3359                                       |
| 1447   | 3233   | 5019  | 6805  | 784CIP2C_34   | 3432                                       |
| 1448   | 3234   | 5020  | 6806  | 784CIP2C_35   | 3438                                       |
| 1449   | 3235   | 5021  | 6807  | 784CIP2C_36   | 3439                                       |
| 1450   | 3236   | 5022  | 6808  | 784CIP2C_39   | 3463                                       |
| 1451   | 3237   | 5023  | 6809  | 784CIP2C_40   | 3466                                       |
| 1452   | 3238   | 5024  | 6810  | 784CIP2C_41   | 3466                                       |
| 1453   | 3239   | 5025  | 6811  | 784CIP2C_42   | 3467                                       |
| 1454   | 3240   | 5026  | 6812  | 784CIP2C_43   | 3468                                       |
| 1455   | 3241   | 5027  | 6813  | 784CIP2C_44   | 3483                                       |
| 1456   | 3242   | 5028  | 6814  | 784CIP2C_45   | 3484                                       |
| 1457   | 3243   | 5029  | 6815  | 784CIP2C_46   | 3488                                       |
| 1458   | 3244   | 5030  | 6816  | 784CIP2C_47   | 3491                                       |
| 1459   | 3245   | 5031  | 6817  | 784CIP2C_48   | 3493                                       |
| 1460   | 3246   | 5032  | 6818  | 784CIP2C_49   | 3494                                       |
| 1461   | 3247   | 5033  | 6819  | 784CIP2C_50   | 3495                                       |
| 1462   | 3248   | 5034  | 6820  | 784CIP2C_51   | 3496                                       |
| 1463   | 3249   | 5035  | 6821  | 784CIP2C_52   | 3503                                       |
| 1464   | 3250   | 5036  | 6822  | 784CIP2C_53   | 3503                                       |
| 1465   | 3251   | 5037  | 6823  | 784CIP2C_54   | 3504                                       |
| 1466   | 3252   | 5038  | 6824  | 784CIP2C_55   | 3511                                       |
| 1467   | 3253   | 5039  | 6825  | 784CIP2C_56   | 3531                                       |
| 1468   | 3254   | 5040  | 6826  | 784CIP2C_57   | 3536                                       |
| 1469   | 3255   | 5041  | 6827  | 784CIP2C_58   | 3546                                       |
| 1470   | 3256   | 5042  | 6828  | 784CIP2C_59   | 3548                                       |
| 1471   | 3257   | 5043  | 6829  | 784CIP2C_60   | 3551                                       |
| 1472   | 3258   | 5044  | 6830  | 784CIP2C_61   | 3553                                       |
| 1473   | 3259   | 5045  | 6831  | 784CIP2C_62   | 3564                                       |
| 1474   | 3260   | 5046  | 6832  | 784CIP2C_63   | 3567                                       |
| 1475   | 3261   | 5047  | 6833  | 784CIP2C_64   | 3572                                       |
| 1476   | 3262   | 5048  | 6834  | 784CIP2C_65   | 3573                                       |
| 1477   | 3263   | 5049  | 6835  | 784CIP2C_66   | 3574                                       |
| 1478   | 3264   | 5050  | 6836  | 784CIP2C_67   | 3583                                       |
| 1479   | 3265   | 5051  | 6837  | 784CIP2C_68   | 3615                                       |
| 1480   | 3266   | 5052  | 6838  | 784CIP2C_69   | 3623                                       |
| 1481   | 3267   | 5053  | 6839  | 784CIP2C_70   | 3629                                       |
| 1482   | 3268   | 5054  | 6840  | 784CIP2C_71   | 3666                                       |
| 1483   | 3269   | 5055  | 6841  | 784CIP2C_72   | 3667                                       |
| 1484   | 3270   | 5056  | 6842  | 784CIP2C_73   | 3906                                       |
| 1485   | 3271   | 5057  | 6843  | 784CIP2C_74   | 3912                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 1486   | 3272   | 5058  | 6844  | 784CIP2C_75   | 3924                                       |
| 1487   | 3273   | 5059  | 6845  | 784CIP2C_76   | 3928                                       |
| 1488   | 3274   | 5060  | 6846  | 784CIP2C_77   | 3935                                       |
| 1489   | 3275   | 5061  | 6847  | 784CIP2C_78   | 3959                                       |
| 1490   | 3276   | 5062  | 6848  | 784CIP2C_79   | 3981                                       |
| 1491   | 3277   | 5063  | 6849  | 784CIP2C_80   | 3989                                       |
| 1492   | 3278   | 5064  | 6850  | 784CIP2C_81   | 4295                                       |
| 1493   | 3279   | 5065  | 6851  | 784CIP2C_82   | 4300                                       |
| 1494   | 3280   | 5066  | 6852  | 784CIP2C_83   | 4360                                       |
| 1495   | 3281   | 5067  | 6853  | 784CIP2C_84   | 4362                                       |
| 1496   | 3282   | 5068  | 6854  | 784CIP2C_85   | 4371                                       |
| 1497   | 3283   | 5069  | 6855  | 784CIP2C_86   | 4373                                       |
| 1498   | 3284   | 5070  | 6856  | 784CIP2C_87   | 4376                                       |
| 1499   | 3285   | 5071  | 6857  | 784CIP2C_89   | 4378                                       |
| 1500   | 3286   | 5072  | 6858  | 784CIP2C_90   | 4382                                       |
| 1501   | 3287   | 5073  | 6859  | 784CIP2C_91   | 4409                                       |
| 1502   | 3288   | 5074  | 6860  | 784CIP2C_92   | 4421                                       |
| 1503   | 3289   | 5075  | 6861  | 784CIP2C_93   | 4421                                       |
| 1504   | 3290   | 5076  | 6862  | 784CIP2C_94   | 4426                                       |
| 1505   | 3291   | 5077  | 6863  | 784CIP2C_95   | 4430                                       |
| 1506   | 3292   | 5078  | 6864  | 784CIP2C_96   | 4435                                       |
| 1507   | 3293   | 5079  | 6865  | 784CIP2C_97   | 4436                                       |
| 1508   | 3294   | 5080  | 6866  | 784CIP2C_98   | 4439                                       |
| 1509   | 3295   | 5081  | 6867  | 784CIP2C_99   | 4440                                       |
| 1510   | 3296   | 5082  | 6868  | 784CIP2C_100  | 4441                                       |
| 1511   | 3297   | 5083  | 6869  | 784CIP2C_101  | 4442                                       |
| 1512   | 3298   | 5084  | 6870  | 784CIP2C_102  | 4455                                       |
| 1513   | 3299   | 5085  | 6871  | 784CIP2C_103  | 4462                                       |
| 1514   | 3300   | 5086  | 6872  | 784CIP2C_104  | 4466                                       |
| 1515   | 3301   | 5087  | 6873  | 784CIP2C_105  | 4469                                       |
| 1516   | 3302   | 5088  | 6874  | 784CIP2C_106  | 4477                                       |
| 1517   | 3303   | 5089  | 6875  | 784CIP2C_107  | 4481                                       |
| 1518   | 3304   | 5090  | 6876  | 784CIP2C_108  | 4483                                       |
| 1519   | 3305   | 5091  | 6877  | 784CIP2C_109  | 4484                                       |
| 1520   | 3306   | 5092  | 6878  | 784CIP2C_110  | 4486                                       |
| 1521   | 3307   | 5093  | 6879  | 784CIP2C_111  | 4490                                       |
| 1522   | 3308   | 5094  | 6880  | 784CIP2C_112  | 4499                                       |
| 1523   | 3309   | 5095  | 6881  | 784CIP2C_113  | 4503                                       |
| 1524   | 3310   | 5096  | 6882  | 784CIP2C_114  | 4506                                       |
| 1525   | 3311   | 5097  | 6883  | 784CIP2C_115  | 4509                                       |
| 1526   | 3312   | 5098  | 6884  | 784CIP2C_116  | 4514                                       |
| 1527   | 3313   | 5099  | 6885  | 784CIP2C_117  | 4516                                       |
| 1528   | 3314   | 5100  | 6886  | 784CIP2C_118  | 4522                                       |
| 1529   | 3315   | 5101  | 6887  | 784CIP2C_119  | 4525                                       |
| 1530   | 3316   | 5102  | 6888  | 784CIP2C_120  | 4527                                       |
| 1531   | 3317   | 5103  | 6889  | 784CIP2C_121  | 4528                                       |
| 1532   | 3318   | 5104  | 6890  | 784CIP2C_122  | 4529                                       |
| 1533   | 3319   | 5105  | 6891  | 784CIP2C_123  | 4532                                       |
| 1534   | 3320   | 5106  | 6892  | 784CIP2C_124  | 4537                                       |
| 1535   | 3321   | 5107  | 6893  | 784CIP2C_125  | 4538                                       |
| 1536   | 3322   | 5108  | 6894  | 784CIP2C_126  | 4551                                       |
| 1537   | 3323   | 5109  | 6895  | 784CIP2C_127  | 4552                                       |
| 1538   | 3324   | 5110  | 6896  | 784CIP2C_128  | 4559                                       |
| 1539   | 3325   | 5111  | 6897  | 784CIP2C_129  | 4567                                       |
| 1540   | 3326   | 5112  | 6898  | 784CIP2C_130  | 4568                                       |
| 1541   | 3327   | 5113  | 6899  | 784CIP2C_132  | 4585                                       |
| 1542   | 3328   | 5114  | 6900  | 784CIP2C_133  | 4592                                       |
| 1543   | 3329   | 5115  | 6901  | 784CIP2C_134  | 4609                                       |
| 1544   | 3330   | 5116  | 6902  | 784CIP2C_135  | 4616                                       |
| 1545   | 3331   | 5117  | 6903  | 784CIP2C_136  | 4617                                       |
| 1546   | 3332   | 5118  | 6904  | 784CIP2C_137  | 4618                                       |
| 1547   | 3333   | 5119  | 6905  | 784CIP2C_138  | 4620                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|--|--|
| 1548   | 3334   | 5120  | 6906  | 784CIP2C_139   | 4624                                       |
| 1549   | 3335   | 5121  | 6907  | 784CIP2C_140   | 4632                                       |
| 1550   | 3336   | 5122  | 6908  | 784CIP2C_141   | 4634                                       |
| 1551   | 3337   | 5123  | 6909  | 784CIP2C_142   | 4638                                       |
| 1552   | 3338   | 5124  | 6910  | 784CIP2C_143   | 4639                                       |
| 1553   | 3339   | 5125  | 6911  | 784CIP2C_144   | 4643                                       |
| 1554   | 3340   | 5126  | 6912  | 784CIP2C_145   | 4644                                       |
| 1555   | 3341   | 5127  | 6913  | 784CIP2C_146   | 4655                                       |
| 1556   | 3342   | 5128  | 6914  | 784CIP2C_147   | 4668                                       |
| 1557   | 3343   | 5129  | 6915  | 784CIP2C_148   | 4677                                       |
| 1558   | 3344   | 5130  | 6916  | 784CIP2C_149   | 4677                                       |
| 1559   | 3345   | 5131  | 6917  | 784CIP2C_150   | 4677                                       |
| 1560   | 3346   | 5132  | 6918  | 784CIP2C_152   | 4682                                       |
| 1561   | 3347   | 5133  | 6919  | 784CIP2C_153   | 4690                                       |
| 1562   | 3348   | 5134  | 6920  | 784CIP2C_154   | 4691                                       |
| 1563   | 3349   | 5135  | 6921  | 784CIP2C_155   | 4727                                       |
| 1564   | 3350   | 5136  | 6922  | 784CIP2C_156   | 4730                                       |
| 1565   | 3351   | 5137  | 6923  | 784CIP2C_157   | 4734                                       |
| 1566   | 3352   | 5138  | 6924  | 784CIP2C_158   | 4757                                       |
| 1567   | 3353   | 5139  | 6925  | 784CIP2C_159   | 4764                                       |
| 1568   | 3354   | 5140  | 6926  | 784CIP2C_160   | 4786                                       |
| 1569   | 3355   | 5141  | 6927  | 784CIP2C_161   | 4793                                       |
| 1570   | 3356   | 5142  | 6928  | 784CIP2C_162   | 4825                                       |
| 1571   | 3357   | 5143  | 6929  | 784CIP2C_163   | 4826                                       |
| 1572   | 3358   | 5144  | 6930  | 784CIP2C_164   | 4850                                       |
| 1573   | 3359   | 5145  | 6931  | 784CIP2C_165   | 4853                                       |
| 1574   | 3360   | 5146  | 6932  | 784CIP2C_166   | 4855                                       |
| 1575   | 3361   | 5147  | 6933  | 784CIP2C_167   | 4856                                       |
| 1576   | 3362   | 5148  | 6934  | 784CIP2C_168   | 4867                                       |
| 1577   | 3363   | 5149  | 6935  | 784CIP2C_169   | 4869                                       |
| 1578   | 3364   | 5150  | 6936  | 784CIP2C_170   | 4878                                       |
| 1579   | 3365   | 5151  | 6937  | 784CIP2C_171   | 4880                                       |
| 1580   | 3366   | 5152  | 6938  | 784CIP2C_172   | 4942                                       |
| 1581   | 3367   | 5153  | 6939  | 784CIP2C_173   | 4945                                       |
| 1582   | 3368   | 5154  | 6940  | 784CIP2C_174   | 4950                                       |
| 1583   | 3369   | 5155  | 6941  | 784CIP2C_175   | 4952                                       |
| 1584   | 3370   | 5156  | 6942  | 784CIP2C_176   | 4954                                       |
| 1585   | 3371   | 5157  | 6943  | 784CIP2C_177   | 4958                                       |
| 1586   | 3372   | 5158  | 6944  | 784CIP2C_178   | 4961                                       |
| 1587   | 3373   | 5159  | 6945  | 784CIP2C_179   | 5590                                       |
| 1588   | 3374   | 5160  | 6946  | 784CIP2C_180   | 5599                                       |
| 1589   | 3375   | 5161  | 6947  | 784CIP2C_181   | 5692                                       |
| 1590   | 3376   | 5162  | 6948  | 784CIP2C_182   | 5732                                       |
| 1591   | 3377   | 5163  | 6949  | 784CIP2C_183   | 5765                                       |
| 1592   | 3378   | 5164  | 6950  | 784CIP2C_184   | 5771                                       |
| 1593   | 3379   | 5165  | 6951  | 784CIP2C_185   | 5774                                       |
| 1594   | 3380   | 5166  | 6952  | 784CIP2C_186   | 5793                                       |
| 1595   | 3381   | 5167  | 6953  | 784CIP2C_187   | 5806                                       |
| 1596   | 3382   | 5168  | 6954  | 784CIP2C_188   | 5852                                       |
| 1597   | 3383   | 5169  | 6955  | 784CIP2C_189   | 5892                                       |
| 1598   | 3384   | 5170  | 6956  | 784CIP2C_190   | 6057                                       |
| 1599   | 3385   | 5171  | 6957  | 784CIP2C_191   | 6061                                       |
| 1600   | 3386   | 5172  | 6958  | 784CIP2C_192   | 6109                                       |
| 1601   | 3387   | 5173  | 6959  | 784CIP2C_193   | 6160                                       |
| 1602   | 3388   | 5174  | 6960  | 784CIP2C_194   | 6297                                       |
| 1603   | 3389   | 5175  | 6961  | 784CIP2C_195   | 6398                                       |
| 1604   | 3390   | 5176  | 6962  | 784CIP2C_196   | 6398                                       |
| 1605   | 3391   | 5177  | 6963  | 784CIP2C_197   | 6415                                       |
| 1606   | 3392   | 5178  | 6964  | 784CIP2C_198   | 6448                                       |
| 1607   | 3393   | 5179  | 6965  | 784CIP2C_199   | 6469                                       |
| 1608   | 3394   | 5180  | 6966  | 784CIP2C_200   | 6476                                       |
| 1609   | 3395   | 5181  | 6967  | 784CIP2C_201   | 6561                                       |



| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 1610   | 3396   | 5182  | 6968  | 784CIP2C_202  | 6574                                       |
| 1611   | 3397   | 5183  | 6969  | 784CIP2C_203  | 6578                                       |
| 1612   | 3398   | 5184  | 6970  | 784CIP2C_204  | 6662                                       |
| 1613   | 3399   | 5185  | 6971  | 784CIP2C_205  | 6672                                       |
| 1614   | 3400   | 5186  | 6972  | 784CIP2C_206  | 6691                                       |
| 1615   | 3401   | 5187  | 6973  | 784CIP2C_207  | 6695                                       |
| 1616   | 3402   | 5188  | 6974  | 784CIP2C_208  | 6746                                       |
| 1617   | 3403   | 5189  | 6975  | 784CIP2C_209  | 6898                                       |
| 1618   | 3404   | 5190  | 6976  | 784CIP2C_210  | 6938                                       |
| 1619   | 3405   | 5191  | 6977  | 784CIP2C_211  | 6943                                       |
| 1620   | 3406   | 5192  | 6978  | 784CIP2C_212  | 7110                                       |
| 1621   | 3407   | 5193  | 6979  | 784CIP2C_213  | 7200                                       |
| 1622   | 3408   | 5194  | 6980  | 784CIP2C_214  | 7212                                       |
| 1623   | 3409   | 5195  | 6981  | 784CIP2C_215  | 7218                                       |
| 1624   | 3410   | 5196  | 6982  | 784CIP2C_216  | 7249                                       |
| 1625   | 3411   | 5197  | 6983  | 784CIP2C_217  | 7500                                       |
| 1626   | 3412   | 5198  | 6984  | 784CIP2C_218  | 7509                                       |
| 1627   | 3413   | 5199  | 6985  | 784CIP2C_219  | 7523                                       |
| 1628   | 3414   | 5200  | 6986  | 784CIP2C_220  | 7544                                       |
| 1629   | 3415   | 5201  | 6987  | 784CIP2C_221  | 7564                                       |
| 1630   | 3416   | 5202  | 6988  | 784CIP2C_222  | 7568                                       |
| 1631   | 3417   | 5203  | 6989  | 784CIP2C_223  | 7631                                       |
| 1632   | 3418   | 5204  | 6990  | 784CIP2C_224  | 7813                                       |
| 1633   | 3419   | 5205  | 6991  | 784CIP2C_225  | 7831                                       |
| 1634   | 3420   | 5206  | 6992  | 784CIP2C_226  | 7843                                       |
| 1635   | 3421   | 5207  | 6993  | 784CIP2C_227  | 7907                                       |
| 1636   | 3422   | 5208  | 6994  | 784CIP2C_228  | 7943                                       |
| 1637   | 3423   | 5209  | 6995  | 784CIP2C_229  | 8175                                       |
| 1638   | 3424   | 5210  | 6996  | 784CIP2C_230  | 8216                                       |
| 1639   | 3425   | 5211  | 6997  | 784CIP2C_231  | 8225                                       |
| 1640   | 3426   | 5212  | 6998  | 784CIP2C_232  | 8271                                       |
| 1641   | 3427   | 5213  | 6999  | 784CIP2C_233  | 8397                                       |
| 1642   | 3428   | 5214  | 7000  | 784CIP2C_234  | 8466                                       |
| 1643   | 3429   | 5215  | 7001  | 784CIP2C_235  | 8503                                       |
| 1644   | 3430   | 5216  | 7002  | 784CIP2C_236  | 8953                                       |
| 1645   | 3431   | 5217  | 7003  | 784CIP2C_237  | 9106                                       |
| 1646   | 3432   | 5218  | 7004  | 784CIP2C_238  | 9139                                       |
| 1647   | 3433   | 5219  | 7005  | 784CIP2C_239  | 9555                                       |
| 1648   | 3434   | 5220  | 7006  | 784CIP2C_240  | 9650                                       |
| 1649   | 3435   | 5221  | 7007  | 784CIP2C_241  | 9889                                       |
| 1650   | 3436   | 5222  | 7008  | 784CIP2C_242  | 9933                                       |
| 1651   | 3437   | 5223  | 7009  | 784CIP2C_243  | 9953                                       |
| 1652   | 3438   | 5224  | 7010  | 784CIP2C_244  | 9981                                       |
| 1653   | 3439   | 5225  | 7011  | 784CIP2D_1  | 746  |
| 1654   | 3440   | 5226  | 7012  | 784CIP2D_2  | 3558                                       |
| 1655   | 3441   | 5227  | 7013  | 784CIP2D_3  | 3558                                       |
| 1656   | 3442   | 5228  | 7014  | 784CIP2D_4  | 3633                                       |
| 1657   | 3443   | 5229  | 7015  | 784CIP2D_5  | 3658                                       |
| 1658   | 3444   | 5230  | 7016  | 784CIP2D_6  | 3732                                       |
| 1659   | 3445   | 5231  | 7017  | 784CIP2D_7  | 4004                                       |
| 1660   | 3446   | 5232  | 7018  | 784CIP2D_8  | 4700                                       |
| 1661   | 3447   | 5233  | 7019  | 784CIP2D_9  | 4703                                       |
| 1662   | 3448   | 5234  | 7020  | 784CIP2D_10   | 4774                                       |
| 1663   | 3449   | 5235  | 7021  | 784CIP2D_11   | 4894                                       |
| 1664   | 3450   | 5236  | 7022  | 784CIP2D_12   | 4918                                       |
| 1665   | 3451   | 5237  | 7023  | 784CIP2D_13   | 5159                                       |
| 1666   | 3452   | 5238  | 7024  | 784CIP2D_14   | 7443                                       |
| 1667   | 3453   | 5239  | 7025  | 784CIP2D_15   | 8673                                       |
| 1668   | 3454   | 5240  | 7026  | 784CIP2D_16   | 8679                                       |
| 1669   | 3455   | 5241  | 7027  | 784CIP2D_17   | 8727                                       |
| 1670   | 3456   | 5242  | 7028  | 784CIP2D_18   | 8734                                       |
| 1671   | 3457   | 5243  | 7029  | 784CIP2D_19   | 8756                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 1672   | 3458   | 5244  | 7030  | 784CIP2D_20   | 8818                                       |
| 1673   | 3459   | 5245  | 7031  | 784CIP2D_21   | 8844                                       |
| 1674   | 3460   | 5246  | 7032  | 784CIP2D_22   | 8846                                       |
| 1675   | 3461   | 5247  | 7033  | 784CIP2D_23   | 8912                                       |
| 1676   | 3462   | 5248  | 7034  | 784CIP2D_24   | 8918                                       |
| 1677   | 3463   | 5249  | 7035  | 784CIP2D_25   | 8918                                       |
| 1678   | 3464   | 5250  | 7036  | 784CIP2D_26   | 8941                                       |
| 1679   | 3465   | 5251  | 7037  | 784CIP2D_27   | 8941                                       |
| 1680   | 3466   | 5252  | 7038  | 784CIP2D_28   | 8951                                       |
| 1681   | 3467   | 5253  | 7039  | 784CIP2D_29   | 8951                                       |
| 1682   | 3468   | 5254  | 7040  | 784CIP2D_30   | 9007                                       |
| 1683   | 3469   | 5255  | 7041  | 784CIP2D_31   | 9012                                       |
| 1684   | 3470   | 5256  | 7042  | 784CIP2D_32   | 9013                                       |
| 1685   | 3471   | 5257  | 7043  | 784CIP2D_33   | 9025                                       |
| 1686   | 3472   | 5258  | 7044  | 784CIP2D_34   | 9053                                       |
| 1687   | 3473   | 5259  | 7045  | 784CIP2D_35   | 9054                                       |
| 1688   | 3474   | 5260  | 7046  | 784CIP2D_36   | 9054                                       |
| 1689   | 3475   | 5261  | 7047  | 784CIP2D_37   | 9113                                       |
| 1690   | 3476   | 5262  | 7048  | 784CIP2D_38   | 9134                                       |
| 1691   | 3477   | 5263  | 7049  | 784CIP2D_39   | 9152                                       |
| 1692   | 3478   | 5264  | 7050  | 784CIP2D_40   | 9152                                       |
| 1693   | 3479   | 5265  | 7051  | 784CIP2D_41   | 9211                                       |
| 1694   | 3480   | 5266  | 7052  | 784CIP2D_42   | 9223                                       |
| 1695   | 3481   | 5267  | 7053  | 784CIP2D_43   | 9223                                       |
| 1696   | 3482   | 5268  | 7054  | 784CIP2D_44   | 9231                                       |
| 1697   | 3483   | 5269  | 7055  | 784CIP2D_45   | 9236                                       |
| 1698   | 3484   | 5270  | 7056  | 784CIP2D_46   | 9236                                       |
| 1699   | 3485   | 5271  | 7057  | 784CIP2D_47   | 9303                                       |
| 1700   | 3486   | 5272  | 7058  | 784CIP2D_48   | 9309                                       |
| 1701   | 3487   | 5273  | 7059  | 784CIP2D_49   | 9314                                       |
| 1702   | 3488   | 5274  | 7060  | 784CIP2D_50   | 9326                                       |
| 1703   | 3489   | 5275  | 7061  | 784CIP2D_51   | 9339                                       |
| 1704   | 3490   | 5276  | 7062  | 784CIP2D_52   | 9348                                       |
| 1705   | 3491   | 5277  | 7063  | 784CIP2D_53   | 9376                                       |
| 1706   | 3492   | 5278  | 7064  | 784CIP2D_54   | 9382                                       |
| 1707   | 3493   | 5279  | 7065  | 784CIP2D_55   | 9407                                       |
| 1708   | 3494   | 5280  | 7066  | 784CIP2D_56   | 9414                                       |
| 1709   | 3495   | 5281  | 7067  | 784CIP2D_57   | 9439                                       |
| 1710   | 3496   | 5282  | 7068  | 784CIP2D_58   | 9485                                       |
| 1711   | 3497   | 5283  | 7069  | 784CIP2D_59   | 9493                                       |
| 1712   | 3498   | 5284  | 7070  | 784CIP2D_60   | 9501                                       |
| 1713   | 3499   | 5285  | 7071  | 784CIP2D_61   | 9526                                       |
| 1714   | 3500   | 5286  | 7072  | 784CIP2D_62   | 9526                                       |
| 1715   | 3501   | 5287  | 7073  | 784CIP2D_63   | 9551                                       |
| 1716   | 3502   | 5288  | 7074  | 784CIP2D_64   | 9557                                       |
| 1717   | 3503   | 5289  | 7075  | 784CIP2D_65   | 9568                                       |
| 1718   | 3504   | 5290  | 7076  | 784CIP2D_66   | 9588                                       |
| 1719   | 3505   | 5291  | 7077  | 784CIP2D_67   | 9597                                       |
| 1720   | 3506   | 5292  | 7078  | 784CIP2D_68   | 9615                                       |
| 1721   | 3507   | 5293  | 7079  | 784CIP2D_69   | 9628                                       |
| 1722   | 3508   | 5294  | 7080  | 784CIP2D_70   | 9649                                       |
| 1723   | 3509   | 5295  | 7081  | 784CIP2D_71   | 9652                                       |
| 1724   | 3510   | 5296  | 7082  | 784CIP2D_72   | 9660                                       |
| 1725   | 3511   | 5297  | 7083  | 784CIP2D_73   | 9662                                       |
| 1726   | 3512   | 5298  | 7084  | 784CIP2D_74   | 9725                                       |
| 1727   | 3513   | 5299  | 7085  | 784CIP2D_75   | 9746                                       |
| 1728   | 3514   | 5300  | 7086  | 784CIP2D_76   | 9777                                       |
| 1729   | 3515   | 5301  | 7087  | 784CIP2D_77   | 9787                                       |
| 1730   | 3516   | 5302  | 7088  | 784CIP2D_78   | 9790                                       |
| 1731   | 3517   | 5303  | 7089  | 784CIP2D_79   | 9842                                       |
| 1732   | 3518   | 5304  | 7090  | 784CIP2D_80   | 9842                                       |
| 1733   | 3519   | 5305  | 7091  | 784CIP2D_81   | 9848                                       |

| SEQ ID NO:<br>of full-<br>length<br>nucleotide<br>sequence | SEQ ID<br>NO: of<br>full-<br>length<br>peptide<br>sequence | SEQ ID NO:<br>of contig<br>nucleotide<br>sequence | SEQ ID<br>NO:<br>of contig<br>peptide<br>sequence | Priority<br>docket number_<br>corresponding<br>SEQ ID NO: in<br>priority<br>application | SEQ ID<br>NO: in<br>U.S.S.N.<br>09/488,725 |
|--|--|---|---|---|--|
| 1734   | 3520   | 5306  | 7092  | 784CIP2D_82   | 9867                                       |
| 1735   | 3521   | 5307  | 7093  | 784CIP2D_83   | 10010                                      |
| 1736   | 3522   | 5308  | 7094  | 784CIP2D_84   | 10011                                      |
| 1737   | 3523   | 5309  | 7095  | 784CIP2D_85   | 10052                                      |
| 1738   | 3524   | 5310  | 7096  | 784CIP2D_86   | 10057                                      |
| 1739   | 3525   | 5311  | 7097  | 784CIP2D_87   | 10085                                      |
| 1740   | 3526   | 5312  | 7098  | 784CIP2D_89   | 10139                                      |
| 1741   | 3527   | 5313  | 7099  | 784CIP2D_90   | 10142                                      |
| 1742   | 3528   | 5314  | 7100  | 784CIP2D_92   | 10165                                      |
| 1743   | 3529   | 5315  | 7101  | 784CIP2D_93   | 10173                                      |
| 1744   | 3530   | 5316  | 7102  | 784CIP2D_94   | 10173                                      |
| 1745   | 3531   | 5317  | 7103  | 784CIP2D_95   | 10273                                      |
| 1746   | 3532   | 5318  | 7104  | 784CIP2E_1  | 3121                                       |
| 1747   | 3533   | 5319  | 7105  | 784CIP2E_2  | 3628                                       |
| 1748   | 3534   | 5320  | 7106  | 784CIP2E_4  | 3673                                       |
| 1749   | 3535   | 5321  | 7107  | 784CIP2E_5  | 4018                                       |
| 1750   | 3536   | 5322  | 7108  | 784CIP2E_6  | 4467                                       |
| 1751   | 3537   | 5323  | 7109  | 784CIP2E_7  | 4865                                       |
| 1752   | 3538   | 5324  | 7110  | 784CIP2E_8  | 4916                                       |
| 1753   | 3539   | 5325  | 7111  | 784CIP2E_9  | 4923                                       |
| 1754   | 3540   | 5326  | 7112  | 784CIP2E_10   | 4926                                       |
| 1755   | 3541   | 5327  | 7113  | 784CIP2E_11   | 4962                                       |
| 1756   | 3542   | 5328  | 7114  | 784CIP2E_12   | 4963                                       |
| 1757   | 3543   | 5329  | 7115  | 784CIP2E_13   | 4964                                       |
| 1758   | 3544   | 5330  | 7116  | 784CIP2E_14   | 4988                                       |
| 1759   | 3545   | 5331  | 7117  | 784CIP2E_15   | 5835                                       |
| 1760   | 3546   | 5332  | 7118  | 784CIP2E_16   | 7682                                       |
| 1761   | 3547   | 5333  | 7119  | 784CIP2E_17   | 7682                                       |
| 1762   | 3548   | 5334  | 7120  | 784CIP2E_18   | 7699                                       |
| 1763   | 3549   | 5335  | 7121  | 784CIP2E_19   | 7707                                       |
| 1764   | 3550   | 5336  | 7122  | 784CIP2E_20   | 7707                                       |
| 1765   | 3551   | 5337  | 7123  | 784CIP2E_21   | 7752                                       |
| 1766   | 3552   | 5338  | 7124  | 784CIP2E_22   | 8357                                       |
| 1767   | 3553   | 5339  | 7125  | 784CIP2E_23   | 9065                                       |
| 1768   | 3554   | 5340  | 7126  | 784CIP2E_24   | 9324                                       |
| 1769   | 3555   | 5341  | 7127  | 784CIP2F_1  | 2976                                       |
| 1770   | 3556   | 5342  | 7128  | 784CIP2F_2  | 3559                                       |
| 1771   | 3557   | 5343  | 7129  | 784CIP2F_3  | 4021                                       |
| 1772   | 3558   | 5344  | 7130  | 784CIP2F_4  | 4474                                       |
| 1773   | 3559   | 5345  | 7131  | 784CIP2F_5  | 4566                                       |
| 1774   | 3560   | 5346  | 7132  | 784CIP2F_6  | 4705                                       |
| 1775   | 3561   | 5347  | 7133  | 784CIP2F_7  | 4707                                       |
| 1776   | 3562   | 5348  | 7134  | 784CIP2F_8  | 4712                                       |
| 1777   | 3563   | 5349  | 7135  | 784CIP2F_9  | 5008                                       |
| 1778   | 3564   | 5350  | 7136  | 784CIP2F_10   | 5009                                       |
| 1779   | 3565   | 5351  | 7137  | 784CIP2F_11   | 5015                                       |
| 1780   | 3566   | 5352  | 7138  | 784CIP2F_12   | 5015                                       |
| 1781   | 3567   | 5353  | 7139  | 784CIP2F_13   | 7724                                       |
| 1782   | 3568   | 5354  | 7140  | 784CIP2F_14   | 7725                                       |
| 1783   | 3569   | 5355  | 7141  | 784CIP2F_15   | 8828                                       |
| 1784   | 3570   | 5356  | 7142  | 784CIP2F_16   | 8830                                       |
| 1785   | 3571   | 5357  | 7143  | 784CIP2F_17   | 9739                                       |
| 1786   | 3572   | 5358  | 7144  | 784CIP2F_18   | 9896                                       |

TRADOC:1416247.1(%CS7011.DOC)

TABLE 7

| SEQ ID NO: | Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence | Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence | Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  |
|------------|--|--|--|
| 5359       | 337  | 1131   | AHLARLSALILDEVAITLPAPQNLSTNMKHLMLWSPVIAAG<br>ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPZCDVDDITA<br>TVPYNLVRVATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMBI<br>TKDGFHLVIBLEDLGPQFEFLVAYWRREPAGAEHVKMVRSGGIP<br>VHLETMEPGAAYCVKAQTFFVKAIGRYSAFSQTECEVEQGEAIP<br>VLALFAFVGPMILLVVPLFVWKMGRLLQ/YLLLPRGSSQTPW<br>KITQF  |
| 5360       | 2  | 1115   | PRVRSSGGQEDPASQOWARPRFTQPSKMRRRVIARPVGSSVRLK<br>CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED<br>SGKYTCRVSNRAGAINATYKVDVIQRTSRKPVLTGTHPVNTTVD<br>FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSIDVGGQKF<br>VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS<br>FRSAFLTLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL<br>GTLWLWCQAQKKPCTPAPAPPLPGHRPGTARDRSGDKDLPSL<br>AALSAGPGVGLCEEHGSAPAPQHLLGPGPVAGPKLYPKLYTGHS<br>TPHTYTHPPSCQLNSSH  |
| 5361       | 3  | 925  | HEGSISSANILLDDQFQPKLTDFAHAFRSHLEHQSCITNMTSS<br>SSKHLMYMPBEYIROGKLSIKTDVYSFGIVIMEVLTGCRVVLDD<br>PKHIQLRDLRLHELMKRGDLSCLSLDKKVPPCPRNFSAKLFCL<br>AGRCATRAKLRPSNDEVLNLTLESTQASLYFAEDPPTSLKSRFC<br>PSPLFLENVPSIPVEDDESQNNLLPSDEGLRIDRMTQKTPFEC<br>SQSEVMFLSLDKKPKESKRNEEACNMPSSSCSESWFPKYIVPSQD<br>LRPYKVNIDPSSSEAPGHSCRSRPVSSCS9KPSWDEYEQYKKE  |
| 5362       | 2  | 4879   | SCQVEGCTRTYNSSQSIGKHMKTAPDQYAAFKMQRKSKKGQKA<br>NNLNTPNNGKFVYFLPSVNVSSNPFFTSQTANGNPACSAQLQH<br>VSPPIFFAHLASVSTPLSSMESVINPNITSQDKNEQGGMLCSQ<br>MENLPSTALPAQMEDLTKTVLPLNIDRGSDFLLSLPAESSSIDL<br>FSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA<br>VFPSQVNVANFSSSTNAQSAPEKVKKDRGRGTGKERKPKHKN<br>RAKWPALIRDGKFCISRCYRAFTNPRSLGGHLSKRSYCKPLDGA<br>ETAOELLQSNQPSLLASMIILSTNAVNLQPPQSTFNPEACFKD<br>PSFLQLLAENRSPAFLPNTFPRSGVTNFTNSVSQEGSEIIQAL<br>ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLH<br>TVCHPNTLLTNQNRSTNSKTSSIEECSSLPVFPTNDLLKTVEN<br>GLCSSSFPSGGPSQNFSTNSSRVSVISGPONTRSSHLNKKGNS<br>ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH<br>SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT<br>VLAPLTKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFECT<br>LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNILQPSVNTVQ<br>NNKLDPSSP/FSSFISVMPTESNIPOSE/VSHKBDQIQEILEGL<br>QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE<br>MINIQFNDKVNKPFVCQNGCNYSAMTKDALFKHYGKIHOYTPE<br>MILEIKKNQLKFAFKCVVPTCTKTFTNRNSNLRAHCQLVHHFTT<br>EEMVKLKIIRPYGRKKSQSENVASRSTQVKKQLAMTEENKESQ<br>PALELRAETQNTHSNVAVIPEKQLIEKKSFDKTESSLQVITVTS<br>EQCNTNALTNTQTKGRKIRRHKKKEEKKRKKPVQSLEFPTRY<br>SPYRPHYRCVHQGCFAAFTIQONLILHYQAVHKSDDLPAFSAEVEE<br>ESEAGKESEETETKQTLKEFRQVSDCSRIFQAITGLIQHYMKL<br>HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD<br>HGIGLRASKTEEDGVYKDCCEGCDRIYATRSNLLRHFNKHNDK<br>HKAHLIRPRRLTPGQENMSSKANQEKSKSRGRTKMSRCGKEGI<br>KMPKTRKKNLNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN<br>DALSECTSRFVTQYPCMIKGCTSVVTSESNIRHYKCHKLSKAF<br>TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKSDTCVSESND<br>NSRTIATVSQKEVEKNE*DEMDLTELFTKLINEDSTSVETQA<br>NTSSNVSNDFQEDNLQSERQKASNLKRVNKEKNVSQNKRRKVE<br>KAEPASAAELSSVRKEETAVAIQIEHPASFDWSSFKPMGFE<br>VSFLKFLEESAVKQKNTDKDHPNTGNKKGSHSNRKNIDKTAV<br>TSGNHVCPCKESETFVQFANPSQLQCSDNVIVLDKLNKDCDEL |

| SEQ ID NO: | Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence | Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence | Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)   |
|------------|--|--|---|
| 5363       | 8066   | 703  | <p>VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDLSIGKATGRGQY</p> <p>RLCCTGGGEGTPEGASGKRGPAATTSVLVLCIPSVPPVPFPTLWP</p> <p>PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML</p> <p>RGPGLLLAVLCLGTAVPSTGASKSKRQAQMQVQPSPVAVS</p> <p>QSKPGCYDNGKHVQINQWERTYLGNALVCTCYGSSRGFNCEK</p> <p>PEAETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS</p> <p>CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT</p> <p>CKPIAEKCFDHAAGTSYVVGETWEKPYQGMWVDCTCLGEGSGR</p> <p>ITCTSRNRCDQDRTSYRIGDTSKKNRGNLLQICITGNGRG</p> <p>HWKCRHTSVQTTSSGSGPFTDVRAAVYQPPHPPPPYGHCVT</p> <p>DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG</p> <p>GNSNGEPCVLPFTYNGRTFYSCCTEGRQDGLWCSTTSNYEQDQ</p> <p>KYSFCTDHTVLVQTRGGNSGALCHFPFLYNHNYTDOCTSEGR</p> <p>DNMKWCGTTQNYDADQKFGFCMAAHEEICTTNEGVMYRIGDQW</p> <p>DKQDMGHMMRCTCVGNGRGWETCIAYSQLRDQCIVDDITYNVN</p> <p>DTFHKRHEEGHMLNCTCFGQGRGKNCDFVQCDQDSETGTFYQI</p> <p>GDSWEKYVHGVRQCYCYGRGIGENHCQPLQTYPSSSGPVEVFI</p> <p>TETPSQPNSHPIQWNAQPPSHISKYILRWRPKNSVGRWKEATIP</p> <p>GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTSTST</p> <p>PVTSNT\VTGETTFFPLVATSESVTEITASSFVVSWSASDVT</p> <p>SGFRVEYELSEEGDEPQYLVPSTATSV\NIP\DLLPGRKYIVN</p> <p>VYQISEDGEQSLILSTSQTAPDAPPDPTVDQVDDTSIVVWRWS</p> <p>QAPITGYRIVYSPSVEGSSSTELNLPETANSVTLSDLQPGVQYN</p> <p>ITIIYAVEENQESTPVVIOQETTGTTPRSDTVPSRDLQFVEVTDV</p> <p>KVTIMWTPPESAVTGYRVDVIVNLPGHEGQRLPLSRNTF\AEN</p> <p>TGLSPGVITYYFKVFAVSHGRESKPLTAQQTTL\DAPTNLQFVN</p> <p>ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPVSYSKY</p> <p>PLRNLPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIIPPYN</p> <p>TEVTETTIVITWTPAPRIGFKLGVRPSQGGAPREVTSDSGSIV</p> <p>VSGLTGVEYVYTIQVLRDQERDAP\IVNK\VVTPLSPTNLH</p> <p>LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV</p> <p>HADQSSCTF\DNLEVPGLYVNSVYTVKDDKESVPISDTIIPAV</p> <p>PPPTDLRFTN\ILGPDTRMTW\APPPSIDLTNLFVRYSPVKNE</p> <p>GRMLQSLSIFFLSDN\AVLTNLPLGTEYVVSVSVEQHESTP</p> <p>\LRGRQKTGLDSP\TGIDFS\DTA\NSFT\VHW\IAPRA\TPI</p> <p>TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLNLTPGTEYV</p> <p>SIVALNGREESPLLIGQSTVSDVPRDLEVAATPTSLLI\SWD</p> <p>APAVTVRYRITYGETGGNSFPVQEFVPGSKSTATISGLKPGVD</p> <p>YTTIVYAVTGRGDSPASSKRPISINRYTEIDKPSQMQVTDVQDNS</p> <p>ISVKNLPSSSPVTGYRVTT\PKNGPG\PTKTKTAGPDQTEMTI</p> <p>EGLQPTVEYVVSVAQNPSGESQPLVQTAVTNIDRPGGLAFTDV</p> <p>DVDSIKIAWESPPQQVSRVRYVYSSPEDGIHELFPAPDGEZDTA</p> <p>ELQCLRPGEYTVSVVALHDDMESQPLIGTQSTAIAPDPTDLKET</p> <p>QVTPTSLSAQWTPPNVQLTGYRVVTPKKTGPMKEINLAPDSS</p> <p>SVVVSGLMVATKYEVSVYALKDITLSRPAQGVVTTLENVSPRR</p> <p>ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP</p> <p>DVRSYITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS</p> <p>NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP</p> <p>RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKTDEL</p> <p>QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT</p> <p>SGQQPSVGQQMIFEEHGFRTTPTTATPIRHRPRPYPPNVGQE</p> <p>ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT</p> <p>LTGLTRGATYNIIVEALKDQQRHKVREEVTVGNSVNEGLNQPT</p> <p>DDSCFDPTYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD</p> <p>SSRWCHDNGVNYKIGEKWDRQGENGQMSCTCLGNGKGEFKCDP</p> <p>HEATCYDDGKTYHVGEQWQKEYLGAI CSCTCFGGQRCWRCDNR</p> <p>RPGGEPSPGTTGQSYNQYSQRYHQRTNTNVNCP IECFMPDLVQ</p> <p>ADREDSRE</p> |
| 5364       | 8066   | 703  | <p>RLCCTGGGEGTPEGASGKRGPAATTSVLVLCIPSVPPVPFPTLWP</p> <p>PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML</p> <p>RGPGLLLAVLCLGTAVPSTGASKSKRQAQMQVQPSPVAVS</p>   |

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|------------|--|--|---|
|            |  |  | QSKPGCYDNGKHVQINQWERTYLGNALVCTCYGSGRGFNCESK<br>PEAETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGRIS<br>CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT<br>CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCICLGEGRS<br>ITCTSRNRNDQDTRTSYRIGDTHSKKDNRRGNLLQCICITGNRGR<br>EWK CERHTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT<br>DSGVVYSVGMQLA*KTQGNKQML\CTCLNGVSCQETA VQTQTYG<br>GNSNGEPCVLPFTYNGRTFYSCCTEGRQDGHLCSTTSNYEQDQ<br>KYSFCTDHTVLVQTRGCGNSGALCHFPFLYNNHNYTDCITSEGR<br>DNMKWCGTTQNYDADQKFGFCPMAAHZEICTTNEGVMYRIGDQW<br>DKQHDGMHMRCTCVGNRGEWTCIAYSQLRDQCIVDDITYNVN<br>DTFHKRHEEGHMLNCTCFGGGRGWKCDPVDQCDSETGTFYQI<br>GDSWEKYVHGVRVYQCYCGRGIGEWHCQPLQTYPSSSGPVEFI<br>TETPSQPNSHPIQWNPQPSHISKYILRWRPKNSVGRWKEATIP<br>GHLNSYTIKGLKPGVVYEGQLISIQYGHQEVTRFDFTTSTST<br>PVTSTNT\VTGETTPFSPLVATSESVTEITASSFVSVWSASDVT<br>SGFRVEYELSEEGDEPQYLVLSTATSV\NIP\DLLPGRKYIVN<br>VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR<br>PQAPITGYRIVYSPSVESSTELNLPETANSVTLSDLPQGVQYN<br>ITIIYAVEENQESTPVVQQEITGTTPRSDTVPSPRDLQFVEVTDV<br>KVTIMWTPEASVTGYRVDVIFVNLPGEGHQRLLPSRNTF\AEN<br>TGLSPGVTYFYKVFVAVSHGRESKPLTAQQTTKL\DAPTNLQFVN<br>ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY<br>PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN<br>TEVTETTIVITWTPAPRIGFKLGVRPSQGGAPREVTSDSGSIV<br>VSLTPGVEYVYTIQVLRDGOERDAP\IVNK\VVTPLSPPTNLH<br>LEANPDTGVLTVSWERSTPDTITGYRITTTPTNGQQGNSLEEVV<br>HADQSSCTF\DNLEVPGLYNSVYTVKDDKESVPSIDTIIIPAV<br>FPPTDLRFTN\ILGPDTRMTW\APPPSIDLTNLFVRXSPVKNE<br>GRMLQSLSIFFLSDN\AVVLTNI.LPGTEYVSVSSVYEQHESTP<br>\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA\TPI<br>TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLNLTPGTEYVV<br>SIVALNGREBSPLLIQQSTVSDVPRDLEVVAATPSTLLI\SWD<br>APAVTVRYRITYGETGCGNSPVQEFVTPGSKSTATISGLKPGVD<br>YITIVYAVTGRGDSPASSKPIISINRYTEIDKPSQMQVTDVQDNS<br>ISVKWLPSSSPVTGYRVTT\PKNGPG\PTKTKTAGPDQTEMTI<br>EGLQPTVEYVSVYVQAQNSGESQPLVQTA VTNIDRPKGLAFTDV<br>DVDSIKIAWESPOGQVSRYRVYSSPEDGIHELFPAPDGEEDTA<br>ELQQLRPGSEYTVSVVALHDDMESQPLIGTQSTAI PAPTDLKFT<br>QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS<br>SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPRRR<br>ARVTDATETITISWRKTETITGQVDAVPANGQTP IQRTIKP<br>DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS<br>NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP<br>RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDDEL<br>QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT<br>SGQQPSVGQQMIFEEHGFRRTPPTTATPIRHRPRPYPPNVGQE<br>ALSQTTISWAPFQDTSEYIISCHPVGTDDEPLQFRVPGTSTSAT<br>LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT<br>DDSCFDPTYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRC<br>SSRWCHDNGVNYKIGEKWDRQENGQMMSCCTCLGNGKGEFKCDP<br>HEATCYDDGKTYHVGEQWQKEYLGAICSCCTCFGGQRGWRCDNCR<br>RPGGEPSPGTTGQSYNQYSQRYHQRTNTNVCNPIECFMPLDVQ<br>ADREDSRE |
| 5365       | 8066   | 703  | RLCCTGGGEGTPGASGKRGPAAATSLVLCIPSVPPPPVFPPTLWP<br>PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML<br>RPGPGGLLLAVLCLGTAVPSTGASKSKRQAQMVQPSVAVS<br>QSKPGCYDNGKHVQINQWERTYLGNALVCTCYGSGRGFNCESK<br>PEAETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGRIS<br>CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT<br>CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCICLGEGRS   |

| SEQ<br>ID<br>NO: | Predicted<br>beginning<br>nucleotide<br>location<br>corresponding<br>to first<br>amino acid<br>residue of<br>amino acid<br>sequence | Predicted end<br>nucleotide<br>location<br>corresponding<br>to first<br>amino acid<br>residue of<br>amino acid<br>sequence | Amino acid segment containing signal peptide<br>(A=Alanine, C=Cysteine, D=Aspartic Acid, E=<br>Glutamic Acid, F=Phenylalanine, G=Glycine,<br>H=Histidine, I=Isoleucine, K=Lysine,<br>L=Leucine, M=Methionine, N=Asparagine,<br>P=Proline, Q=Glutamine, R=Arginine,<br>S=Serine, T=Threonine, V=Valine,<br>W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop<br>Codon, /=possible nucleotide deletion,<br>\=possible nucleotide insertion)   |
|------------------|---|--|---|
|                  |   |  | <p>ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNRG<br/> EWKCEHRTSVQTTSSSGSPFTDVRAAVYQPPHPQPPYPGHCVT<br/> DSGVVYSVGMQLA*KTQGNKQML\CTCLGNVSCQETA VQTQY<br/> GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGLHWCSTTSNYEQDQ<br/> KYSFCTDHTVLVQTRGNSNGALCHFFLYNNHNYTDCTSEGR<br/> DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW<br/> DKQHDGMHMRCTCVGNRGGEWT CIAYSQLRDOCI VDDITYNVN<br/> DTFHKRHEEGHMLNCTCFGQGRGRWKC DPVDQCDQDSETGT FYQI<br/> GUSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI<br/> TETPSQPNSHPIQWNAQPSHISKYILRWRPKNSVGRWKEATIP<br/> GHLNSYTIKGLKPGVYEGQLISIQQYGHQEVTRFDTTSTST<br/> PVTSTNT\VTGETTFFSPLVATSESVTEITASSFVSVWSASDTV<br/> SGFRVEYELSEEGDEPQYLVL PSTATSV\NIP\DLLPGRKYIVN<br/> VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR<br/> POAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLPQGVQYN<br/> ITIIYAVEENQESTPVVIQOETTGT PRSDTVPSPRDLQFVEVTDV<br/> KVTIMWTPPEASVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN<br/> TGLSPGVTYFYKVFVAVSHGRESKPLTAQQTTL\DAPTNLQFVN<br/> ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPVSVKY<br/> PLRNLPASEYTVSLVAIKQXQESPKATGVFTTLQPGSSIPPYN<br/> TEVTETTIVITWTPAPRIGFKLGVPRPSQGGAPREVTSDSGSIV<br/> VSGLTPGVEYVYTIQVLRDQERDAP\IVNK\VVTPLSPTNLH<br/> LEANPDTGVLTVSWERSTT PDITGYRITTTPTNGQQGNSLEEVV<br/> HADQSSCTF\DNLFVPGLEYNVSVYTVKDDKESVPI SDTIIIPAV<br/> PPPTDLRFTN\ILGPDTRVTVW\APPPSIDLTNLFVRYSPVKNE<br/> GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVS SVSYEQHESTP<br/> \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA\TPI<br/> TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPTGTEYV<br/> SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD<br/> APAVTVRYRITYGETGGNSPVQEFVPGSKSTATISGLKPGVD<br/> YTIIVYAVTGRGDSPASSKPISINRYTEIDKPSQM QVTDVQDNS<br/> ISVKWLPSSSPVTGYRVTT\PKNGPG\PTKTKTAGPDQTEMTI<br/> EGLQPTVEYVVS VYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV<br/> DVDSIKIAWESPPQQVSRYRVYSSPEDGIHELFPAPDGEEDTA<br/> ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTA\PAPTDLKFT<br/> QVTPTSLSAQWTPPNVQLTGYRVVTPKEKTGPMKEINLAPDSS<br/> SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPRR<br/> ARVTDATETITISWRKTETITGFQVDVAVPANGQTPQRTIKP<br/> DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS<br/> NLRFLATTPNLSLVSWQPPRARITGYIIKYEKPGSPPREVVRP<br/> RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDLP<br/> QLVTLPHPNLHGPEILDVPSVQKTFVTHPGYDTGNGIQLPGT<br/> SGQQPSVGQOMIFEHGFRRTPPTTATPIRHRPRPYPPNVGQE<br/> ALSQTTISWAPFQDSEYIIISCHPVGTDEEPLQFRVPGTSTSAT<br/> LTGLTRGATYNIIVEALKDQQRHKVREVVTVGNSVNEGLNQPT<br/> DDSCFPDPTVSHYAVGDEWERMSESGFKLLCCLGFGSGHFRCD<br/> SSRWCHDNGVNYKIGEKWDRQGENGQMMSCCTCLGNGKGEFKCDP<br/> HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGQGRGWRCDNCR<br/> RPGGBSPPEGTTGQSYNQYSQRYHQRTNTNVNCFIECFMPLDVQ<br/> ADREDSRE</p> |
| 5366             | 8066  | 703  | <p>RLCCTGGGEGTPEGASGKRGAATTSVLVCIPSVPPVPVPTLWP<br/> PPSWRRQPPGGIRDRFSRRLRREANLVATCLPVRA SLPHRLNML<br/> RGPGLGLLLAVLCLGTAVPSTGASKSKRQAQMMVQPSPVAVS<br/> QSKPGCYDNGKHXYINQQWERTYLGNALVCTCYGSGRGFNCE<br/> PEAEETCFDKYTGNTYRVGDYTERPKDSMIWDCCTCIGAGRGRIS<br/> CTIANRCHEGGQSYKIGDTHRRPHETGGYMLECVCLGNGKGEWT<br/> CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCCTCLGEGSGR<br/> ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNRG<br/> EWKCEHRTSVQTTSSSGSPFTDVRAAVYQPPHPQPPYPGHCVT<br/> DSGVVYSVGMQLA*KTQGNKQML\CTCLGNVSCQETA VQTQY<br/> GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGLHWCSTTSNYEQDQ</p>  |

| SEQ ID NO: | Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence | Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence | Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)   |
|------------|--|--|--|
|            |  |  | <p>KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCSTSEGR</p> <p>DNMKWCGTTONYDADQKFGFCMAAHEEICTNEGVMYRIGDQW</p> <p>DKQHDMGHMMRCTCVGNRGGEWTCIAYSQLRDQCIVDDITYNVN</p> <p>DTFHKRHEEGHMLNCTCFGGQGRGWKCDPVDQCDSETGTFFYQI</p> <p>GDSWEKYVHGVRQCYCYGRGIGENHCQPLQTYPSSSGPVEVFI</p> <p>TETPSQPNSHPIQWNAPOPSHISKYILRWPRKNSVGRWKEATIP</p> <p>GHLNSYTIKGLKPGVVYEGQLISIQOYGHQEVTRFDFTTSTST</p> <p>PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWSASDTV</p> <p>SGFRVEYELSEEGDEPOYLVLPLSTATSV\NIP\DLLPGRKYIVN</p> <p>VYQISEDGEQSLILSTSQTAPDAPPDPTVDQVDDTISIVRWSR</p> <p>PQAPITGYRIVYSPSVEGSSTELNLPTANSVTLSDLQPGVQYN</p> <p>ITIYAVEENQESTPVVIQOETTGTTPRSDTVPSRDLQFVEVTDV</p> <p>KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN</p> <p>TGLSPGVITYYKFVAVSHGRESKPLTAQOTTKL\DAPTNLQFVN</p> <p>ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY</p> <p>PLRNLQPASEYTVSLVAIKGNQESPKATGVPTTLQPGSSIPPYN</p> <p>TEVTETTIVITWTPAPRIGFKLGVPRPSQGEAPREVTSDSGSIV</p> <p>VSGLTPGVEYVYTIQVLRDQGERDAP\IVNK\VVTPLSPTNLH</p> <p>LEANPDGTGLTVSWERSTTPDITGYRITTTPTNGQOGNSLEEVV</p> <p>IADQSSCTF\DNLEVPGLYXVSVYTVKDDKESVPSIDTIIIPAV</p> <p>PPPTDLRFTN\ILGPDTRVTV\APPPSIDLTNLFVRYSPVKNP</p> <p>GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSEVYQHESTP</p> <p>\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA\TPIT</p> <p>GYRIR\HHPEHF\SGRPREDR\VPHSRNSITLNLTPGTEVVV</p> <p>SIVALNGREESPLLIGQSTVSDVPRDLEVAATPTSLLI\SWD</p> <p>APAVTVRYRITYGETGGNSPVQEFVTPGSKSTATISGLKPGVD</p> <p>YITIVYAVTGRGDSPASSKPIISINYRTEIDKPSQMQVTDVQDNS</p> <p>ISVKWLPSSSPVTGYRVTT\PKNGPG\PTKKTAGPDQTEMTI</p> <p>EGLQPTVEYVVSVAQNPSGESQPLVQTAVTNIDRPGKLAFTDV</p> <p>DVDSIKIAWESPOGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA</p> <p>ELOGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPPTDLKFT</p> <p>QVTPTLSAQWTPPNVQLTGYRVVTPKEKTGPMKEINLAPDSS</p> <p>SVVVSGLMVATKYEVSVYALKDTLSRPAQGVVTTLENVSPRR</p> <p>ARVTDATETITISWRKTETITGFQVDAVPANGQPTPIQRTIKP</p> <p>DVRSYITITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS</p> <p>NLRPLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP</p> <p>RPQVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDLP</p> <p>QLVTLPHPNLHGPEILOVPSTVQKTPFVTHPGYDTGNGIQLPGT</p> <p>SGQPSVGQMI FEEHGFRTTPTTATPIRHRPRPYPPNVQOE</p> <p>ALSQTTISWAPFQDTSEYIISCHPVGTDDEPLQFRVPGTSTSAT</p> <p>LTGLTRGATYNIIVEALKDQQRHKVREEVTVGNSVNEGLNQPT</p> <p>DDSCFDPTYVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD</p> <p>SSRWCHDNGVNYKIGEKWDRQGENGQMMSCCTCLNGKGFEKCDP</p> <p>HEATCYDDGKTYHVGEQWQKEYLGAICSCCTCFGGQRCWRCNCR</p> <p>RPGEPSPEGTGQSYNQYSQRYHQRTNTNVNCPICFCMPLDVQ</p> <p>ADREDSRE</p> |
| 5367       | 235  | 3591   | <p>KKILNMLCKKNIVIEVLADILYEVLYGFCFSGIKKYLIIHVLRL</p> <p>ILELWMTRLLLEKSVSLQTYLLLVKILSWFFPKEMRHHLQIM</p> <p>EVMMRKQDS/RIVONGSEQQLQKELADVLMDPPMDQPGKEBLV</p> <p>KRSQLDGECDGPLSNQLSASSTINPVPLVGLOKPEMSLPVKPGQ</p> <p>GDSEASSPFTPVAEDSVVPSKLTYLGCASVNAPRSEVEALRNM</p> <p>SILRSQCQISLDVTLSPNVSEGI VRLDLPQNTNTEIANYPYIKI</p> <p>LCVVRGHDGTPESDCFAFTESHYNALFRIHVFRCEIQEAVSRI</p> <p>LYSFATAFRRSKQTPLSATAAPQTPDSDI FTFSVSLKEDDG</p> <p>KGYFSAVPKDKDRQCFKLKRGIDKKIYVYVQTTNKEIAIERCF</p> <p>GLLLSPGKDVRNSDMHLLDLESMSGKSSDGKSYVITGSWNPKSPH</p> <p>FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCS</p> <p>NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVCLLS</p> <p>ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDEBEDNDEPLL</p> <p>SGSGDVSKECAEKILETWGELLSKNHLNLRVPKQLSSLVNRGV</p> <p>PEALRGEVWQLLAGCHNNDHLVEKYRILITKESQDSATTRDIN</p>   |



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|------------|--|--|--|
|            |  |  | RTFFAHDFKDTGGDQDSLYKICKAYSVDDEEIGYCGQSFLA<br>AVLLHMPPEEQAFSVLVKIMFDYGLRELKQNFEDLHCKFYOLE<br>RLMQEYIPDLVYNHFLDISLEAHMYASQWFLTLFTAKFPLVMVFH<br>IIDLLCEGISVIFNVALGLLKTSKDDLLJ.TDFEGALKFFRVQL<br>PKRYRSEENAKKLMELACNMKISQKLLKYEKEYHTMREQQAQQ<br>EDPIERFERENRRLQENMRLEQENDDLAHELVTSKIALRKDL<br>NAEEKADALNK3LLMTKQLIDAEEEKRRLEESAHLLKKMCRRE<br>LKAESSEIKKNSIIIGDYKQICSLSERLEKQQTANKVEIEKIR<br>QKVDCCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL<br>REMELELAQTKL\QLVEASCKIQD\LEHPF*GLPFNE\VQAA\K<br>RTWNRTLSSIKTATGVQKQKTC   |
| 5368       | 573  | 2014   | GAAAGAADPRRGSLLGRTMLDFAIFAVTFLLALVGAIVLYLPAS<br>ROAGIPGITPTPEEKDGNLDPDIVNSGSLHEFLVNLHERYGPVVS<br>FWFGRRLVSVLGTVDVLKQHINPNKTL/LF*NHAEVIKVSIN<br>WQCE*KP\QRKKLYENGVTDSLKSNFALLKLPEELLDKWLSY<br>PETQH\VLPSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG<br>TVWSEIGKGLDGLSDKNMTRKKQYEDALMQLESVLNRIKERK<br>GRNFSQHIFIDSLVQGNLNDQILEDSMIFSLASCIITAKLCTW<br>AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVL<br>ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLVALGVVLQDP<br>NTWSPHKKFDPDRFDELVMKTFSSLGFSGTQCEPELRFAYMVT<br>TVLLSVLVKRLHLLSVEGQVIETKYELVTSSEEAWITVSKRY   |
| 5369       | 1  | 6622   | PRSLCFSLWAEAAVLADGGLRRRRRLRGTMASAFVPGASLED<br>CHCNLFCLADLTGIKWKYVWQGPSAPILFPVTEEDPILSSFS<br>RCLKADVLG/VWRDORPERRE\L*IFWGGEDP\VLTLTFTMTY<br>QKKKMECGRMDPMMNAVLCFSKAVHNLLERCLMNRNFRVIGKWF<br>VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVINQHQPVY<br>LLEEHITLAQSSNSPFQVILCFGLNGTLTGQAFKMSDSATKK<br>LIGEWKQFYPISCCLEKMESEKQEDMDWEDDSLAAVEVLVAGVR<br>MIYPACFVLVPQSDIPTSPVGSSTHCSSSCLGVHQPASTROPA<br>MSSVTLTPPTSPBEVQTVDPQSVQKWKVFSVSDGFNSDSTSHH<br>GGKIPRKLANHVVDVWQECNMNRAQNKRYASASSGGLCEEATA<br>AKVASWDFVEATORTNCSCLRHKNLKS RNAGQQGQAPS LGQQQQ<br>ILPKHKTNEKQEKSEKPKRPLTPPHHRVSVSDVGM\ADS\A<br>SQRV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPO<br>PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPPTDPLVPSKPM<br>EDRIDLSQSFPFPQYQEAVEPTVYVGTAVNLBEDEANIWKYK<br>FPKKKDVFLPQLPSDKFKDDPVGPFQGESVTSVTELMVQCKK<br>PLKVSDELVQYQIKNQCLSATASDAEQEPKIDPYAFVEGDEEF<br>LFPDKDRONSEREAGKKHVEDGTSSVTLSHEEDAMSLFSPS<br>IKQDAPRPTSHARPSTSLIYDSDLAVSYTDLNLFNSDEDEL<br>PGSKRSANGSDDKASCKRKTGNLDPLSCISTADLHKMYPTPPS<br>LEQHIMGFSPMNMNKEYGSMDDTPGGTVLEGNSSSIGAQFKIE<br>VDEGFCSPKPSKIDFSYVYKPCNCQILVGCSPFAPLKTLP SQY<br>LPLIKLPEECIYRQSWTVGKLELLSSGSPMPFIKEGDGNSNDQ<br>YGTAYTPQTHTSCGMPSSAPPNSGAGILPSPSTPRFPPTPTPT<br>RTPTPTPRGAGGPASAGSVKYENS DLYSPASTPTCTRPLNSVEP<br>ATVPSIPEAHSYLVNLI LSESVMNLFKDCNSDSCCICVCNMNIK<br>GADVGVYIPDPTQEAQYRCTCGFSAMNKRKFGNNSGLFFEDELD<br>IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL<br>LQDQCTNLFSPFGAADQDPFPKSGVISNWRVEERDCCNDCYLA<br>LEHGRQFMDNMSGGKVDLAVKSSCLHPWSKRNDVSMQCSQDIL<br>RMLLSLQPVLDQAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG<br>TDESPEPLPIPTFLGYDYDYLVSFPALPYERLMLEPYGSQR<br>DIAYVVLCPENEALLNGAKSFRODLTAIYESCRLGQHRFVSRLL<br>TDGIMRVGSTASKKLEKLVAEWFSQAADGNNFAFSKLYAQV<br>CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA<br>NTPSATLASAASSTMTVTSGVAISTSVATANSTLTASTSSSSS<br>SNLNSGVSSNKLPSFPFGSMNSAAGSMSTQANTVQSGQLGQ<br>QTSALQTAGISGESSLPTQPHDPVSESTMDRDKVGIPTDGDH<br>AVTYPPAIVVYIIDPPTYENTDESTNSSSVWTLGLLRCPLEMVO |

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|------------|--|--|--|
|            |  |  | <p>TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF<br/> TQCRRLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP<br/> FILAPVKDKQTELGETFGAEGQKYNVLFVGYCLSHDQRWILASC<br/> TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCGLGV<br/> QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRLQSLSKRLKDM<br/> CRMCGISAADSPSILSACLVAPEQGSFVIMPDSVSTGVSFVGRS<br/> TTLNMQTSQNLTPQDTSCTHILVFPPTSASVQVASATYTTENLDL<br/> AFNPNNDGADGMGIFDLDLTDGDDLPDIINILPASPTGSPVHSP<br/> GSHYPHGGDAGKQGSTDRLLSTEPHEEVFNILQQPLALGYFVST<br/> AKAGPLPDWFWASACPAQYQCPLFLKASLHLHVPVSQSDLLHS<br/> KHSPLDSNQTSDVLRFLVLEQYNALSWLTCDPATQDRRSCLPIH<br/> FVVLNQLYNFIMNML</p>   |
| 5370       | 1226   | 716  | <p>RWSRKLELRRAAQATESRPPQSQEMHPTGKEVHALKRLRDSAN<br/> ANDVETVQQLLEDGADPCAAADDKGRITALHFAECNGNDQIVQLL<br/> DHGADPNQRDGLGNTPLHLAACTNHVPVITTLRGGARVDALDR<br/> AGRTPLHLAKSKLNLQEGHAQCLKAVR/HGGEADHPYAEVSG<br/> APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR<br/> AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACSTLPVG<br/> GCISWL</p>   |
| 5371       | 1331   | 167  | <p>IAAMLWKLLLRSSQSCRLCSFRKMRSPPKYRPFACFTYTTDKQS<br/> SKENTRTVEKLYKCSVDIRKIRR\*KGYF*RMKPMKKLRI/F<br/> LQELGADETAVASILERCEAIVCSPTAVNTORKLWQLVCKNEE<br/> ELIKLIEQFPESFFTIDQENQKLVQFFQELGLKNVVISRLLT<br/> AAPNVFHNFPVEKNQKQVRILQESYLDVGGSEANMKVWLLKLLSQ<br/> NPFILLNSPTAIKETLEFLQEOGFTSFELQLLKLKGLFQLC<br/> PRSIQNSISFSKNAFKCTDHLKQLVLKCPALLYSVFVLEERM<br/> QGLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG<br/> HLANLNGSKKEFEANFGKIQAQKVRPLFNVPAPLNVEE</p>  |
| 5372       | 51   | 857  | <p>SPGAQFLWAAPDMPDLFSAVQKDEILHKALCFPCWLGKGGME<br/> PLRLILFLVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR<br/> RKAWCRQLGEGPCQVRVSTHNLWLLSFLRRWNGSTAITDDTLG<br/> GTLTITLRLNLPDAGLYQCQSLHGSADTLRKVLVEVLADPLD<br/> HRDAGDLWFPGLDLRASRMZMWSTASPGASWKEKSPSHPLPSFS<br/> SWPASFSR*QPAPSGLQPGMDRSQGHHPVNTVMTQGISS<br/> KLCQG</p>  |
| 5373       | 2814   | 346  | <p>VKTKSIFNSAMQEMEYVENIRRKFGVFNYSPFRTPYTPNSQY<br/> QMLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG<br/> TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE<br/> ESMDFLDKSTASPASTKTGQAGSLSGSPKPPSPQLSAPITTKTD<br/> KTSTTGSILNLDNRKAEMDLKELSESVOQSTPVPLISPKRQ<br/> IRSRFQNLNLDKTIESCQAQLGINEISEDVYTAVEHSDSESEKS<br/> DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKPKP<br/> TNPEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS<br/> PHPIKDKLKGDETDSPVHLGLDSDSE\NELVIDLGEDHSGRE<br/> GRKNKKEPKESPQDVGKTPPSTTVGSHSPPETPVLTRSSAQ<br/> TSAAGATATSTSTSTVTVPAPAAATGSPVKQRPLLPKE\TAP<br/> AVQRSCGTSSSTVQKEITQSPSTSTITLVTSTQSSPLVTSSGSM<br/> STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI<br/> YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQEEL\SEMKN<br/> LELTMAEMRQSWEQERDLIAEVKKQLELEKQQAQVDETKKKQWC<br/> ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ<br/> \QADAE\VNTETLNKSSQSSSSSTQSAPSETASA\SKEKETSA<br/> EKSKEGSTDLDGSRTPSSILLGSNQSDHSR\SNKSSWSSS<br/> DEKRG\TRSDH\TPSTQHGRSLLPKESRAGTPFLGTSK</p> |
| 5374       | 2814   | 346  | <p>VKTKSIFNSAMQEMEYVENIRRKFGVFNYSPFRTPYTPNSQY<br/> QMLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG<br/> TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE<br/> ESMDFLDKSTASPASTKTGQAGSLSGSPKPPSPQLSAPITTKTD<br/> KTSTTGSILNLDNRKAEMDLKELSESVOQSTPVPLISPKRQ<br/> IRSRFQNLNLDKTIESCQAQLGINEISEDVYTAVEHSDSESEKS<br/> DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKPKP</p>   |

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|------------|--|--|--|
|            |  |  | TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS<br>PHPIKDKLKGKDETDSPVHLGLDSDSE\NELVIDLGDHSGRE<br>GRNKKKEPKESPQKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ<br>TSAAGATATTSTSTVTVTAPAPAATGSPVKKQRPPLPKETAP<br>AVQRSCGTSSTVQKEITOSPSTSTITLVTSTQSSPLVTSSGSM<br>STLVSSVNGDLPITGASADVAADIAYTSKL\MDAIGKTM\TEI<br>YNDLSKV\TTWKAQLAEDSQGLRIEIEKLQWLHQQL\SEMKNH<br>LELTMAEMRQSWEQERDRLAEVKKQLELEKQQAQVDETKKKQWC<br>ANFKKEAIFCCWNTSYCDYPCQ\QAHWPBH\MKSCQTSATAPO<br>\QEADAE\VNTETLNKSSQSSSSSTQAPSETASA\SKEKETSA<br>EKSKEGSGTLDLSSGRETPSSILGSGNQGSDHSR\SNKSSWSSS<br>DEKRGST\TRSDHN\TPSTQHGSRLLPGKESRAGTPFLGTSK  |
| 5375       | 2907   | 1116   | HIFLAEEEPMLERRCRGPLAMGPAQPRLLSGPSQESPTLKGES<br>RGLRQOGTSVA\QSGAQAPGRAHRCACRRHFPGWVA\LWLHTR<br>RCQA\RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH<br>LCQSGFRGWVALVLHLRAHSAKAGPPACPKMARDAFWRRKAAS<br>SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV<br>SRRP*ERGPPAKVFWGPRPRGPTGDTPPGPGGDAVDRPF\QCA<br>CCGKRFRHK\PNLIRSHAACISGERPHQ/CSRECG\KRFTNKPY<br>LTS\HRRITHTARQPYPCKECCGRRFRHKPNLLSHSKIHKRSEGS<br>AQAAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP<br>QDPIEAPPSLYSCDDCGRSFRLERFLRAHQHQHTGERPFTCAEC<br>GKNFGKKTHLVAHSRVHSGERPFLARKCGRRFLPRASQSGGRN<br>SAEPNAPRFGPFVCPDCGKAFRHKPYLAHRPIATPAEKPYVCP<br>DCRKAFSQKSNL\VSHRRHTGERPYACPCDRSFSQKSNLITH<br>RKSHIRDGAFFCAICGQTFDDEERLLAHQKKHVD   |
| 5376       | 4504   | 591  | VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS<br>ARPLRVGSRVEVIGKGRGTIVAYVGATLTFATGKVVGVILDEAKG<br>KNDGTVOGRKYFTCEGHGIFVRQSQIQVFEDGADTTSPETPDS<br>SASKVLKREGTDTTAKTSKLRLGLKPKAPTARKTTTRRPKPTRP<br>ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP<br>VLTPSGAVPPLPSPSKEEGLRAQVRDLBEKLETLRLKRAEDKA<br>KLKLEKHKIQLEQVQVWKSQMEEQADLQRRLEKARKEAKEAL<br>EAKERYMEEMADTADAIEMATLDKEMAEERAEALQVEALKER<br>VDELTDLLEILKAEIEBKSGSDGAASSYQLKQLEBQENARLKDALV<br>RMRDLSSEKQEHVK\LQKLEKKNQLELVVRQORERLQELSL<br>AESTIDELKEQVDAALGAEMVEMLTDRNLNLEEKVRELRETVG<br>DLEAMNEMNDELQENARETELELRLQDLMAGARVREAKRVEAA<br>QETVADYQQTICKYRQLTAHLQDVNRELINQOEASVERQQQPP<br>ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD<br>SFLRPGGDHDCVLVLLMPRLICKAELIRKQAQEKFELENCSE<br>RPLRGAGAEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR<br>LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQDDETVNVEPLT<br>KAICYQHLYSINLAEQPEDCTMQLADHIKFTQSALDCMSVEVG<br>RLRAFLQGGQBATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT<br>DAPGIPAALAFGPQVSDTLDCRHLTWVAVLQEVAAAAQLI<br>APLAENEGLLVALEELAFKASEQIYGTSSSPYECLRQSCNIL<br>ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA<br>EGLGLKLEDRETVIKBLKSLKIRGEELSEANVRLTLEKKLDS<br>AAKDADERIEKVQTRLEETQALLRKEKEFEETMDALQADIDQL<br>EAEKAEKQLRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR<br>GAIPGQAPGSVPGPGLVKDSPLLQQISAMRLHISQLQHENSIL<br>KGAQMKASLASLPPLHVAKLSHEGPGSELPAALYRKTSLLET<br>LNQLSTHTHVVDITRTSPAASPSAQLMEQVAQLKSLSDTVEKL<br>KDEVLKETVSQRPGATVPTDFATFPSSAF\LRKEEQQDDTVYMG<br>KVTFSCAAGFGQRHRLVLTQEQHLQHLHSLIS |
| 5377       | 762  | 1106   | DVPCRVLPAAEQKGLTLSCGESGEEG\F*YHEVRQAEGES*<br>/WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX<br>SS*WPGYDGGWGGQYIFIFRGMREEQP   |
| 5378       | 2009   | 664  | QASGTTLRPLPDLPLQKRRRATSRNRALKPRGLVLMTSCLPAL<br>RFIATPRLSAMPHIDNDVKLDFKDVLLRPRKSTLKSRSSEVDLTR   |

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|------------|--|--|---|
|            |  |  | SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWDPQMGCVFLIYKFLTLKWKMLLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV EBLILSGADI IKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA HGLKGHI ISDGGCSCPGDVAKAFGAGADFVMLGMLAGHSESGG ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNPIFSEAC  |
| 5379       | 2009   | 664  | QASGTTLRPLPDLPLQKKRREATSRNRALKPRGRVLVMTSCLPAL RFIATPRLSAMPHIDNDVKLDFDKVLLRPKRSTLKRSEVDLTR SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWDPQMGCVFLIYKFLTLKWKMLLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV EBLILSGADI IKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA HGLKGHI ISDGGCSCPGDVAKAFGAGADFVMLGMLAGHSESGG ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNPIFSEAC  |
| 5380       | 2  | 2050   | PSRAGGAERGRAAAARSPPGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAPQDELGGRGSSSSSESQKPCALRGLSSLSIHLGME SFIIVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHVHSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLKSKKLIHQAAFPRRPPPRGTRPAPGGCIQP RGP I\EQVYQEI A\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKLPLSEDQARFYFQDLIKGIEYLYOKI I H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGT P FMAPELSLSETRKIFSGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEP LPSDENCTLVEVTEEEVENSVKHIPS LATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESELKT*KISPLPACCKVT*EPPHPSGCRPSCWQPPFLHTHSQPR *PEPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFLSTSWL PDLVGAPGSHFCFLNIALRLYNSHTM |
| 5381       | 2  | 2050   | PSRAGGAERGRAAAARSPPGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAPQDELGGRGSSSSSESQKPCALRGLSSLSIHLGME SFIIVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHVHSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLKSKKLIHQAAFPRRPPPRGTRPAPGGCIQP RGP I\EQVYQEI A\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKLPLSEDQARFYFQDLIKGIEYLYOKI I H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGT P FMAPELSLSETRKIFSGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEP LPSDENCTLVEVTEEEVENSVKHIPS LATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESELKT*KISPLPACCKVT*EPPHPSGCRPSCWQPPFLHTHSQPR *PEPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFLSTSWL PDLVGAPGSHFCFLNIALRLYNSHTM |
| 5382       | 1536   | 203  | GARGSQQDAPALQEAVERGPRAQPARGRMTKARLFRLWLVLGS VEMILLIIVWDSAGAAHFYLHTSFSPRPHGPPLPPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPKETEQQPPAPGSMEE SVRG YDWSPRDARRSPDQGRQAERRSVLRGFCANSSLAFTKERPF D DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMI VLSGSL LH RGAPYRDLPI PREHVHNASAHLTFNKFWRRYKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFLENEEF/*PQVRRHAAAV RQPHQPARLGARGLP RPWQ\VSFANFIQYLLDPHTEKLAPFNEH WRQVYRLCHPCQIDYDFVGKLETLEDAAQLQLQLQVLDLAPLP  |

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|------------|--|--|--|
| 5383       | 45   | 5250   | <p>PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP ENLLRD</p> <p>VERLLGCRNSKRTWRMLISKNNPWRRLQGISFGMYSAEELKKLS VKSITNPRYLDLSGNPSANGLYDLALGADSKVCSTCVQDFEN CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI HLLLCQLRVLEVGAQAVYELERILSRFLEENADPSASRIEEL EQYTTEIVQNNLLGSQGAHVKNVCESKSLIALFWKAHMNAKRC PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQXDSEPLGIEEAQ IGRGYLTPTSAREHLSALWKNEGFFLNLYLFSGMDDDGMESRFN PSVFFLDLFVPPSRSPVSRSGDQMFNTNGQTVNLQAVMKDVVL IRKLLALMAQEQLPEEVATPTTDEEKDSLAIADRSPLSTLPQO SLIDKLYNIWIRLQSHVNIIVDSEMDKLMMDKYPGIRQILEKKE GLFRKHMGMKRVDYAARSVICPDYINTNEIGIPMVFPATKLTYP QPVTWNVQELRQAVINGPNVHPGASVINEGDSRTALSADVMT QREAVAKQLLTPATGAPKPGQTIVCRHVKNQDILLNRQPTLH RPSIQAHRRARILPEEKVLRHLHYANCKAYNADFDGDEMNAHFPQS ELGRAEAYVLACTDQQLVLPKDGQPLAGLIQDHMVSGASMTTRG CFFTREHYMELVYRGLTDKVGVRKLLSPSILKPPFLWTGKQVVS TLLINII PEDHILPLNLSGKAKITGKANVKETPRSPVGFNPDSMC ESQVIREGELCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVQRORIEESTH CGQAVRAALNLPAAASYDEVGRKWQDAHLGKDQDQDFNMIDLFK KEEVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT MQISCIHQIELEGRSTPLMASGKSLPCFEPYFTPRAGGFVTG RFLTGIKPPEFFHCHMAGREGLVDTAVKTSRSGYLQRCIIKHLE GLVVQYDLTVRDSGVSQVQFLYGEDGLDIPKTQFLQPKQFPFLA SNYEVIMKSOHLHEVLSRADPKKALHFFRAIKKQSKHPNTLLR RGAPLSYSQKIQEAVKALKLESENRRGR/RPWS/G/RMLRMWY ELDEESRRKYQKKAACPDPSLSVWRPDIYFASVSETFETKVDD YSQEWAAQTEKSYEKSELSDRLRLTLQL\KWORSCEPGEAVG LLAAQSIGEPSTQMTLNTFFHAGRGEMNVTLGIPRLREILMVAS ANIKTPMMSVPVNLTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESFCMEEKQNKQVYQLRFQFLPHAYYQEKCLRPEDILRFMET RFFKLLMESIKKKNKASAFRNVNTRRATQDRLDNAGELGRSRG EQEGDEEEEGHIVDAEAEEDGADASDAKRKEQBEEDVYSEEE EREGEENDEDDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV PSRPDDAAPETHQPGAPGA\EAMERRVQAVREIHPFIDDYQYD TEESLWCQVTVKPLPMKINFDMSSSLVSLAHGAVIYATKGITRC LNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIADVPRHLSLVADYMCF EGVYKPLNRFGRSNSSPLOQMTFETSQFLKQATMLGSHDEL R SPSACLVGKVVVRGGTGLFELKQPLR</p> |
| 5384       | 196  | 886  | <p>QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGBPGQSGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD</p>   |
| 5385       | 326  | 799  | <p>LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVS HKKNKIHM SPTFRRPCTL*LRRQPKYPWKSTPRRNKLDHVVIIKFPLTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLQ SDGERKAYVRLAPDYDALVVATKIGIT</p>  |
| 5386       | 326  | 799  | <p>LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVS HKKNKIHM SPTFRRPCTL*LRRQPKYPWKSTPRRNKLDHVVIIKFPLTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLQ SDGERKAYVRLAPDYDALVVATKIGIT</p>  |
| 5387       | 2  | 2117   | <p>FVVAASGGCWFVLGERRAGSLLSASYGT FAMPGMVLFGRWATA SDDLVPFGFFELVVRVLWWIGILTLYLMHRGKLCAGGALLSSY LIVLMILLAVICTVSAIMCVSMRGTCNPGPRKSMKLLYIRL ALFPPEMVWASLGAAWVADGVQCDRTVVNGIATVVVSWIIIAA TVVSIIVFDPLGGKMAPYSSAGFSLDSDHSSQLLNLKLTAT</p>  |

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|------------|--|--|---|
|            |  |  | SVWETRIKLLCCCGKDDHTRVAFSSSTAELEFSTYFSDTDLVPSD<br>IAAGLALLHQQDNIRNNQEPAPQVVCCHAPGSSQEAADLDAELKNC<br>HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGCCRSKNPQMTMT/M<br>VGGDQLQL/CTSAPILHTRAAVOGLHPRQLPWTRFTELPFLVA<br>LDHRKESVVAVRGTMSLQDVLTDLSAESEVLDECEVQDRLAH<br>KGISQAARYVYQRLINDGILSOAFSIAPEYRLVIVGHSLGGGAA<br>ALLATMVRAAYPQVRCYAFSPRGLWSKALQEYSQSFIIVSLVLG<br>KDVIPRLSVTNLEDLKRRIIRVVAHCNKPKYKILLHGLWYELFG<br>GNPNLPTELDGGDQEVLTQPLLGEQSLLRWSPAYSFSSDSPL<br>DSSPKYPPPLYPPGRIIHLQEGAGRGCCSAHYSAKWSHEAE<br>FSKILIGPKMLTDHMPDILMRALDSVVSRAACVSCPAQGVSSV<br>DVA   |
| 5388       | 1569   | 753  | TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRRRAACQAEPAARS<br>KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMCLSTGCGFYGNPR<br>TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQALDST<br>SSMQPSPVSNQSLLESVASSQLDSTSDKAVPETEDVQASVS<br>DTAQQPSEEQSKLE\NRNKKRIAVSCAGRKWDLGLNAGVEMF<br>TVVYTVTQMYTIALTITKQMLKNFVFOQEFKSFSGSFHQQLLEYK<br>LLEHLQTKN  |
| 5389       | 1569   | 753  | TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRRRAACQAEPAARS<br>KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMCLSTGCGFYGNPR<br>TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQALDST<br>SSMQPSPVSNQSLLESVASSQLDSTSDKAVPETEDVQASVS<br>DTAQQPSEEQSKLE\NRNKKRIAVSCAGRKWDLGLNAGVEMF<br>TVVYTVTQMYTIALTITKQMLKNFVFOQEFKSFSGSFHQQLLEYK<br>LLEHLQTKN  |
| 5390       | 217  | 1332   | EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI<br>EGGADDSITRDDNIAAFKRIIRLPRYLDRVSEVDTRTTIQGEEI<br>SAPICIAPTGPHCLVWPDGEMSTARAAQAA\GICYITSTFASCS<br>LEDIVIAAPEGRLRFQLYVHPDLQNLKLIQRVESLGFKALVIT<br>LDTFVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAPYFQMTPI<br>TSLCWNDSLWFSITRLPIILKGILTKEDAEALAVKHNVQGIIVS<br>NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK<br>ALALGAKCIFLGDAILWALASKGEHGVKEVLNLTNEFHTSMA\<br>LTGCRSVAEINRNVLQFSL   |
| 5391       | 1  | 1292   | VKKAAGRSRGPTTAGQRCEAPGTVMERRLOVRANVKENROS?<br>QPPVCNKLMIHQEQKVMFVGGPNTKDYHIEEGEEVFYQLEGDM<br>VLRVLEQGGKHRDVIQGEIFLLPARVPHSPQRFANTVGLVVER<br>RRLETELDGLRYVVDITMDVLEKWFYCKDLGTQLAPIIQEFFF<br>SEQYRTGKPIPDQLLKEPPPLSTRSIMPEMSLDALDSSHREI<br>QAGTPLSLFGDTYETQVLAQGGSSEGLRQNVVWLWQLEGSSV<br>VTMGRRRLSLGPMWDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q<br>DPAKKS PWGEPSC HGLKAATGV PSTLEVPSLENNSPSPHYLSV<br>YCRVPHRPAHCHPPSCPSQPRCHAPGRAAPHLLWQTQPTAL<br>PVLPGGLPPAPLLP I PLSLQTCSTSTPRRPSIKAS   |
| 5392       | 1  | 1623   | IRGSNAQKVVGASGSGGAGPQDFAGPGGVPALAAAVLGACEPR<br>CAAPCPLPALSRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS<br>FIHKPAHGNLHPDARVLGPGVS YVVRVMGCI EVLRSMRSLDFNT<br>RTQVTREAINRLHEAVPGVRGSKKKAPNKALASVLGKSNLRF<br>GMSIS IHISTDGLSLSPATROVIANHHMPSISFASGGDTMDT<br>YVAVAKDPINQRACHILECCEGL\AQSIISTVGOAFELRFKQY<br>LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYNSIPGKEPPL<br>GGLVDSRLALTQPCALTALDQGPSPLRDACSLPVDVSGTGAP<br>PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR<br>PFEDALKLHECSVAAGVTAAPLPLEDQWPSPTTRAPVAPTEEQ<br>LRQEPWYHGRMSRAAERMLRADGDFLVRDSVTNPGQYVLTGMH<br>AGQPKHLLLVDPGVVTRTKDVL FESISHLIDHILQNGQPIVAE<br>SELHLRGVVSREP |
| 5393       | 2  | 982  | GGDSAGMTMETQMSQNVCPRLWLLQPLTVLLLLASADSQAAP<br>PKAVLKLEPPWINVLQ\EDSVTLTCQGAQP/ERSDSIQWFHNG   |

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|------------|--|--|--|
|            |  |  | \NLIPHTHTQPS\YRFKANN\DSGEYTCQTGQTS\SDPVHLTV<br>LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK<br>SQKFSHLDPFTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVITIV<br>QVPSMGSSSPMGIIIVAVVIATAVAIIAAVVALIYCRKKRISAN<br>STDPVKAAQFEPFGQMIAIRKRQLEETNNDYETADGGYMTLNP<br>RAPTDDDKNIIYLTLPNDHVNSNN  |
| 5394       | 2  | 982  | GGDSAGMTMETQMSQNVCPRLWLLQPLTVLLLLASADSQAAP<br>PKAVLKLEPPWINVLQ\EDSVTLTCQGAQP/ERSDSIQWFHNG<br>\NLIPHTHTQPS\YRFKANN\DSGEYTCQTGQTS\SDPVHLTV<br>LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK<br>SQKFSHLDPFTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVITIV<br>QVPSMGSSSPMGIIIVAVVIATAVAIIAAVVALIYCRKKRISAN<br>STDPVKAAQFEPFGQMIAIRKRQLEETNNDYETADGGYMTLNP<br>RAPTDDDKNIIYLTLPNDHVNSNN   |
| 5395       | 3135   | 531  | RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS<br>SSGNPEAVALAPDAYSTGSSSASSTLKRTKKRPPPSLKKKQTTK<br>KPTETPPVKETQEQPDEESLVPSGENLASETKTESAKTEGSPSPA<br>LLEETPLEPAAGPKAACPLDSESEGVVPPASGGGRVQNSPPVG<br>RKTLPPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS<br>SWDNQQENPPPTKKIGKPKVAKMPLRRPKMKKTPEKLDNTPASP<br>PRSPAEPNDIPIAKGTYTTFIDKWDDPNFNPFSSTSKMQESPCL<br>PQQSYNFDPTCDESVDPFKTSSTKPSSPSKSPASFEIPASAME<br>ANGVDGDLNPKAKKKKTPKTDTFRVKKS PKRSPLSDPPSQDP<br>TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMTVDLEADKQD<br>YPQPSDLSTFVNETKFSSPTEELDYNRSYEIYMEKIGSSSLPQD<br>DDAPKKQALYLMFDTSQESPVKSSPVRMSSEPTPCSGSSFEETE<br>ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELEAMGLGTP<br>SEAIETAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN<br>PPLFAQKLQREAAHPTDVSISKALYSRIGTAEVEKPAGLLFQD<br>PDLDSALQIARAEIITKEREVSEWKDKYERSRREVMEMRKIVAE<br>YEKTIQMIEDEQREKSVS\HQTVOQLVLEKEQA\LADLNSVEK<br>\SLADLFRRYEKMKEVLEGFRRKNEEVLKRCQAQYLSRVKKEEQR<br>YQALKVHA\BEKLDRAE\IAQVRGKAQEQAAHQASLAERSS<br>CRV\DALERTLEQKNKEIEBLTKICDELIAMGKS |
| 5396       | 3135   | 531  | RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS<br>SSGNPEAVALAPDAYSTGSSSASSTLKRTKKRPPPSLKKKQTTK<br>KPTETPPVKETQEQPDEESLVPSGENLASETKTESAKTEGSPSPA<br>LLEETPLEPAAGPKAACPLDSESEGVVPPASGGGRVQNSPPVG<br>RKTLPPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS<br>SWDNQQENPPPTKKIGKPKVAKMPLRRPKMKKTPEKLDNTPASP<br>PRSPAEPNDIPIAKGTYTTFIDKWDDPNFNPFSSTSKMQESPCL<br>PQQSYNFDPTCDESVDPFKTSSTKPSSPSKSPASFEIPASAME<br>ANGVDGDLNPKAKKKKTPKTDTFRVKKS PKRSPLSDPPSQDP<br>TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMTVDLEADKQD<br>YPQPSDLSTFVNETKFSSPTEELDYNRSYEIYMEKIGSSSLPQD<br>DDAPKKQALYLMFDTSQESPVKSSPVRMSSEPTPCSGSSFEETE<br>ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELEAMGLGTP<br>SEAIETAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN<br>PPLFAQKLQREAAHPTDVSISKALYSRIGTAEVEKPAGLLFQD<br>PDLDSALQIARAEIITKEREVSEWKDKYERSRREVMEMRKIVAE<br>YEKTIQMIEDEQREKSVS\HQTVOQLVLEKEQA\LADLNSVEK<br>\SLADLFRRYEKMKEVLEGFRRKNEEVLKRCQAQYLSRVKKEEQR<br>YQALKVHA\BEKLDRAE\IAQVRGKAQEQAAHQASLAERSS<br>CRV\DALERTLEQKNKEIEBLTKICDELIAMGKS |
| 5397       | 3135   | 531  | RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS<br>SSGNPEAVALAPDAYSTGSSSASSTLKRTKKRPPPSLKKKQTTK<br>KPTETPPVKETQEQPDEESLVPSGENLASETKTESAKTEGSPSPA<br>LLEETPLEPAAGPKAACPLDSESEGVVPPASGGGRVQNSPPVG<br>RKTLPPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS<br>SWDNQQENPPPTKKIGKPKVAKMPLRRPKMKKTPEKLDNTPASP<br>PRSPAEPNDIPIAKGTYTTFIDKWDDPNFNPFSSTSKMQESPCL  |

| SEQ<br>ID<br>NO: | Predicted<br>beginning<br>nucleotide<br>location<br>corresponding<br>to first<br>amino acid<br>residue of<br>amino acid<br>sequence | Predicted end<br>nucleotide<br>location<br>corresponding<br>to first<br>amino acid<br>residue of<br>amino acid<br>sequence | Amino acid segment containing signal peptide<br>(A=Alanine, C=Cysteine, D=Aspartic Acid, E=<br>Glutamic Acid, F=Phenylalanine, G=Glycine,<br>H=Histidine, I=Isoleucine, K=Lysine,<br>L=Leucine, M=Methionine, N=Asparagine,<br>P=Proline, Q=Glutamine, R=Arginine,<br>S=Serine, T=Threonine, V=Valine,<br>W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop<br>Codon, /=possible nucleotide deletion,<br>\=possible nucleotide insertion)   |
|------------------|---|--|---|
|                  |   |  | PQQSYNFDPTCDSEVDFFKTSSTKSPSSPSKSPASFEIPASAME<br>ANGVDGDLNKPAAKKKTKPLKTDTPRVKKSPPKRSPLSDPPSQDP<br>TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMTVDLEADKQD<br>YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSSLPQD<br>DDAPKKQALYLMFDTSQSPVKSSPVRMSPTPCSGSSFEETE<br>ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELEAMGLGTP<br>SEAIEITAPEGSPASADALLSRLAHPVSLCGALDYLEPDLAEXN<br>PPLFAQLQREAAHPTDVSISKALYSRIGTAIEVEKPAGLLFQQ<br>PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE<br>YEKTIAMIEDEQREKSVS\HQTQQQLVLEKEQA\LADLNSVEK<br>\SLADLFRRYEKKMEVLEGFKNNEEVLKRCQBYLSRVKKEEQ<br>YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHOASLAERSS<br>CRV\DALERTLEQKNKEIEBELTKICDELIAKMGKS   |
| 5398             | 56  | 5426   | SGEVCRMESNENQEGVPRPSYVFSADPIARPSEINFDGKILDL<br>HEFSLVAPNTEANSFESKDYLVCLIRIPFTQSEKELESEGCVH<br>ILDSQTVVLKEPQCILGRLEKSSG\QM\AQKFSFPFGFLGPAT<br>TQKEFFQGCIMHP\VKDLLKGQSLIFTYGLTNSGKTYTFOGTE<br>ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSRBYRLSSSQEK<br>EETASKSALLRQIKEVTVHNSDDTLYGSLTNSLNISEFEESIK<br>DYEQANLNMANSIKFSVWVSFFFIYNEYIYDLFVPVSSKFQKRR<br>MLRLSQDVKGYSFIKDLQWQVSDSKAYRLKLGIXHQSVAF<br>KLNNASSRSHSIPTVKILQIEDSEMSRVIRVSELSLCLAGSER<br>TMKTQNEGERLRETGNINTSLTLGKCNVNLKSEKSKFQKHVP<br>FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETNLNLFPS<br>ATAQKVCVPTLNSSEKLFQGVKSSQDVSLDSNNSKILNVKR<br>ATISWENSLEDLMEDEDLVELENAEETD/VGETKLDEDLK<br>TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE<br>EVTQFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG<br>KCDTREAAKDICKATKVETEBATACLELKFNQIKAEKAKTGEL<br>IKTKEELKKRENESSLIQELETSSNKIITQNRKIKELINIIDQ<br>KEDTINEFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV<br>PKDSKSKICSRKRVNENELQDEPPAKKSGSIHVSSAITEQKK<br>SEVRPNIAEIEDIRVLQENNEGLRAFLLTIEENELKNEKEKAE<br>LNKQIVHFQOELSLSEKKNLTLSKEVQIQSNYDIAIAELHVOK<br>SKNQEQEEKIMKLSNEIETATRSITNNVSIQKLMHTKIDELRTL<br>DSVQISNIDLNLRLDLSNGSEEDNLPTQLDOLLGNDYLVSKQV<br>KEYRIQBPNNRENSFHSSIEAIWEECKEIVKASSKKSHQIEELEQ<br>QIEKLQAEVKGKEDNNRLKEKEHKNQDDLLKEKETLIQOLKEE<br>LQEKVTLQVQIQHVVEGKRALSELTCQVTCYKAKIKELETILE<br>TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHQDSVKNT<br>KDLNVKELKKEETITQLTNNLQDMKHLQLKEEEEETNRQETEK<br>LKEELSASSARTQN\LNADLQRKEEDYADLKEKLTDAKKQIKQV<br>QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQRTIOQLK<br>EQLINQKVEEAIQQYERACKDLNVKEKIIDMRMTLEBEQEQTV<br>EQDQVL\SAKLSEVERLATELDRWRVKCNDETQNNQSRNKEHE<br>NNTDVLGKLTNLQDELQSESEQYNADRKKNWLEKMMMLITQAKEA<br>ENIRNKEMKKYADRERFFKQQNEMLTAQLTEKDSDLQKWRE<br>ERDQLVALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI<br>MDIKPKRISSADPKLQTEPLSTSPFISRNKIEDGSVVLDSCEV<br>STENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK<br>ARKRKSNEEEDLVKCNKKNATPRTNLKFPIISDRNSSVKKEQ<br>KVAIRPSSSKTYSLSQASIIIGVNLATKKKEGTLQKFGDFLQHS<br>PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRLTYSE<br>ISSPIDISGQVILMDQMKMESDHQIIKRLRLTKTAK |
| 5399             | 705   | 230  | GPRMAFLSQDQINEYKECFSLYDKQQRGKIKATDLVAMRCLG<br>ASPTPGEVQRHLQTHGIDNGELDFSTFLTIMHMQIKQEDPKKE<br>ILLAMLVVDKEKKGYVMASDLRSKILTSLGKLTKEV\DDLFRE<br>\ADIEPNGKVYDEFIHKITSYLDGT   |
| 5400             | 931   | 248  | SHCSSGMEIPTNYPASRAALVAQNYINQQGTGPHRVFEVQXVK<br>QASMEDIPGRGHKYLKFAVEEIIQKQKVNCTAEVLYPSTGQE<br>TAPEVNETFEGETGKNPDEEDNTFYQRLKSMKPFLEAQNI\PDN   |



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|------------|--|--|---|
|            |  |  | FGNVSPMTLVHLAWVACGYIIMQNSTEDTWYKMKYIQTVKQV<br>QRNDDFIELDYTILLHNIASQEIIPWQMQLWHPQYGTQVKHNS<br>RLPKEVQLE  |
| 5401       | 3  | 1360   | TGWSVGPTSLAFLAPRDFPFPKLLIHPQAVVRLSCGAGSMGS<br>QAAAEWRNWSWEGSSSLSGCSMGCFKDDRIWTFWTFSTYFME<br>KWAPRQDDMLFYVRRKLAYSSESGADGRKAAEPEVEVEVYRRD<br>SKKLPLGDDPDIDWEESVCLNLILQKLDYMTCAVCTRADGGDI<br>HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFNMIDSF\BE\<br>VFSDMTVGKGMVCLVASDKTNTFQGVIFQGSIRYBALKKVY<br>DNRVSVAAARMAQK\MSFGFSKYSNMEF\VR\MKGPQKGHAEMA<br>VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA<br>FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT<br>NLRSRSLSGTGRSLVGSWLKLNLRADGNFLLYAHLTYVTLPLHRI<br>LTDILEVRQKPIMLT   |
| 5402       | 3445   | 1563   | GECEIMAAVVQNDLVFEFASNVMEDEQLGDPPIFPAVIVEHV<br>PGADILNSYAGLACVEEPNDMITESSLDVAEEIIDDDEDDITL<br>TVEASCHDGETIETIEAAEALLNMDSPGPMLEKRINNIFSS<br>PEDDMVAVPVTHVSVTLGDIPEVMETQQVQEKYADSPGASSPEQ<br>PKRKKGRKTKPPRDPSPATTPNISVKKKNKDGKNTIYLWEFLL<br>ALLQDKATCPKYIKWTQREKGIKFLVDSKPVSLWRKHKNKP\D<br>MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE<br>DPSSSIESSDPSLSSSATSNNRQTSRVRVSSSPGVKGGATTVLK<br>PGNSKAAKPKDPVEVAQSEVLRTVQPTQSPYPTQLFRTVHVQ<br>PVQAVPEGEAARTSTMQDETINSSVQSIR\TIQAPTQVPVVVSP<br>RNQQLHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPISSQP<br>MTVLKENVMLQSQKAGSPPSIVLGPARGV\QQVLTSNVQTCINGT<br>VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ<br>ETKTLTQVEVEKSEDLKENTKTEQQPQPYVMVSSSNGFTS<br>QVAMQNELLEPNSF |
| 5403       | 3445   | 1563   | GECEIMAAVVQNDLVFEFASNVMEDEQLGDPPIFPAVIVEHV<br>PGADILNSYAGLACVEEPNDMITESSLDVAEEIIDDDEDDITL<br>TVEASCHDGETIETIEAAEALLNMDSPGPMLEKRINNIFSS<br>PEDDMVAVPVTHVSVTLGDIPEVMETQQVQEKYADSPGASSPEQ<br>PKRKKGRKTKPPRDPSPATTPNISVKKKNKDGKNTIYLWEFLL<br>ALLQDKATCPKYIKWTQREKGIKFLVDSKPVSLWRKHKNKP\D<br>MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE<br>DPSSSIESSDPSLSSSATSNNRQTSRVRVSSSPGVKGGATTVLK<br>PGNSKAAKPKDPVEVAQSEVLRTVQPTQSPYPTQLFRTVHVQ<br>PVQAVPEGEAARTSTMQDETINSSVQSIR\TIQAPTQVPVVVSP<br>RNQQLHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPISSQP<br>MTVLKENVMLQSQKAGSPPSIVLGPARGV\QQVLTSNVQTCINGT<br>VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ<br>ETKTLTQVEVEKSEDLKENTKTEQQPQPYVMVSSSNGFTS<br>QVAMQNELLEPNSF |
| 5404       | 187  | 1111   | LPVTLIFAKMKTLLQSTLLLLLVPLIKPAPPTQDSRIIYDGT<br>DNFEESI FSQDYEDKYLKGNIKEKETV IIPNEKSLQLQKDEAI<br>TPLPPKKENDEMPTECLLCVCLSGSVYCEEVDIDAVPLPKESAY<br>LYARPKNKIKLT\AKDFADIPNLRLDFTGNLIEDIEDGTFSKL<br>SLVEELSLAENQLLKLPLVLPKLTLEFNAXYNIKSRGIKANAFK<br>KLNNLTFLYLDHNALESVPLNLPESLRVHLQFNNIASITDDTF<br>CKANDTSYIRDRIEIRLEGNP IVLGKHPNSFICLRLPIGSYF  |
| 5405       | 2199   | 1220   | QNSRSLHMDPQNHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA<br>ILSLDQIKAIRGSNEYTEGSPVVKRPAPRTAPRQEKHERTHEII<br>PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS<br>NSSASSEQGLLGRSPPTRPVPGHRSERAI RTOPKOLIVDDLKGS<br>LKEDLTQHKFICEQCGKCKGECTAPRTLPSCLACNRQCLCSAE<br>SMVEYGTMCML\VKGI FYHCSNDDEGDSYSDNPCSCSQSHCCSR<br>YLCMGAMSLFLPCLLCYPPAKGCLKLCRCYDWIHRPGCRCKNS<br>NTVYCKLESCPSRGQKPS   |
| 5406       | 279  | 2732   | WRRTYNVEGPLTFMDVAIEFCLEENQCLDTAQONLYRVNMLENY  |

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|------------|--|--|--|
|            |  |  | <p>RNLVFLG/I IAVSKPDLITCLEQEKEPWEPMRRHEMVAKPVMC<br/> SHFTQDFWPEQHIKDPFQKATLRRYKNCHEKNVHLKDKHSVDE<br/> CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS<br/> HTEKKLFKCKEKGKSF CMLSHLAQHKI IHTRVNFCCKEKGKAF<br/> NCPSSIITKHKRINTGKPYTCBEGKVFVNSSRLTTHKKNYTRY<br/> KLYKCECGKAFNKSSILTHKII RTGKFKYKCEKAKAFNQSS<br/> NI TEHKKIHPGKPYKCECGKAFNWPSTLT KHKRINTGKPYT<br/> CECGKAFNQSNLTTHKR IHTA\ EKFKYKTECGEAFSRS\ SNL<br/> TKHKEIHTKPKYKCECGKAFKWSKLT EHKLTHTGKPKYKCE<br/> KCGKAFNCPSSIITKHNRINTGKPYTCBEGKVFVNSSRLTTHK<br/> KNTRYKLYKCECGKAFNKSSILTHKIIHIEKFKYKCECGK<br/> AFKWSKLT EHKIHTGKPYKCECGKAFNHFSILT KHKR IHT<br/> GKPKYKCECGKAFNQSNLTTHKIIHTGKFKYKCECGKAFQ<br/> SSNLTTHKIIHTGGKPYKCECGKAFNQSTLT KHKI IHT EKP<br/> YKCECGKAFKNSSTLT KHKI IHTGKPYKCECGKAFKLSST<br/> LSHKIIHTGKPYKCECGKAFNRPSNLI EHKIHTGKPYKCE<br/> EECGKAFNYSSHLNTHKR IHTKEQPYKCECGKAFNQSNLTTH<br/> NKIHTGKLYKPEDVTVILTTPTQTFSNIK</p>  |
| 5407       | 3  | 659  | <p>RPRRRQSSCCTGWLAGWLLRAAPFCRRRTETDMEQGRGLAVLIL<br/> AII LLQGT LAQSIKGNHLVKVYDYQEDGSVLLTCDAAKNITWF<br/> KDGKMI GFLTEDKKKWNLSNAKDPGRMYQCKGSONKSKPLQVY<br/> YRMQCNCIELNAATISGFLFAEIVSIFDLAVGVYFIAGTGMEFR<br/> QS\RASDKQTLPL\NDPAPTQPLKDKPRKMTQYSHLQGN\QLRRN</p>  |
| 5408       | 2745   | 6128   | <p>QGSKGTCHPQAQQPWDEGVWQEAQSEPWGQSQEPPTMPQRLP<br/> HARQHTPLPLGSADYRRVSVRPQGPHRDPKDSRDAAKREQGS<br/> APRPVPASRGKTLCKGYRQAPPGPPAQFORPICSASPPWASRF<br/> STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLWKSM<br/> RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWAECGE<br/> VRNKDMSWPEEMSF IANSSKIDRHKVPTEKGATGLSNLGNTCFM<br/> NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYG<br/> LVQELWSGTQKNVAPLKLRTIAYAPRFNGFQQQDSQELLAFL<br/> LDGLHEDLNRVHEKPYVELKDS DGRPDWEVAAEAWDNHLRRNRS<br/> IVVDLFHQGLRSQVKCKTCGHISVRFPFNFLSLPLPMDSYMHL<br/> EITVIKLDGTTVPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL<br/> LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP<br/> TQTDFFSSSPSTNEMFTLTNGDLPRPFIIPNGMPTVVPCTEX<br/> NFTNGMVNGHMPSLPDSPTGYIIAVHRKMMRTELYFLSSQKNR<br/> PSLFGMPLIVPCTVHTRKLDYDAVWIVQVSLASPLPQEASNH<br/> AQDCDDSMGYQYPFTLRVQKDGNSCAWCPWYRFRGCKIDCGE<br/> DRAFIGNAYIADVWHPTALHLRYQTSQERVVDEHESVEQSRRQ<br/> VEPINLDSCLRAFTSEELGENEMYCCKKTHCLATKKLDLWR<br/> LPPILI IHLKRPQFVNGRWIKSQIKVFPRESFDPASFLVPRDP<br/> ALCOHKPLTPQDELSEPRILAREVKVDAQSSAGEEDVLLSKS<br/> PSSLSANI ISSPKGSPSSSRKSGTSCPSKNSPNSPRTLGSR<br/> KGRRLRPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH<br/> VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSGNLG<br/> NHSEEDSTDDQREOTRIKPIYNLYAISCHSGILGGGHVYTYAKN<br/> PNCWKYCYNDSSCKELHPDEIDTDSAYILFYEQGIDYQAFLEPK<br/> TDGKKMADTSSMEDDFESDY\ EKYCVLQ</p> |
| 5409       | 2745   | 6128   | <p>QGSKGTCHPQAQQPWDEGVWQEAQSEPWGQSQEPPTMPQRLP<br/> HARQHTPLPLGSADYRRVSVRPQGPHRDPKDSRDAAKREQGS<br/> APRPVPASRGKTLCKGYRQAPPGPPAQFORPICSASPPWASRF<br/> STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLWKSM<br/> RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWAECGE<br/> VRNKDMSWPEEMSF IANSSKIDRHKVPTEKGATGLSNLGNTCFM<br/> NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYG<br/> LVQELWSGTQKNVAPLKLRTIAYAPRFNGFQQQDSQELLAFL<br/> LDGLHEDLNRVHEKPYVELKDS DGRPDWEVAAEAWDNHLRRNRS<br/> IVVDLFHQGLRSQVKCKTCGHISVRFPFNFLSLPLPMDSYMHL<br/> EITVIKLDGTTVPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL<br/> LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP</p>  |

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|------------|--|--|---|
|            |  |  | TQTFSSSPSTNEMPTLTNGDLPRPFIPIPNMGMPNTVVPCTGTEK<br>NFTNGMVNGHNPSPDPSPFTGYIIAVHRKMMRTLYFLSSQKNR<br>PSLFGMPLIVPCTVHTRKKDLYDAVWVQVSRSLASPLPQEQASNH<br>AQDCDDSMGYQYPTTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE<br>DRAFIGNAYIAVDWHTALHLRYQTSQERVVDEHESVEQSRRQA<br>VEPINLDSCLRAFTSEEEELGENEMYCCKKTHCLATKKLDLWR<br>LPPILIIHLKRFQVNGRWIKSQKIVKFPRESFDPSPAFVLPDRP<br>ALCQHKPLTPQGDSESPRILAREVKKVDAQSSAGEEDVLLSKS<br>PSSLSANIISSPKGSFSSSRKSGTSCPSSKNSSPNSSPRTLGRS<br>KGRRLRPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH<br>VLGGSQPELVTPQDHEVALANGFLYEACGNGCGNGYSNGQLG<br>NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHVVTYAKN<br>PNCKWYCYNDSSCKELHPDEIDTDSAYILFYRQQGIDYAFQFLPK<br>TDGKKMADTSSMDEDFESDY\EKYCVLQ   |
| 5410       | 2  | 710  | LRPPGQARHVWLAARMQAPHEKLYKLLVIGDLGVGKTSIIKRY<br>VHGNFSSHYRATIGVDFALKVLHWDPETVVRLQLNDIAGQERFG<br>NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNLDSKLSLPLNG<br>KPVSVVLLANKCDQKQKVLMMNGLKMDQFCKEHGFVGFETSAK<br>ENTNIDEASRCLVKHILANECMLMESIEPDVVKPHLTSTKVASC<br>SG\CAKILVGFIFAGVW   |
| 5411       | 1302   | 289  | TGPAAAGRRKALGSFGKPSVPTGLRAARRRRTRPSAPAAPSVC<br>GKRRES DAGAGGERASVRTGSGRRGRMTAGDSEQLQNHQPN<br>GGEFFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVILS<br>QDSFYRVLTSEQKAKALKQGFNFDPDAFDNELILKTLKEITTEG<br>KTVQIPVYDFVSHSRKEETVTVPADVVLFEGLAFYSQBR/IR<br>DLFQMKLFVDTDADTRLRRVLKDISERGRDLEQILSSSTLRFV<br>KPA\FEEFCLPPK\KYADVIIIPR\GADN\RVPINLIVQHIQ\DI<br>LNGGPS\NRQTNGCLNGYTPSRKROASESSSRPH  |
| 5412       | 3180   | 313  | QGISNFFHKEANFWFEVSGYLISPLRS PFVDFALEWSLMA SPWN<br>KMEGBSSRFEIHTPVSDKKKKKCSIHKERPKQKHSHEIFRDS SLV<br>NEQSQITRRKKRKKDFQHLISSPLKKSRI CDETANATSTLKKRK<br>KRRYSALEVDEBAGVTVVLVDKENINNTPKHFRKDDVDVVCVMS<br>IEQKLPK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQ<br>KAASWBSORA\RDTPQSEFPTQESWLSVCGGGEITELP\ASA<br>HKNSKKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV<br>GLDDETQPLLGPHTKKKKKKKKKKSNHQEFESLAMPEGSQVGS<br>EVGADMQES\RPVGLHGETAGIPAPAYKNKSKKKKKSNHQEF<br>EAVAMPESLESAYPEGSQVGSVEGTVEGSTALKGFKESNSTKKK<br>SKKRKLT SVKARVSGDDFVPSKNSBSTLFDSEVGDMAMEEG<br>VKSRRPQKKTQACLASKHVQEA PRLEPANEHNVTAEDESEIRY<br>LSADSGDADSDADLGS AVKQLQEFIPN IKRATSTIKRMYRDD<br>LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD<br>KLLYTD RYPEEKSVITNLKRRYSFRLHIG\RN IARPWKLIYYRA<br>KKMFVNNYKGRYSEGDTEKLMYHSLLGNDWKTIGEMVARRSL<br>SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVLKMKSPQBLK<br>EVD SKLQENPESCLSI VREKLYKGISWVEVEAKVQTRNWMQCKS<br>KWTEILT KRMTNGRRIYGMNALRAKVS LIERLYEINVEDTNEI<br>DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFQKKTFPEI IDYL<br>YETTLPLLKEKLEKMEKKGT KIQTPAAPKQVFPFRDIFYEDD<br>SEGGHHRKRKRPRRRHAWPTPVIPVLWEAKAGWII |
| 5413       | 3753   | 1304   | RFPAGVAPRRAMNVSKKVSWSGRDRDDEEAAPLLRRTARPGGG<br>TPLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DM DPP<br>HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHIAFR<br>TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKRYVIGKNID<br>KFTEKGGLSFSLLLWATLNAAPVLVGSVIVAFIEPVAAGSGIPQ<br>IKCFLNGVKIPHVVRLKTLVIKVS GVL SVVGGLAVGKEGPMIH<br>SGSVIAAGISQGRSTSLKRD FKI FEYLRRDTEKRD FVSAGAAAG<br>VSAAFGAPVGVLFSL EEGASFNNQFLTWRIF FASMISTFTLNF<br>VLSIYHGNMWDLS SPGLINFGFRDSEKMYITHEIPVFIAMGVV<br>GGVLGAVFNALNYLTMFRIRYIHRPCLQVIEAVLVAAVTATVA<br>FVLIYSSRDCQPLQGGMSYPLQLFCADGEYNSMAAAFNTPEK   |

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|------------|--|--|---|
|            |  |  | SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP<br>SLLI GAAGWGRLLFGISLSYLTGAAIWADPGKYALMGAAQGGIV<br>RMTLSLTVMMEATSNVTYGFPIMLVMTAKIVGDVFIIEGLYDM<br>HIQLQSVFPLHWEAPVTSLSLTAREVMSTPVTCLRRREKVGIV<br>DVLSDTASNHNHGFVVEHADDTPARLQGLILRSQILVLLKHKV<br>FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSDERECTMD<br>LSEFMNPSPYTVPQEASLPRVFKLFRALGLRHLVVVDNRNQVVG<br>LVTRKDLARYRLGKRGLEELSLAQ   |
| 5414       | 2130   | 390  | QVASAWDRALFSPLLSPTSRSVPRTSPPRCVSTETGRRDRARVPS<br>QWCSVLQKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR<br>AGAAPRDHGRVRHRRPSSARRMTRTTGOC LAPRGCGQPRGTRSP<br>RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINILNMYNDRFTV<br>AGVLPDIEQFFNIGDSSSGLIQTVFISSYMLAPVFGYLGDRYN<br>RKYLMCGGIAFWSLVTLGSSFIPEGHFWLLLLTRGLVGVGEASY<br>STIAPTLIADLFVADQSRSMLSIFYFAIPVGSGLGYIAGSKVKD<br>MAGDWHWALRVTPGLGVVAVLLFLVVRPPRGAVERHSDLPPL<br>NPTSWWADLRALARNPSFVLSSLGFTAVAPVTGSLALWAPAPLL<br>RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGLVGLGVGEI<br>SRLRHSNPRADPLVCATGLGSAFFLFLSLACARGSIVATYIF<br>IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD<br>AGSPYILGLISDRLRNWPSPFLSEFRALQFSLMLCAFVGALGG<br>AAFLGTAHLH   |
| 5415       | 693  | 2986   | IPPKTKLELQKH\LTTLT\NQEQTIFEEVQKLRPRNEQRENE<br>IISFLRCLFEBKQKEHIIHIGEMKQTSQMAENIGSELPPSATRF<br>RLDMLKNKAKRSLTESLESILSRGNKARGLQEHISISVDLSSLS<br>STLNTSKEPSVCEKEALPISESSPKLLGSSSEDLSSDSESHLPE<br>EPAPLSPOQAFRRRANTLSHFPIECQE?POPARGSPGVSQRKLM<br>RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQOIFL<br>RVATPQKACDSSSRVEDYSELGELPPRSLEPVCEDGPPGPPPE<br>EKKRTSRELRELWQKAILQIILLRMEKENQKIQASENDLLNKR<br>LKLDYEEITPCLKEVTVWEKMLSTPGRSKIKFDMKMHSAVGQ<br>GVP\RHHRGEIWKFLAEQFHLKHQPPSKQKQKDVVPYKELLKQLT<br>SQQHAILIDLGRFTPTHPYFSAQLGAGQSLYNI LKAYSLLDQZ<br>VGQCQGLSFVAGILLHMHSEEAFFKMLKFLMFMGLRKQYRPDM<br>IILQIQMYQLSRLLDYHRDLYNHLBEHEIGPSLYAAPFWLTFM<br>ASQFPLGVARVFDMIPLQGTETVIFKVALSLLGSHKPLILQHEN<br>LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIKQLQAYEVEYH<br>VLQEEIDSSPLSDNQRMDEKLEKTNSLRKQNLDLLEQLQVANG<br>RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS<br>AKPSDREPECTQPEPTGD   |
| 5416       | 27   | 4074   | KSQLFCFWGGKAGDILSGDQKEQKDPYFVETPYGVQLDLDFLK<br>YVDDIQKGNITIKRLNIQKRRKPSVPCPEPRITSGQQGIWSTES<br>LSSNSDDNKQCPNPLIARSQVTSTPI SKPPPLETSLPFLTIP<br>ENRQLPPPSQPLKHNHVTKLTMTETRRLEQERATMQMTPEF<br>RRPRLASFGMGTTSSLPFVSGNHNPAKHQLQNGYQNGDYG<br>SYAPAAPTTSSMGSSIRHSPSSGISTPVTNVS PMHLQHIREQM<br>AIALKRLKELBEQVRTIPVLQVKISVLQEEKQLVSQLKNQRAA<br>SQINVCVGRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME<br>TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC<br>RSVAVGAENMNDIVVYHRGSRSCDAAVGLVEMRNCGVSVTE<br>AMLGVMTEADKEIELQQOTIESLKEKIYRLEVQLRETTDREMT<br>KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH<br>MDLVDTCVGTSVETNSVGISCQPECKNKVVGPPELPMNWWIVKER<br>VEMHDCAGRSVEMCDKSVSVSVCTGTSNTEESVNDLTLLKT<br>NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTAEVQVEAAV<br>MAVPRTADQDSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ<br>TSQTQVTRTVAVGRGRVKDINSSTKTRSIGVGTLLSGHSGFDR<br>PSAVXTKESGVGQININDNYLVGLKMRITACGPPQLTVGLTASR<br>RSVGVGDDPVGESLENPQAPLGMMTGLDHYIERIQRLAEQQ<br>TLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST<br>EELRNPDFQKTSLGKITGSYLYTCKCGGLQSGSPLSSQTSQPE |

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|------------|--|--|--|
|            |  |  | QEVGTSEGKPISSLDAPFTQEGTLPVNLTDQIAAGLYACTNN<br>ESTLKSIMKKKDGKDSNGAKKNLQFVINGGYETSSDDSSSD<br>ESSSESDDDECDVIEYPLEEEEEDEBTRGMAEGHHAHVNI<br>KSARVEDEMQVQCEPEKVEIRERYELSEKMLSACNLLKNTIND<br>PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDIYAFAEI<br>SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVNCVD<br>HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG<br>QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG<br>HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA<br>HVNFAKAQSPGTPRLGRKTSPPGTHRGSD   |
| 5417       | 27   | 4074   | KSQPCFPGGKAGDILSGDQKEQKDPYFVETPYGYQLDLDLFLK<br>YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRITSSGQGIWSTES<br>LSSNSDDNKQCPNFIARSQVTSTPISKPPPLETSLPFLTIP<br>ENRQLPPSPQLPKHNLHVTKTLMETRRRLQERATMQMTPGEB<br>RRPRLASFGMGMTSSLPFVSGNHNPAKHQLQNGYQNGDYG<br>SYAPAAPTTSSMGSSIRHSLSSGISTPVTNVPMLHQHIREQM<br>AIALKRLKELEEQRVTPVLQVKISVLQEEKRLVSLKNQRAA<br>SQINVCGRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME<br>TVEQSTQRIKEFRQLTACMQALEQKIQDSSCEASSELRENGEC<br>RSVAVGAENMNDIVVYHRGSRSCDAVGLVEMRNCVSVTE<br>ANLGVMTBADKEIQLQQTIESLKEKIVRLEVQLRETHDREMT<br>KLKQELQAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH<br>MDLVDTCVGTSVETNSVGI SCQPECKNKVVGPELPMNWHIVKER<br>VEMHDCAGRSVEMCDKSVSVSVCTGSNTESVNDITLLKT<br>NLNLKEVRSIGCGDCSDVDVTCSPKECASRGVNTAVSQVEAAV<br>MAVPRADQDSTDLBQVHQFTNTETATLIESCTNTCLSTLQK<br>TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR<br>PSAVKTKESGVQGININDYLVGLKMRITACGPPQITVGLTASR<br>RSVGVGDDPVGESLENPQAPLGMGTGLDHYIERIQKLLAEQQ<br>TLAENYSELAEAFGEPHSQMGSLSQLISTLSSINVMKSAST<br>EELRNPDFQKTSGLKITGSYLGYTCKCGGLQSGSPSSQTSQPE<br>QEVGTSEGKPISSLDAPFTQEGTLPVNLTDQIAAGLYACTNN<br>ESTLKSIMKKKDGKDSNGAKKNLQFVINGGYETSSDDSSSD<br>ESSSESDDDECDVIEYPLEEEEEDEBTRGMAEGHHAHVNI<br>KSARVEDEMQVQCEPEKVEIRERYELSEKMLSACNLLKNTIND<br>PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDIYAFAEI<br>SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVNCVD<br>HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG<br>QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG<br>HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA<br>HVNFAKAQSPGTPRLGRKTSPPGTHRGSD |
| 5418       | 24   | 1133   | SVPRAGGDMRTGAELYDQALGILQHVGNVQDFLRVLFGFLYR<br>KTDYFRLLRHPSDRMGFPFGAAQALVLQVFKTFDHMARQDDEKR<br>RQLEEEKIRKKEEEAKTVSAAAEKEPVVPVQEIETDSTTEL<br>DGHQVEKQVPPGPKMAHGSQEAEPAGVAGAAEVPR\EPPI<br>LPRIQEQQFQKNPDSYNGAVRENYTWSQDYTDLEVRVVPKHVVK<br>GKQVSVALSSSIRVAMLEENGERVLMGKLTHTKINTESSLSL<br>EPGKCVLVNLSKVGEYWNAILGEEEPIDIDINKERSMATVDE<br>EEQAVLDRLTFDYHQKLGKQPSHELKVMELKKGNDAGSPFR<br>GQRFDPAMFNISPGAVQF   |
| 5419       | 1395   | 259  | GTHPLDPLVSRVSVQGPLMTMACPGMSDTEESPFLLGPRAAEG<br>SESEACEAFGRRKSEEGRRSDTSGFGRSRKHVNNKHPERADA<br>KDPASLPQC/LGP/DCVRPAQPSKYCSDDCGMKLANRIYELL<br>PQRIQWQQSPCIAEEHGKLLERIRREQQSARTRLOEMERRFH<br>ELEAII LRKQAVREDEESNEGSDDTDLQIFCVSCGHEINPR<br>VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT<br>YCKRLQVLCPEHSRDPKVPADVCGCPLVRDVFELTGDFCRLPK<br>RQCNRYHCWEKLRAEVDLERVRVWYKLDLFEQERNVRTAMTN<br>RAGLLALMLHQTIQHDPLTTDLRSSADR   |
| 5420       | 117  | 1733   | NEAGGACPFKGGASGRLYLSFRLPRVSVAGCEERPLGWVVLGG<br>GGFLPARFPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR  |

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|------------|--|--|--|
|            |  |  | ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPSTRL/LLELCTFTLAIALGAVLLLPFSIIISNEVLLSLPRNYIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLRGV YETVVMMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP YLYSCISFLGVLLLVCTPLGLARMFVSVTGKLLVKPRLLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPDLMELHRRQVLALQTRVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPGRMGQTSLGQVSFSKLGSGGAVIQVVLIFYLMVSSVVG F YSSPLFRSLRPRNHDAMTQIIGNCVCLLVSSALPVFSRTLGL TRFDLLGDFGRFNWLGNYIVFLYNAAFAGLTTCLVKTFATAV RAE LIRAFGERE  |
| 5421       | 117  | 1733   | NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWWVVLGG GGFLPARPPRAQRHLGFSAEQSMEADPYEVLSVREQLFHERIR ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPSTRL/LLELCTFTLAIALGAVLLLPFSIIISNEVLLSLPRNYIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLRGV YETVVMMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP YLYSCISFLGVLLLVCTPLGLARMFVSVTGKLLVKPRLLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPDLMELHRRQVLALQTRVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPGRMGQTSLGQVSFSKLGSGGAVIQVVLIFYLMVSSVVG F YSSPLFRSLRPRNHDAMTQIIGNCVCLLVSSALPVFSRTLGL TRFDLLGDFGRFNWLGNYIVFLYNAAFAGLTTCLVKTFATAV RAE LIRAFGERE   |
| 5422       | 3  | 1263   | SCGESLPTWLAGASRPGIGRKGAWGGRRGSSPAQVLLSEGPVF KAGCNWHLSDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD YRSTVLCVSKMEADLSGFNIDAPRWQRTFLGRVKHFLNITDPR TVFVSERELDKAKVMVEKSRMGVVPVPGTQVEQI\IYAKKLYDSAF HPDTGEKMNVIQRMSFQLPGGMIITGFMLQFYRTMPAVIFWQHV NQSFNALVNYTNRAASPTSVRQMALSYFTATTAVATAVGMNM LTKKAPPLVGRWVPAFAVAANCVNIPMMRQBELIKGICVKDRN ENEIGHSRRAAIGITQVVISRITMSAPGMILLPVIMERLEKLH FMQKVVL/SAPLQVMSGCCFLIFMVPVACGLFPQKCELPVSYL EPKLQDTIKAKYGELEPYVYFNKGL  |
| 5423       | 3186   | 905  | GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSEBQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGSPRAHQPOASD ANREPVAERSEPALSGLPATMGSGDLLSGESQVEKTKLSSSE EFFQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAPSSCSISASSTGSSSQGHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVLGPRPQWSPQPVFSGGDASGL GRRRLSFQAEYWACVLPDLSLPPSPDRHSPLMNPNKEYEDLLDYT YPLRPGFQLPKHLSRVFADPVLQDSGVLDLSFSVSPASTLKSP TNVSPNCPPAEATALPFGSGPREPSLKQWPSRVPOKQGGMGLASW SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTRDRGWPSRPREREKRTSQSARRPTCTESRWKSBEVESDDEY LALPARLTQVSSLVSYLGSISTLVLTPTGDIKQSPLEVSDDSG PASFPSSSSQSLPPGAALQSGDPEGQNPCLRSFVRAHDSAG EGSIGSSQALGVSSGLLKTREPSLPARLDRWFFSDPDVEGQLPRK GGEQKESLVQC\VKTFC\QLEELICWLYNV\ADVTDHGTTPAR SNLTSLK\SSLQLYRQFKDIDEHQSLTESVLQKGEILLQCLLE NTPVLEDVLGRIAKQSGELESADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV |
| 5424       | 3186   | 905  | GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSEBQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGSPRAHQPOASD ANREPVAERSEPALSGLPATMGSGDLLSGESQVEKTKLSSSE EFFQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAPSSCSISASSTGSSSQGHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVLGPRPQWSPQPVFSGGDASGL GRRRLSFQAEYWACVLPDLSLPPSPDRHSPLMNPNKEYEDLLDYT YPLRPGFQLPKHLSRVFADPVLQDSGVLDLSFSVSPASTLKSP TNVSPNCPPAEATALPFGSGPREPSLKQWPSRVPOKQGGMGLASW  |

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|------------|--|--|---|
|            |  |  | SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL<br>RTRDRGWSPSPRPEREKRTSQSARRPTCTESRWKSEBEVESDDEY<br>LALPARLTQVSSSLVSYLGSISTLVTLPTGDIKQSPLEVSDSDG<br>PASFPSSSSQSQLPPGAALQSGDPEGQNPFCFLRSFVRAHDSAG<br>EGSLGSSQALGVSSGLLKTREPLPARLDRWPFSDDPDVEGQLPRK<br>GGEQKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTTPAR<br>SNLTSLK\SSQLYRQFKKDIDEHQSLTESVLQKGRILLQCLLE<br>NTPVLEDVLGRIAKQSGELESADRLYDSILASLDMLAGCTTLP<br>DKKPMAMEHPCEGV  |
| 5425       | 1086   | 115  | GFCPSPSLGHQPPRVLHPTMSMAVETFGFMATVGLNLGVTLF<br>NSYWRVSTVHGNVITNTI FENLWFSCATDSLGVYNCWEFFPSML<br>ALSGYIOACRALMITAILLGLGILLGLIAGLCTNIGGLELSRK<br>AKLAATAGAPH\ILPGICGMVAI\SNYAFNITR\DFSDPLYPGT<br>KYELGPALYLGNASLISILGGLCLCSACCGSDEDDPAASARRP<br>YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA<br>PKRGPGRGPFPYPSNLGRPRPVVAPPRPRPRVLHSHGPSQAK<br>NCSWEVAYLPSEAGSLIF   |
| 5426       | 42   | 3435   | ATSSQSLGRADPPRGGTMEERSPGEGSPSPMDQPSAPSDDPTDQ<br>PAAHAKPDPGSGGQPPAGPGAAGEALAVLTSFGRRLVLIPVYLA<br>GAVGLSVGFVLFGALALYLGWRRVRDEKERSLRAARQLDDEEQ<br>TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK<br>LLAETVAPAVRGSNPHLQTFFTFTRVELGEKPLRIIGVKVHPGQR<br>KEQILLDLNISYVGDVQIDVEVKYFCKAGVKGMQLHGVLRVIL<br>EPLIGDLFPVGAUSMFFIRRPDLINWTGMTNLLDIPGLSSLS<br>TMIMDSIAAFLVLPNRLVLPVLPDQDVAQLRSPLPRGIIRIHL<br>LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN<br>PQWGETYEVVHEVPGQEIIEVEVFDKDPDKDDFLGRMKLDVGKV<br>LQASVLDWFPPLQGGQGVHLRLLEWLSLLSDAEKLEQVLQWNWG<br>VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKGNKEPNP<br>MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV<br>KDDSRALTGLALTPLARLLTAPELILDQWFQLSSSGPNSRLYM<br>KLVMRILYLDSEICFPTVPGCCPGAWDVDSNPQRGSSVDAPPR<br>PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY<br>VKLKLGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF<br>DKDLDDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRHLRL<br>ERLTTPRTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAE<br>LPLRKGTKHLSPYATLTVGDSHKTITISQTSAPVWDESASFLI<br>RKPHTESLELQVRGEGTGVLSLSLPLSELLVADQLCDRWFTL<br>SSGQGVLLRAQLGILVSQHSQGVAAHSHSYSHSSSSLSSEPELS<br>GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTWYYS<br>ERKLVSIHVGCRLRQNGRDPDPYVSLLLLPDKNRGTKRRTSQ<br>KRTLSPEFNERFEWELPLDEAQRRLDVSVKNSSSFMSREREL<br>LGKVQLDLAETDLSQGVARWYDLMDNKKDKGSS |
| 5427       | 42   | 3435   | ATSSQSLGRADPPRGGTMEERSPGEGSPSPMDQPSAPSDDPTDQ<br>PAAHAKPDPGSGGQPPAGPGAAGEALAVLTSFGRRLVLIPVYLA<br>GAVGLSVGFVLFGALALYLGWRRVRDEKERSLRAARQLDDEEQ<br>TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK<br>LLAETVAPAVRGSNPHLQTFFTFTRVELGEKPLRIIGVKVHPGQR<br>KEQILLDLNISYVGDVQIDVEVKYFCKAGVKGMQLHGVLRVIL<br>EPLIGDLFPVGAUSMFFIRRPDLINWTGMTNLLDIPGLSSLS<br>TMIMDSIAAFLVLPNRLVLPVLPDQDVAQLRSPLPRGIIRIHL<br>LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN<br>PQWGETYEVVHEVPGQEIIEVEVFDKDPDKDDFLGRMKLDVGKV<br>LQASVLDWFPPLQGGQGVHLRLLEWLSLLSDAEKLEQVLQWNWG<br>VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKGNKEPNP<br>MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV<br>KDDSRALTGLALTPLARLLTAPELILDQWFQLSSSGPNSRLYM<br>KLVMRILYLDSEICFPTVPGCCPGAWDVDSNPQRGSSVDAPPR<br>PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY<br>VKLKLGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF<br>DKDLDDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRHLRL  |

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|------------|--|--|--|
|            |  |  | ERLTPRPTAAEEVLQVNSLIQTQKSAELAAALLSIYMERAE<br>LPLRKGTKHLSPYATLTIVGDSSHKTITISQTSAPVWDESASF<br>RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCDRWFTL<br>SSGQGQVLLRAQLGILVSQHSQVEAHSHSYSHSSSSLSSEPELS<br>GGPPIHTSSAPEV\RQRLTHVDSPLAPAGPLGQVKLTWYYSE<br>ERKLVSIHVHGRSLRQNGRDPDPYVSLLLLPDKNRGCTKRRTSQ<br>KKRTLSPEFNERFEWELPLDEAQRKLDVSVKSNSSFSREREL<br>LGKVQLDLAETDLSQGVARWYDLMDNKKDKGSS   |
| 5428       | 3  | 1839   | SSRERLSACATAPPVWVSSRPAPQALQRPQKMWEDGAELED<br>LVHFSVSELPSRGYGVMEIIRRGKLCVTLKIGDHKFSARHIV<br>LAASIPYFHAMFTNDMECKQDEIVMQGMDPSALEALINFAYNG<br>NLAIQQNVQSLMGASFLQLQSIKDACCTFLRERLHPKNCGLV<br>RQFAETMMCAVLYDAANSFIHQHFVEVSMSEFLALPLEDVLEL<br>VSRDELNVKSEEQVFEAALAWVRVYDREQRGTFL\RLQSNIRLL<br>PCRPPQLSDRVQDDLVRCCHCKRDLVDEAKDYLLMPERRPHLP<br>AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVDFPIANCWER<br>CRPMTTARSRVGVAVVNGLLYAIGGYDQQLRLSTVQAYNTETDT<br>WTRVGMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSVVETYSPE<br>TDKWTVVTSMSNSR\GVTVFEGRIYVSGHDLQIFSSVZEH<br>YNHHTATWHPAGMLNKRRCRGAASLGSKMPVCGGYDGSGLFI<br>AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGPAVGRLYAVWGV<br>TGQSNL\SSVGDVLTPELTCWTFM\APMACHEGGVGVGCIPLLT<br>I |
| 5429       | 828  | 202  | RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF<br>AQRRERFHRFQPTYPYLQHEIDLPTTISLSDGEEPPPYQGCTLQ<br>LRDEPQQLNRESVRAPPNRTIFDSDLMSARLGGPCPPSSNS<br>GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFHQQSSGPPSL<br>LEGTRLHHTHIAPLESAAIWSKEDKQKQKHPL   |
| 5430       | 441  | 1507   | QKRRKRRRKIMKTIQPKMHSISWAIPTGLAALCLFQGVVPRS<br>GDATFPKAMDNTVRQGESATLRCTIDNRVTRVAWLNRSITLYA<br>GNDKWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPYTCSVQTDN<br>HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEP<br>TVIWRHISPKAVGVPSEDEYLEIQGITREQSGDYECASNDV\A<br>APV\VRVVKVTVNPYPYISEAKGTGVPVQKGTQLQCEASAVPSA<br>EFQWYKDDKRLI\EGKKGKVENRPFSLKLIFFNVSEHDYGNVT<br>CVASNLGHTNASIMLFGPGAVSEVSNGTSSRRACGVLLPLLV<br>HLLKF   |
| 5431       | 2  | 1312   | AAAAPGSRRRRPLPDRPHMAHGYEAPPPAPRSPAWRARSKPV\<br>LPGITINP\TIAEGPSP\TSEGASEANLVDLQKLELELDEQQ<br>KKRLEAFLTQKAKVGLKDDDFERISELGAGNGGVVTKVQHRPS<br>GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGYGAFY<br>SDGEISICMEHMDGGSLLDQVLKEAKRIPEEILGKVSIAVLRGLA<br>YLREKHQIMHRDVKPSNVLNVRGEIKLDFGVSGQLIDSMANS<br>FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPPIPP<br>DAKLEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP<br>AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA<br>DLKMLTNHTFIKRSEVEEVDFAWLCCTLRNLNQPPTPTTAV   |
| 5432       | 2  | 1312   | AAAAPGSRRRRPLPDRPHMAHGYEAPPPAPRSPAWRARSKPV\<br>LPGITINP\TIAEGPSP\TSEGASEANLVDLQKLELELDEQQ<br>KKRLEAFLTQKAKVGLKDDDFERISELGAGNGGVVTKVQHRPS<br>GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGYGAFY<br>SDGEISICMEHMDGGSLLDQVLKEAKRIPEEILGKVSIAVLRGLA<br>YLREKHQIMHRDVKPSNVLNVRGEIKLDFGVSGQLIDSMANS<br>FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPPIPP<br>DAKLEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP<br>AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA<br>DLKMLTNHTFIKRSEVEEVDFAWLCCTLRNLNQPPTPTTAV   |
| 5433       | 360  | 1885   | SVQEDKVGFEFLHLCSSWRARACPTWPHC/CTGLLECLGFAGV<br>LFGWPSPVLFVFKNEDYFKDLGCPDAGPIGNATGQADCKAQDERF<br>SLIFTLGSFMNNFTFPTGYIFDRFKTTVARLIAIFFYTTATLI  |



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|------------|--|--|--|
|            |  |  | IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI<br>ITLYNGAPDSSSAVFLIILKLYEKGISLR/VLLHLHLCLQYLAC<br>STHFPPDAPGAHPIPTAPQLQNLVPVFWHHKKGREG/QQLSMKT<br>GYSQSSSFQRRKRPQGGRSRNSAPSGATL/CSRRFAWHLVWL<br>SVIQLWHYLFITGLNSLLTNMAGGDMARVSTYTNAFAFTQFVGL<br>CAPWNGLLMDRLKQKYQKEARKTGSSTLAVLCSTVPSLALTSL<br>LCLGFALCASVPILPLQYLTPILQVISRSFLYGSNAFLTLAEP<br>SEHFGKLFGLVMALSAVVSLLQFPITFLIKGSLQNDFFVNVVMF<br>MLAILLTFHFPFLVYRECRWKESSPAIA   |
| 5434       | 66   | 652  | RYAALIISLIQHLWLRNQHCSRVCVIMSFAQSAAGLNWLF/GSGK<br>HGFPLGCSQYPACDYVRPLKSSADGHIVKVLGQVCPACGANLV<br>LRQGRFGMFIGCINYPECEHTLIDKPDETAITCPCRTGHLVQ<br>RRSRVYKTFHSCDRYPECQFAINFKPIAGECECHYPLLEKKT<br>AOGVKHFCASKQCGKPVSAE   |
| 5435       | 4704   | 1597   | PGDSSQRLAEMSNKAKRKHAKMRNQTNTVLTSSGFVADRGVKH<br>HSGGEKPFQAQKQEPHPTSRQRTVNPVHSLPDPEVNRQSSSK<br>GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAASISAMLKAV<br>TQKSSNSLVFQTLPRHMRMRAMSHNVKRLPRRLQEIQAQKEAKA<br>VHQKKEHSKNKCHKARRCHMNRLEFNRRQKKNWLETHIWHAK<br>RFHMVKKWGYCLGERPTVKSHRACYRAMTNRLQDLQSYCCLE<br>LKGKEEELKALSGMCNIDTGLTFAAVHCLSGKRQGSVLVYRVN<br>KYPREMLGPVTFIWKSRQTPGDPSESRLWHLHTLQDILEE<br>IKAACQCVPEIKSAVCIADPLPTPSQESQTELPDEKIGKKRRK<br>KDDGENAKPIKKIIGDGTDRDPCLPYSWISPTTGIIISDLTMMEN<br>RFRILGIPLSHSILTEAIIKAASVHTVGEDTETPHRWIETCKKP<br>DSVSLHCRQEAIFELGGITSPAEPAGTILGLTVGDPRINLPQ<br>KKSALPNPEKQDNEKVRQLLLEGVPECTHSFIWNQDICKSV<br>TENKISDQDLNMRSELLV2GSQLILGPHESKIPIILLIQPGKV<br>TGEDRLGWGSGWDLPLKQWGMFPIPIYRGVRVGGKESAVH<br>SQYKRSPNVPGDFPDPCAGMLFAEEQAKNLEKYKRRPAPKRPN<br>YVKLGTLPFCPPWEQLTQDWESRVQAYEESPVASSPNGKESDL<br>RRSEVPKAMPKKTQPSDEVGTSIEHPREAEVMDAGCQESAG<br>PERITDQEAENHVAATGSHLCVLRSRKLLKQLSAWCGPSSSDS<br>RGRRRAPGRGQGLTREACLILGHFPRALVWVSLSLSKGSPE<br>PHTMICVPKEDFLQLHEDWHYCGPQESKHSDFRSKILKQKEK<br>KKREKRQKP\GRASSDGPAGEEPVAGQEAALTGLWSGPLPRVTL<br>HCSRTLGLGFVTQGDFSMAVGCGEALGFVSLTGLLDMSSQPAAG<br>RGLVLLRPPASLQYRFARIAIEV |
| 5436       | 1781   | 635  | ASDSIPWSEARTTRKLAQRGCQWSLPERMPLVVFCLPYSGKSR<br>RAEELRVALAAEGRVYVDDAAVLGAEDPAVYGDSAREKALRG<br>ALRASVERRLSRHDVILDSLNYIKGFRYELY\CLARAARTPLC<br>LVYCVRPGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA<br>GSSVLRRELHTADSVVNGSAQADVPEKELEREBSGAESPALVTPD<br>SEKSAKHGSAFYSPLEALTLRFEAPDSRNRWDRPLFTLVGL<br>ESPLPLAGIRSALFENRAPPHQSTQSQPLASGSFLHQLDQVTS<br>QVLAGLMEAQSAVPGDLLTLPGTTEHLRFTRLTMAELSRRLR<br>QFISYTKMHPNNENLPQLANMFLQYLSQSLH  |
| 5437       | 739  | 1672   | CQEAASEFGGPLHTPAMFLRLGGWLPWPWGRKKPMRPDPYPPE<br>PRRVDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRASE<br>PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR<br>WDHVDSGGTRRPVSPGGL\GVPGGAPLEKPGREKLLGWLR<br>GEPCAPSRYLGGPEECIQISTNLTILHLELLASALLALCSRPLR<br>AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA<br>CLFGLLQALVLAVSLREPNGDEAATDWRSEGLEREQEQRGDPG<br>KGL   |
| 5438       | 2443   | 1152   | TKPRKRRHPASQQRQRPWSSDSTGDLLARGKGRKEENKGS DRV<br>LAPPSLRPMQSEARQGPBLRAAKNLHFPQLALRRRLGQLSC<br>MSRPALKLRSWPLTVLYLLPFGALRPLSRVGVWEPVSRVALYKS<br>VPTLLSRAWGRNLQVELPHWLRRPVYSLYIWTFGVNMKEAAVE<br>DLHMYRNLSEFFRRKLKQARPVCGLHVSIPSDGRILNFGQVK<br>NCEVEQVKGVTYSLESFLGRMCTEDLPFPPAASCDSEKQNLVT  |

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|------------|--|--|--|
|            |  |  | REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGLMSVNP<br>GMARWIKELFCHNERVVLTDGDKHGFFSLTAVGAT\NWSIRIY<br>FDRDLHTNSPRHSKGSYNDFSFTVHTNREGVPMALRGEHLG/QS<br>FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGALGSL  |
| 5439       | 2443   | 1152   | TKPRKRRHQPASORQRPWSDDTGLLARGKGRKEENKGS DRV<br>LAPPSLRPMQSEARQGPRLRAAKWLFHFPQLALRRRLGQLSC<br>MSRPALKLRSWPLTVLYYLPFGALRPLSRVUGWRPVSRYALYS<br>VPTRLLSRAWGRNLNQVELPHWLRPPVSYLYIWTFGVNMKEAAVE<br>DLHYYRNLSSEFFRRRLKQPAPVCGLSHSVISPSDGRILNFGQVK<br>NCEVEQVKGVTYSLESFLGPRMCTEDLPFPAAASCDSEKQNLVT<br>REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGLMSVNP<br>GMARWIKELFCHNERVVLTDGDKHGFFSLTAVGAT\NWSIRIY<br>FDRDLHTNSPRHSKGSYNDFSFTVHTNREGVPMALRGEHLG/QS<br>FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGALGSL   |
| 5440       | 693  | 253  | EPITVTPDHRILVTMTIHV\QTFSFVNS\GQFPNYEMLKEEQEVA<br>MLGAPHNPAPPMTSTVIRSETSVDPHVVNSLFTLMTNTCLLG<br>FIAFAYSVKSRDRKMVGDDVTGAQAYASTAKCLNIWALILGIFMT<br>ILLIIPVLVVQAQR   |
| 5441       | 2  | 2054   | CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSFIN<br>NSDLWVANIETGEERRLTFCHQGLSNVLDPPKSGAVATFVIEEE<br>FDRFTGYNWCPTASWEGSEGLKTLRLIYEEVDESEVEIHPVSP<br>ALEERKTDYSYRPTGSKNPKIALKLAEFQTDGQKIVSTOEKE<br>LVQPFSSLPKVEYIARAGWTRDGKYAMAMFLDRPQQWLQVLVLL<br>PPALFIPSTENEEQ\RLASARAVPRNVQPVVVEEVTNVWINVH<br>DIFYPFQSEGEDELCLFRANECKTGFCILYKVTAVLKSQGYDW<br>SEPFSPGEQESLTNAIWNNEETKLVIYFQGTQDTPLEHHLVYVS<br>YEAAGEIVRLTTPGFSSHSCMSQNFDMFVSHYSSVSTPPCVHYV<br>KLSGPDDDPLHKQPRFWASMMELAKIHPHTRSDVRLYGMIYKP<br>HALQPGKKHPTVLFVYGGPQVLVNNFSFKGIKYLRLNTLASLGY<br>AVVVIDGRGSCQRLRFEGALKNQMGQVEIEDQVEGLQFVAKY<br>GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVM<br>AYDTGYTERYMDVPENNHQHYEAGSVALHVEKLPNEPNRLILH<br>GFIDENVHFFHTNLFVLSQLIRAGKPYQLQVALPPVSPQIYPNER<br>HSIRCPESGEHYEVTLLHFLQEYL  |
| 5442       | 1  | 3474   | CGQSRRRSPDMPEAKPAAKAPKGDAPKAPKEAPPKEAPAE<br>APKEAPPEDQSPTEAETGVLKPKDSVSVETGKDAVVVAKVNG<br>KELPDKPTIKWFKGKWLGLGSKSGARFSFKESHNSASNYTVEL<br>HIGKVVLDGRGYRLEVKAQDTCDSGCFNIDVEAPQDASGQSL<br>ESFKRTSEKSDTAGELDFSGLLKREVVVEEKKKKKKDDDLG<br>IPPEIWEILLKGAKSEYEKIAFYQGITDLRGLKRLKKAKEVVK<br>KSAFTKKLDPAYQVDRGNKIKLMVEISDPLTLKWPKNQGEIK<br>PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCTELFV<br>KEPPVLIVTPLEDQVQVFGDRVEMAVEVSEEGAQVMWMDGVEL<br>TREDSEFKARYRFPKDKGRHILIFSDVVQEDRGRYQVITNGGQCE<br>AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSEKVTGKWKYK<br>NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDTYFVDPGYAL<br>GSLSAKLNFLKVEYVVKQ\EPKPIPLGFASGGKTSNAD/IV<br>VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE<br>KRVDCCSFVIESAQREDEGRYTIKVTNPIGBDVASIFLQVVDVP<br>DPPEAVRITSVGEDWAILVWEPPMYDGGKPVGTGYLVERKKKGSQ<br>RWMKLNFEVFTBTYESTKMEGILYEMRFAVNAIGVSQPSMN<br>TKPFMPIAPTSEPLHLIVEDVTDTTLKWRPPNRIAGGIDGY<br>LVEYCLEGSEEWVPANTEPVSRGFTVKNLPTGARILFRVVGYN<br>IAGRSEPATLAQPVTTIREIAEPPKIRLPRHLRQTYIRKVGEQLN<br>LVVPFQKPRPQVWVTGKGAPLDTSRVHVRTSDFDTVFFVRQAA<br>RSDSGEYELSVQIENMKDTATIRRVVEKAGPPINVMVKEVWGT<br>NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVEYERNHTSC<br>TVSDLIVGNEYFRVYTNICGLSDSPGVSKNTARILKTGITPK<br>PPEYKEHDFRMAPKFLTPLIDRVVVGYSALNCAVRGHPKPKV<br>VWMKNKMEIREDPKFLITNYQGVLTNLNRRPSPFDAGTYTCRAV<br>NELGEALAECKLEVRVPQ |

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|------------|--|--|--|
| 5443       | 66   | 1003   | SRGQLDAGQSSEQHGGNRQPEQSRSSSSSSSPRRSRSAEPA<br>MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI<br>LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSFVKTDV<br>NKIEFFLEEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS<br>RPEANEALERGLLKTQLKDEYLSPLPDEIDENSMEIKFSTR<br>KFLDGNEMTLADCNLLPKLHIVKVVAKYRNFDIPKEMTGIWRY<br>LTNAYSREFTNTCPSDKEVEI\AYSQVAKRLHQVKSRLKEVS<br>FMSSP   |
| 5444       | 2  | 344  | SGPIGVITGAQMAKWLDRDYLSTFGGRRPPPPPTPDYTESDILRAY<br>RAQKNLDFEDPY*DESRLBDDPAGPGDSKNPGDAKYGSPKHRL<br>IKVEAADMARAKALLGGPGEELEADTEYLDPPDAQHPAPDDG<br>YMEPYDAQVWMSLEPGRGVQLYDTPYEEQDPETADGPPSGQKPR<br>QSRMPQEDERPADEYDQPEWKKDHISRAFAVQFDSPEWERTPG<br>SAKELRRPPPRSPQPAERVDPALPLEKQPFHGLNRAEAESLL<br>SLCKEGSYLVRLSETNPQDCSLSRSSQGFLHLKFARTRENQV<br>LGQSGPFPSVPELVLYSSRPLPVQGAHLALLYPVVTQTP*Q<br>*PDWGDRRPNGQVATGLPELWGAEPASAAHPGLHRRERHPEGLP<br>RAEKPGLRGPLGLREPLGAGPRGPWGLQEPRRCQVWFQAPAH<br>QGGGCGYQSQGSPGRPRGGAGSRH  |
| 5445       | 2364   | 486  | ILSRGFLGSVEICIQPLPASEPVLLLTWARRRWRETSRREPT<br>TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIEYSP<br>EEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANK<br>QRPVSRQVTCRLTQVLEDESDSFCRRHPGLGKAFPSGCSAVSE<br>ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTHGDSKSD<br>QSLPNASADSLGGSQEMVQRPQPHNRAGLDLPTIDTGYDSQPD<br>DVLGIQRLERPLPLTSVCYPQDLRPLRSREFFQPEPQRYPACA<br>QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDPYRAAYQQVIQ<br>ALPGQPLPGASVRGLHPVQKVI LNYPSPWDQERPAORDCSFPG<br>LPRHQDQPHQPPNRAAGPESLECPAELRPQVPQPPSPAAPR<br>PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLV<br>NGFQTAIDIFEDIRGIDIKWMERYLRDKTVMIIVAISPKYKQ<br>DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQSGMNFRIPLVLF<br>PNAKKEHVPTWLQNTHVYSWPKNKNILLRLLEEEYVAPRGP<br>LPTLQVVPL |
| 5446       | 972  | 161  | SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEKYELKEGO<br>TLDVKCDYTLEKFASSQAWQIIRDGEMPKTLACTERPSKNSH<br>VQVGRILEDYHDHGLLRVMVNLQVEDSGLYQCVIYQPPKEPH<br>MLFDRIRLVVTGFGSGTPGSNENSTONVYKIPPTTKALCPLYT<br>TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA<br>GGPLSKSLVPSVLFVAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA<br>KGGRR   |
| 5447       | 207  | 617  | MTARTLSLMASLVAYDDSDSEAEHAGSFNATGQKDTSGVAR<br>PPGQDFASGTLDPKAGAOPTKHGSCEDPGGYRLPLAQLGRSDR<br>GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHPASHMPLAAA<br>RFKQVKLSRNFPSKSFHAQSESETVGKNGSSFQKKCEDCVVY<br>TPRRLRQRLALSTETGKGKDVPEQGPAGRAPAPLYVGPVSEF<br>IQPYLNSHYKETTVPKVLPHLRGHRQPVNTIQWCPVLSKSHML<br>LSTSMCKTFKVVNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL<br>SGGDFDALHLTDLETGTLFSGRSDFRITTLKFHPKXDNIFLCG<br>GFSSEMKAWDIRTGKVMRSYKATIQQTLOILFREGSEFLSST<br>ASTRDSADRTIANDFRTSAKISNQIFHERFTCPSLALHPREP<br>FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG<br>GDLVLTGSADGRVLMYSFRTASRACTLQGHQACVGTIYHPVLP<br>SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL<br>KSPSPSKSLVLLCGRAMFQPATCPQLPALSK                          |
| 5448       | 194  | 1833   | MASKVTDIVWYQKKIGAYDQOIWEKSVEQREIKGLRNKPKKTA<br>HVKPDLDVLRGSAFAKAKPESPWTSLTITGIVRVVFFPFF<br>RWNLQVTSKVIFFWLLVLYLQVAAIVLFCSTSSPHSIPLTEVI<br>GPIWMLLLGTVHCQIVSTRTPKPELSTGGKRRRKLKAAHLEV<br>HREGDSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAFFLS<br>GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIONHEPQCET   |

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|------------|--|--|---|
|            |  |  | IRPEETAWNTGTLRNGPSKDTQRTITNVSDVSSSEEGPETGYSLRRHVDRTSEGVLNRNRKSHHYKKHYPNEJAPKSGTSCSSRCSSSRQDESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPCVKKEYRDDPPHQSHLPWLHSSHPGLEKISAIWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMVIIISFVVRVSLVWIFFFLLCVAERTYKQVGIM  |
| 5449       | 194  | 1833   | MASKVTDALVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTAHVKPDLDVLDVRGSFAFAKAKPESPWTSLTTKGIVRVVFFPFFFRWLQVTSKVIFFWLLVLYLQVAAIVLFCSTSSPHSIPLTVEVIGPINWMLLLGTVHCQIVSTRTPKPPPLSTGGKRRRKLRAAHLEVRHREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAFFLSGSKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIONHEPQCSTIRPEETAWNTGTLRNGPSKDTQRTITNVSDVSSSEEGPETGYSLRRHVDRTSEGVLNRNRKSHHYKKHYPNEJAPKSGTSCSSRCSSSRQDESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPCVKKEYRDDPPHQSHLPWLHSSHPGLEKISAIWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMVIIISFVVRVSLVWIFFFLLCVAERTYKQVGIM  |
| 5450       | 8136   | 1242   | GQQFASFFG*NHPEVTVAMALTDIDLQQLQFSMSQPEALLLLAAGPADHLLQLLYSGHLQVRLVLQGEELRLQTPAETLLSDSIPTTVLTVVEGWATLSVDGFLNASSAVPGAPLEVPGYGLFVGGTGTGLGLPYLRGTSRPLRGCLHAATLNGRSLRLPLTPDVHEGCAEEFASDDVALGFGSPHSLAAPPAGTQDEGTLEFTLTQSRQAPLAFQAGGRRGDPIYVDIFEGHLRAVVEKGGTVLLHNSVPVADGQPHEVSVHINAHRLAISVDQYPTHTSNRGVLSYLEPRGSLLLGGDLAEASRHLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMAAGCRLEEEYEDDAYGHYEAFTLAPPAWPAPELPEPCVPEPGLPPVFANFTQLLTISPLVVAEGGTANLEWRHVQPTLDLMEALRXSQVLPSTVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHDSGSDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPPHIIFFPHGSLMVILEHTQKPLGPEVFOAYDPSACEGLTFQVLGTSSGLPVERRDQGPGEPAEFSCRELEAGSLVYVHCGGPAQDLTFRVSDGLQASPPATLKVVVAIRPAIQIHRSTGLRLAQQSAMPILPANLSVETNAVGGQDVSVLFRVTGALQFGELOKHSTCGVEGAEWATQAFHQRDVEQGRVRYLSTDPQHAYDTVENLALEVQVQGEILSNLSFPVTIQRATVWMLRLLEPLHTONTQETLTTAHLEATLEEAGPSPTTFHYEVVQAPRKGNLQQLGTRLSDGQGFTQDDIQAGRVTYGTARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNVLLVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRGTDQKTTMVTSTFNEDLLRGRVLYQHDDSETTEDDIPFVATRQGESGDMAWEVVRGVFRVAIQPVNDHAPVQTIISRIHVARGRRLLTTDDVAFSDADSGFADALVLRKDLLFGSIVAVDEPTRPIYRFTQEDLRKRRVLFVHSGADRGWILQVSDGQHQAATALLEVQASEPYLRVANGSSLVVPGGGQGTIDTAVLHLDTNLDIRSGDEVHYHVTAGPRWGQLVRAGQPATAFSQDLDGAVLYSHNGSLSPEDTMAFSVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEIRRDQLEAAQEAAPPADIVFSVKSPPSAGYLVMSRQALADEPPSLDPVQSFSQEAVDTRGVLYLHRSRPEAWSDFSLDVASGLGAPLEGVLELEVLPAIIPLEAQNFVSPEGGSLTAPPLLRVSGPYFFT |

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|------------|--|--|--|
|            |  |  | LLGLSLQVLEPPQHGLQKEDGPQARTLSAFSWRMVEEQIRYV<br>HDGSETLTDSFVLMANASEMDRQSHPVAFVTVLPVNDQPPILT<br>TNTGLQMWEGATAPIPAEALRSTDGDSGEDLVYTIEQPSNGRV<br>VLRGAPGTEVRSFTQAQLDGGVLVFSHRGTLDDGGFFRLSDGEH<br>TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS<br>SAGTDPQLLLYRVVRGPQLGRFLHAQQDSTGEALVNFTQAEVYA<br>GNILYEHEMPPEPFWEAHDTELEQLSSPPARDVAATLAVAVSFE<br>AACQPRPSHLWKNKGLWVPEGQARITVAALDASNLLASVPSPQ<br>RSEHDVLPQVTQFPPSRGQLLVSEEPHAGQPHFLQSQLAAGQLV<br>YAHGGGTQODGFHFRHLQGPAGASVAGPQTSEAFITVRDYN<br>ERPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEQ<br>RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF<br>QLNSDGLASPLPMSLAVDILPSAIEVQLRALPEVPPALGRSSL<br>SQQLRVVSDREEPEAAVRLIQGPQYGHLLVGGRPSTAFSQFQI<br>DQGEVVFATNFSSSHDHFRVLALARGVNASAVNVTVRALLV<br>WAGGPWPGATLRLDPTVLDAEGLANRTGSPFRFLLEGPRHGR<br>VVRVPRARTEPGGSQVLEQFTQDDLEDGRGLGLEVRPEGRAPG<br>AGDSLTLLELWAGGVPPAVASLDFATEPYNAARPYSVALLSVPEA<br>ARTEAGKPESSTPTGEPGPMASPEPAVAKGGLSFLANMFVS<br>IIPMCLVLLALLALILPLLFLYLRKRNTGKHVDVQLTAKPRNGLA<br>GDTETFRKVEPGQAIPLTAVFGQGGPPGGQDPPELLQFCRTNPL<br>ALKNGQYVW |
| 5451       | 1  | 2274   | RDSEEQRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR<br>KNSEPGSPHSLEALRDAAPSQGLNPLLLFTKMLFIENFLFSPPLP<br>TPALICILTFGAAIFLWLITRPQVLPPLLDLNNQSVGIEGGARK<br>GVSQKNNDLTSCCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNP<br>PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW<br>IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ<br>KALVLIGNVEKGFTPSLVKIILMDPFDDDLKQRGEKSGIETLSL<br>YDAENLGKEHFRKPVPSPEDLSVICFTSGTGDGPKGAMITHQN<br>IVSNAAFLKCVHAYEPTDDVAISYLPDAHMERIVQAVVYS<br>CGARVGFQGDRIILLADDMKTLKPTLFPVPRLLNRIYDKVQNE<br>AKTPLKKFLLKLAVSSKFELQKGIIRHDSFWDKLIFAKIQDSL<br>GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT<br>FTLPGDWTSGHVGVPLACNYVKLEDVADMYFTVNNEGEVCIKG<br>TNVFKGYLKDPEKTQEAIDSDGWLHTGDIWRWLPNGTLKIIDRK<br>KNIFKLAQGEYIAPEKIENIYNRSQPVLIQFVHGESLRSSLVGV<br>VVPDITDVLPSFAAKLGKGSFEELCQNVVREAILDLQKIGKE<br>SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKEYFRTO<br>IDSLYEHIQD   |
| 5452       | 1833   | 1138   | SRVPSLCLSLSLSPSREP VAGAPGCGTAGPPAMATLWGGLLR<br>LGSLLSLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS<br>HIYNKNISQKDCDCLHVEPMPVVRGPDVEAYCLRCECKYEBSRS<br>VTIKVTIIYLSILGLLLYMVYLTVEPILKRRLFGHAQLIQS<br>DDDIGHQPFANAHDLARSRSRANVLNKVEYAQQRNKLQVQEQ<br>RKSVFDRHVLS  |
| 5453       | 111  | 1520   | PSIPAAVPQSAPEPHREETVTATATSQVAQQPPAAAAPGEQAV<br>AGPAPSTVPSSSTSKDRPVSPSLVGSKEEPPPARSGSGGSAKE<br>PQEERSQQQDDIELETKAVGMSNDGRFLKFDIEIGRGSFKTVY<br>KGLDTETTVEVAVCELODRKLTKSERQRFKEEAENLKGLOHPNI<br>VRFYDSWESTVKGKKCIVLTELMTSGTLKTYLKRFKVMKIKVL<br>RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD<br>LGLATLKRAFAKSVIGTPEFMAPEMEYEEKYDESVDVYAFGMCM<br>LEMATSEYPYSECQNAQIYRRVTSKVGPASFDKVAIPEVKEII<br>EGCIRONKDERYSIKDLLNHAFFQETGVRVELABEDDGEKIAI<br>KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVRS<br>YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*   |
| 5454       | 111  | 1520   | PSIPAAVPQSAPEPHREETVTATATSQVAQQPPAAAAPGEQAV<br>AGPAPSTVPSSSTSKDRPVSPSLVGSKEEPPPARSGSGGSAKE<br>PQEERSQQQDDIELETKAVGMSNDGRFLKFDIEIGRGSFKTVY<br>KGLDTETTVEVAVCELODRKLTKSERQRFKEEAENLKGLOHPNI  |

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|------------|--|--|--|
|            |  |  | VRFYDSWESTVKGKKCIVLVTLMSTGLTKTYLKRFKVMKIKVL<br>RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD<br>LGLATLKRRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGCMC<br>LEMATSEYPYSECQNAQIYRRVTSGVKPASFDKVAIPEVKEII<br>EGCIRQNKDERYSIKDLLNHAFQFQETGVRVELAEEDDGEKIAI<br>KLWLRIEDIKKLGKGYKDNEAIEFSFDLERNVPEDVAQEMVESG<br>YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*   |
| 5455       | 1359   | 377  | LTMVSPATRKSPLPKVKAMDPTTSTAILELLPGCLGVFGLFRLLQ<br>WVRGKAYLRNAVVTITGATSGLGRECAKVFAAGAKLVLCGRNG<br>GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAEIL<br>QCFGYVDILVNNAGISYRGTIMDTTVDDVKRVMETNYFGPVALT<br>KALLPSMIKRQGHIVAISIQGKMSIPFRSAYAASKHATQAF<br>DCLRAEMEQEIEVTVISPGYIHTNLSVNITADGSRVGMDDTT<br>TAQGRSPVEVAQDVLAAGVKKKDVILADLLPSLAVYLRTLAPC<br>LFFSLMASRARKERKSKNS   |
| 5456       | 2  | 2332   | CGAGLVAAGAVLVLYPASRAGERTVPSSPAPSSLPFLHSPGACG<br>TEVMDPQRSPLLEVKNIELKRPLIXAPSQLPLSGSRILKRRPD<br>QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTPVQTGGQTTA<br>QKVSCKTGPRCSTALATGLKNQKPVPAVPVQKSGTSGVPPMAGG<br>KKPSKRPAWDLKGQCDLNAELKRCRERTQTLDDQENQQLQDQLR<br>DAQQVKALGTERTTLEGLAKVQAQAEQGGQELKNLRACVLEL<br>EERLSTQEGVLQELQKKQVELQEERRGLMSQLEEKERRLOTSEA<br>ALSSSOAEVASLRQETVAQAALLTEREERLHGLEMERRLHNQL<br>QELKGNIRVFCRVRPVLPGEPPTPPGILLFPSPGGGSDPPTRL<br>SLSRSDERRGTLGAPAPPTRHDFSFRVFPFGSGQDEVFEETA<br>MLVQSALDGYPCIFAYGQTGSGKTFTEGGPGGDPQLEGLIPR<br>ALRHLFSVAQELSGQWYTSFVASVYVEIYNETVRDLLATGTRKG<br>QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNR<br>AVARTAQNERSSRSHSVFLQISGEHSSRGLQCGAPLSLVDLAG<br>SERLDPLGALGPGERERLRETQAINSSLTLGLVIMALSNKESH<br>VPYRNSKLTYYLQNSLGGSAKMLMFVNISPLEENVSESLNLR<br>ASKVEPSVLFQTAQSNRKVKTDPDLCVVCVCVCVCVCVCVP<br>MSMYRVRRGRVAGGCFIGWRAPCPRAIK |
| 5457       | 2  | 1540   | DDFVERRRWRTRTCLVRSPPHVPVCGHACSWNGGSLDPLKGT<br>LLRSABRLMRKVKLRLDKENTGSWSRFSLSNSEGAERMATTGTP<br>TADRGDAAATDDPAARFQVQKHSWDGLRSI IHGSRKXSGLI<br>VKNKAPHDFQFVQKTDESGPHSHRLYYLGMYPYGSRENSLYSEI<br>PKKV RKEALLLSWKQMLDHFQATPHHGVYSREBELLRERKRLG<br>VFGITSYDFHSESGFLFQASNSLPHCRDGGKNGFMVSPGPGCV<br>SPMKPLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIET<br>GEERRLTFCHQGLSNVLD DPKSAGVATFVIEEFDRFTGYW<br>WCPTASWEGSEGLKTLRI LYEEVDESEVEV IHVPSPALEER<br>KTD SYRYPRTGSKNPKIALKLAEFQTD SQGKIVSTQEKELVQ<br>PFSSLPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQVLVLLP<br>PALFIPSTENEEQAASLCQSCPQECPAVCGVRGGHQRDLQCS  |
| 5458       | 6642   | 4022   | FVPGLEPQWEPAPQPSATMSAPSEEEYARLVMEAPQEWLRAEV<br>KRLSHELAEATTREKIQAAEYGLAVLEEKHQLKQFEELEVDYEA<br>IRSEMEQLKEAFQOANTHKKVAADGESREESLIQESASKEQYY<br>VRKVLLELQTELKQLRNLVLTNTQSENERLASVAQELKEINQV<br>EIQRRLRDDIKYKFREARLLQDYSELEENISLQKQVSVLRQ<br>NQVEFEGLKHEIKRLEETEYLSQLEDAIRLKEISERQLEBALET<br>LKTEREQKNSLRKELSHYMSINDSFYTSHLHVS LDGLKFSDDAA<br>EPNNDAAELVNGFEHGLAKLP LDKNTSTPKKEGLAPPSPSLVS<br>DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKLEHTRG<br>SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRD<br>SHEDGDYIEVDINGPEILACKYHVAVAEAGELREQLKALRST<br>HEAREAQHAEKGRYEAEQALTEKVSLEKASRDRELLARLEKEL<br>KKVSDVAGETQGSLSVAQDELVTPSEELANLYHHVCMCN<br>NETPNRVMLDYYREGQGGAGRTSPGRTSP EARGRRSPIL<br>LPKGLLAPEAGRADGGTGDSFSPGSSLPSP LDP<br>RREPNIYNLIAIIRDQIKHLQAAVORTTELSRQRIASQELGPAVDK<br>DKEALMBEILKLSLLSTK  |

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|------------|--|--|--|
|            |  |  | REQITTLRTVEKANKQTAEEVALANLKSKEYENKAMVTETMMKLR<br>NELKALKEDAATFSSLRAMPATRCDEYITQLDEMQRQLAAAEDE<br>KKTLSLLRMAIQKQLALTQRLLELLELDHEQTRRGRAKAAPKTK<br>PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD   |
| 5459       | 316  | 1262   | RGGHRLSGMASNFNDIVKQGVVIRSRRLGIYQRCMLVFKKASS<br>KGPKRLEKFSDEAAAYFRCHYKVTETLNNVKNVARLPKSTKKHAI<br>GIYFNDDTSKTFACESDLEADWCVKVLMCEVGTINIDISLGE<br>DLATGVVEREQSERFNVYIMPSPNLGCMGECALQITYEYICLW<br>DVQNPVRKLISWPLSALRRYGRDITWTFEAGRMCEGGLFIF<br>QTRDGEIYQKVHSAALAEQHERLLQSVKNSMLQMKMSERAA<br>SLSTMVPLPRSAWQHITRQSTGQLYRLQDVSSPLKLHRTETF<br>PAYRSEH   |
| 5460       | 45   | 2097   | RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP<br>GLGLAEMPSCGACTCGAAVRLITSSLSAQRGISGGRIHMSVL<br>GRLGTFTETQILQAPLRSFTETPAYFASKDGIKSGSGDGNKKS<br>ASEGSSKKS GSGNSGKGNQLRCPKCGDLCTHVETVSSSTREVK<br>CEKCHFFVVLSEADSKKSIKEPESAAEAVKLAFOQKPPPPPK<br>KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQA<br>VEKQTSLTPRELEIRREDEYRFTKLLQIAGISPHGNALGASMQ<br>QQVNOQIPQEKRGGEVLDSHDDIKLEKSNILLGPTGSGKTL<br>AOTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIKLLQDANYN<br>VEKAQQGIVFLDEVKIGSVPGIHQLRDVGGEGVQGGLLKLE<br>TIVNVPKNSRKLRGETVQVDTTNI LFVASGAFNGLDRIISRRK<br>NEKYLFGTTPSNLGKGRRAAAADLANRSGESNTHQDIEEKDRL<br>LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR<br>NAVIPQYQALFSMDKCELVNTEADALKAIALERKTGARGLRS<br>IMEKLLLEPMFEVFNSDIVCCEVDKEVVEGKPEGYIRAPTKES<br>SEEEYDSGVVEEGWPRQADAANS  |
| 5461       | 1481   | 160  | INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD<br>SHRLPGDCFLLLVLLLYAPVGPCLLVRLFLGIHVFVLSALPD<br>SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH<br>NIVNLLTTCSTPLLSPPSFCWSRGFMEMNGRGLVESLKRFC<br>ASTRLPPTPLLLFPEEEATNGREGLLRFSSWFFSIQDVVQPLTL<br>QVQRPLVSVTVSDASWVSELLWSLFPVFTVYQVRNLRPVHRQLG<br>EANEFEALRVQQLVAKELGQTGTRLTADKAEMKQRHPRLRP<br>QSAQSSFPSPGQSPDVQATLAQRVKEVLPHVPLGVIQRLAK<br>TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASAKFPSSGPV<br>TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD   |
| 5462       | 663  | 3353   | KIKERQMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA<br>RLSNGSFSAPSLTNSRGSVHTVSFLQIGLITRESVTIEAQLSL<br>SAVKDLVCSIVYQKFEPCGFFGMYDKILLFRHDMNSENILQIT<br>SADEIHEGLDVEVLSALATVEDFQIRPHTLYVHSYKAPTFCDY<br>CGEMLWGLVRQGLKCEGCGLNHYHRCFAFKIPNNCSGVRKRLSN<br>VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI<br>WMEKVMVCRVKVPHTFAVHSYTRPTICQYCKRLKGLFRQGMQC<br>KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDIDIPMDIDN<br>NDINSOSSRGLDDTEEPSPPEDKMFLLDPSDLDERDEEAVKTI<br>SPSTSNNIPLMRVVSQIKHTKRKSTMTVKEGWMVHYTSRDNLRK<br>RHYWRDLSKCLTLFQNESGSKYKEIPLSEILRISSPRDFTNIS<br>QGSNPHCFEIIITDMVYFVGENNGDSSHNPVLAATGVGLDVAQS<br>WEKAIRQALMPVTPQASVCTSPGQGDHDKDLSTSISVSNCQIQE<br>NVDISTVYQIFADEVLGSGQFGIVYGGKHKRKTGRDVAIKVIDKM<br>RPTKQESQLRNEVALQNLHHPGIVNLECMFETPERVFMVEK<br>LHGDMLEMILSSEKSRLPERTKFMVTQILVALRNLFKNIVHC<br>DLKPNVLLASAEFPQVKLCDFGFARIIIGKSFRRSVVGTTPAY<br>LAPEVLRSKGYNRS LDMWSGVIIYVSLSGTFFFNEDDEDINDQI<br>QNAAFMYPNPWREISGEAIDLINLLQVKMRKRYSDKSLSH<br>WLQDYQTLWDLREFETRIGBRYITHESDDARWEIHAYTHNLVYP<br>KHFIMAPNPDDMEEDP |
| 5463       | 237  | 1012   | LLSVMTTTSRCSHLPEVLDPDCTSSAAPVVKTVEDCGSLVNGQPQ<br>YVMQVSAKDQQLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL   |

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|------------|--|--|--|
|            |  |  | LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCCHPFAVERKPR<br>PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGWLCLRGAV<br>DHLHFSSRLAEAVGLIALTVALFTIYLFWTLSVFRYHCRLYNEW<br>RTNQRVILLIPKSVNVPNSQPSLLGLHSVKRNSKETVV   |
| 5464       | 195  | 677  | SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL<br>GASILSKIILGDTTLKLQIWDTGQBRVRSVMSTFYKSGDGC<br>LAFDVTDLSEFALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA<br>DRKYQSILENHLTESIKLSPDQSRRC   |
| 5465       | 5278   | 3348   | KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQGGPAAVEA<br>VNVFHHLPYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK<br>PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHLDNLRPSLTPV<br>KELKEPVGQIVCTDKGILAVEQNKVLIPTWNTKFAWGADLSC<br>RLGTYESDKAMTYECLSEWGQILCAICPNKLVITGGTSTVVC<br>VWEMGTSKEKAKTVTLKQALLGHTDVTTCATASLAYHIIVSGSR<br>DRTCIWDLNKLISFLTQLRGHRAPVSALCINELTGDIVSCAGTY<br>IHVWSINGNPISVNTFTGRSQIICCCMSEMNEWDTQNVIVTG<br>HSDGVVRFWRMEFLQVPETFAPEPAEVLMEQEDCPAQIGQEAQ<br>DESDSDSEADEQSISQDPKDTSPQSPSTSHRPRAASCRAAANC<br>TDSGSDSRRWSDQLSDEKDGFIIVNYSEGQTRAHLQGPLSH<br>HPNPIEVNRYSLKPGYRWERQLVFRSKLTMHTAFDRKDNHFA<br>EVTALGISKDHSLILVGDSRGRVFSWSVSDQPGRSAADHWVKDE<br>GGDSCSGCSVRFSLTERRHCRNCGQLFCQKCSRFQSEIKRLKI<br>SSPVVRCQNCYINLQHERGSEDGPRNC   |
| 5466       | 3  | 992  | HACAHASAHASGRVLRWRKRKRSVMGIQTSVPLLASLGVGLVTL<br>LGLAVGSYLVRRSRPQVTLDDPNEKYLLRLDDKTIVSHNTKRF<br>RFALPTAHTLGLPVGKHLYLSTRIDGSLVIRPYTPVTSDEDDQ<br>YVDLVIKVYLGKVHPKFPPEGKMSQYLDLSLVGDVVEFRGPSGL<br>LTYTGKGFHNQPNKKSPPPEPRVAKLGMJAGGTGITPMLQLIR<br>AILKVPEDFTQCFLFANQTEKDIILREDLEELQARYPNRFKLM<br>FTLDHPPKDWAYSKGFVTADMIREHLFAPGDDVLVLLCGPPPMV<br>QLACHPNLCLKGYSQKMRFTY  |
| 5467       | 2103   | 4  | GEALRVGTGRCDRLDPDQARIFIQKKOLEEDESVTAAHLKSRG<br>RSPRKIDQFCNNSNMVHGSVTFRDVAIDFSQBEWECLQPDQRTL<br>YRDVMLENYSHLISLAGSSISKPDVITLLEQKKEPMMVVRKETS<br>RRYPDELKYGPEKVPSPENDTSEVNLPKQVIKQISTTLGIEAFY<br>FRNDSYRQFEGLOGYQEGNINQKMISYEKLPTHTPHASLICNT<br>HKPYECKECGKYFSCGSNLIQHQS IHTGEKPYKCKEKGAFQLH<br>IQLTRHQKFHTGKTEFECKEKGAFNLPTQLNRHKNHTVKKLF<br>ECKEKGKSFNRSSNLTOHQS IHAGVKPYQCKEKGAFNRGNSLI<br>QHKKIHSNEKPPVCKEKGMAFRYHYQLIEHCQIHTGEKPFECKE<br>CGKAFLLTLKLVHRHQKIHTGEKPFECRECGKAFSLNLQNRHKN<br>IHTGEKPFECKEGKSFNRSSNLVQHQS IHAGIKPYECKEKGK<br>FNRGAHLIQHKKIHSNEKPPVCRECEMAFRYHCQLIEHSRIHTG<br>DKPFECQDCGKAFNRGSSLVQHQS IHTGEKPYECKEKGAFRLY<br>LQLSQHQKTHTEKPFECKEGKFFRRGSNLNQHRS IHTGKKPF<br>ECKEKGKAFRLHMHILRHQKLHTGEKPFECKEGKAFRLHMLI<br>RHQKLHTGEKPFECKEGKVFSLPTQLNRHKNHTGEKAS |
| 5468       | 225  | 2976   | SFLTDLFQSLAQLNLCQLYETDTTTLRLQAEKALVEFTNSPD<br>CLSKQQLLLERGSSSYSQLLAATCLTKLVSRNNPLPLEQRIDI<br>RNYVLNLYLATRPKLATFVTOALIQLYARITKLGFDCQKDDYVF<br>RNAITDVTRFLQDSVEYCIIGVTILSQTNEINQVSATAFLIEA<br>DTTHPLTKHRKIASFRDSSSLFDIFTLSCNLLKQASGKNLNLND<br>ESQHGLLMQLLKLTHNCLNDFIGTSTDESSDDLCTVQIPTSWR<br>SAFLDSSTLQSLTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA<br>SASPMDIAVQEGRLTWLVYIIGAVIGGRVFASTDEQDAMDGEL<br>VCRVLQMLNLDSRLAQAGNEKLELAMLSPFEQPRKIYIGDQVQ<br>KSSKLYRRLSEVLGLNDETMLVLSVFIGKIIITNLKYWGRCEPITS<br>KTLQLLNDLSIGYSSVRKLVKLSAVQFMLNHTSBHPSFLGINN<br>QSNLTDNRCTTFYTAGRLMLVLDGEDQYEQFMLPLTAAFE<br>AVAQMFSTNSFNEQEAKRTLVLVRLDRLGIAFAFAKTSFMMFL<br>EWIYPSYMPILQRAIELWYHDPACTTPVLKLMALVHNRSORLQ   |



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|------------|--|--|---|
|            |  |  | FDVSSPFGILLFRETSMITMYGNRIITLGEVPKDQVYALKLKG<br>ISICFSLKKAALSGSYVNFVFRLYGDDALDNLQTFIKLLLSI<br>PHSDLLDYPKLSQSYSLLEVLTDHMFIALEPHVIMYILSS<br>ISEGLTALDMVCTGCCSCLDHIVTYLFPQLSRSTKKRTTPINQ<br>ESDRFLHIMQHPMIQQLSTVLNIIIFEDCRNQWSMSRPLLG<br>LILLNEKYFSDLRNSIVNSQPPEKQAMHLCFENLMEGIERNLL<br>TKNRDRFTQNLASFRREVNDMSKNSTYGVNSNDMMMS   |
| 5469       | 134  | 2653   | DQEFETSLVFWHLPMGWLCSGLLPVSCVLVLLQVASSGNMKVLQ<br>EPTCVSDYMSISTCEWKMGPTNCSTELRLLYQLVFLLEAHTC<br>VPENNGGAGCVCHLLMDVVSADNYTLDLWAGQQLLWKGSKFES<br>EHVKPRAPGNLTVHTNVSDTLTLLTWSNPYPDPNYLYNHLTYAVN<br>IWSNDPADFRIYVNTYLEPSLRIAASTLKSIGSYRVRVRAWAQ<br>CYNWTWSEWSPSTKWHNSYREPFQHLGLGVSVSCIVILAVCLL<br>CYVSIKIKKEWWDQIPNPARSLVAIIQDAQGSQWEKRSRQ<br>EPACPKHWKNCITKLLPCFLEHNMKRDEDPHAAKEMPFQSGSK<br>SAWCPVEISKTLVWPESISVVRCELPEAPVECEEEEEVEEEKQ<br>SFCASPESSRDDFQEGREGIVARLTESLFLDLLEENGFCQDQ<br>MGESCLLPFSGSTSAHMPWDEFFSAGPKEAPPWGKEQPLHLEPS<br>PPASPTQSPDNLTCTETPLVIAGNPAYRSPNSLSQSPCPRSLG<br>PDPLLARHLEEEVEPEMPCVPQLSEPTTVQPEPETWEQILRRNV<br>LQHGAAPVSAPTSGYQEFVHVEQGGTQASAVVGLGPPGEAG<br>YKAFSSLLASSAVSPEKCGFGASSGEEGYKFPQDLIPGCPGDP<br>PVPVPLFTFGLDREPPRSQSSHLPSSSPEHLGLEPGEKVEDMP<br>KPPLPQEQTADPLVDSLQSGIVYSALTCHLCGHLKQCHQEDGG<br>QTPVMASPCCGCCCGDRASPPTPLRAPDPSGGVPLEASLCPA<br>SLAPSGISEKSKSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM<br>RVS |
| 5470       | 17   | 1418   | TACRIRTSINRGIAAVKRDVEMLASYGALSLMKFFETGPMSEF<br>KNUGLVFVNSKRDRTKAVLCMVVAGAAVFEHTLIAYSDLGYYI<br>INKLHVDES VGSKTRRAFLYLAAPFMDAMAWTHAGILLKHXY<br>SFLVGCASISDVIAQVVFVAILHSHLECREPLLIPILSLYMGA<br>LVRCTTLCGLYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA<br>LILATQRISRPVNLVSRDLGSSAATEAVAILTATYVGVHMP<br>YGLTEIRAVYPAFDKNPNPSNKLVSNTVTAAHIKKFTFVCMA<br>LSLTLCFVMFVTPNVSEKILIDIIGVDFAELCVVPLRIFSF<br>PVPVTVRAHLTGWMLTKKTFVLAPSSVLRIIVLIASLVLPYL<br>GVHGATLGVSLLAGFVGESTMDAIAACVYRKQKKKMEENESAT<br>EGEDSAMTDMPTTEEVTDIVEMREENE  |
| 5471       | 1868   | 658  | RSSAPPQQRAAAAATAAAAGVEMAAAAAQGGGGGEPRTTEGV<br>GGVPGVEVMVKGQPFDPVGPRTYQYIGEGAYGMVSSAYDHR<br>KTRVAIKKISPFHQTYCQRTLREIQILLRFRHENVIGIRDILR<br>ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR<br>GLKYIHSANVLRDLKPSNLLINTTCDLKI CDEGLARIADPEHD<br>HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS<br>NRPIFPKHYLDQLNHLGILGSPSQBDLNCI INMKARNYLQSL<br>PSKTKVAAKLFPSKSDSKALDLDRLMTPNPNKRITVEEALAH<br>YLEQYYDPTDEPVAEEPFTFAMELDDLPERLKEKELIFQETARFO<br>PGVLEAP   |
| 5472       | 1469   | 753  | LYVMARYLSDEEVAVSIDRLCKANGRSPIPFGTVRI PGRARVR<br>DPQALWIFGYGSLVWRPDAFYSDSRVGFVRGYSRRFWQDFTFR<br>GSDKMPGRVVTLEDHEGCTWGVAYVQVQGEQVSKALKYLVNREA<br>VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGLGPAPEEA<br>IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA<br>VGTMLPCFCPTQALALV   |
| 5473       | 3  | 2119   | FMNVKLLIQDLEDIEQRVPMDAQYKIITKTAHLITKESPOEEC<br>KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLELEKQMTS<br>FYDSLKGINEIITVLEREAQSSALFKQKHQELLACQENCKKLT<br>LIEKGSQSVQKFVTLNVLKHPDQTRLQRQIADIHVAFQSMVKK<br>TGDWKKHIVETNSRLMKKFESRAELEKVLRIAQEGLEBEKGDPEE<br>LLRRHTEFFSQLDQRVLNAFKACDELTDILPEQEQQLQEA<br>KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAECECRTLDR   |

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|------------|--|--|---|
|            |  |  | KLMPQEGSEKIIKEHRVFFSDKGPHHLCERLQLEELCVKLPV<br>RDPVRDTPGTCHVTLLKELRAAIDSTYRKLMEDPKWKDYTSRFS<br>EFSSWISTNETQLKGIGKEAIDTANHGEVKKRAVEEIRNGVTKRG<br>ETLSWLKSRLLKVLTEVSSSENAQKQGDDELAKLSSSFKALVTLLS<br>EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQAEKILDTE<br>NLFEAQQLLLHHQOKTKRISAKKRDVQQQIAQAQQGEGGLPDRG<br>HEELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKETVVR<br>YLFQTGSSHERFLSFSLSLESLSELEQTKBFKRTESIAVQAEN<br>LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTEEBEYVIDK<br>S                       |
| 5474       | 2  | 780  | TPDVRQLQASRRGIASVSWCSPRWFAGEEMAPVKSGLLRQSTI<br>LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG<br>QECRDTQPPDGKSKCMLQIVCRDGTISLCAESTDDCLAWKET<br>LQDSRTNTAYVGSAMTDETSVVSPPPYTAYAAPEVGRITLS<br>LQQAQYGYGPYGAYPPGTQVYVAANGQAYAVPYQYPYAGLYGQQ<br>PANQVIIRERYRDNDSDLAGMLAGAAATGMALGSLFWVF   |
| 5475       | 2  | 506  | ARGWLESLSLTCQTPPPSPCLLHSPETFIHTMPPNLTGYRYF<br>VSKQNMEDYLQALNISLAVRKIALLLKPKDEIEHQGNHMTVRTL<br>STFRNYTVQFDVGVEFEEDLRSVDGRKCTIVTWEEHLVVCVQK<br>GEVFNRRGWRHLEGEMLYLELTARDAVCEQVFRKVR   |
| 5476       | 192  | 1457   | SDMSLLDCFCSTRTQVESLRPEKQSETSIHQYLVDEPTLSWSR<br>PSTRASEVLCSTNVSHYELQVEIGRFPDNLTSVHLARHTPTGTL<br>VTIKITNLNENCNEERLKAQKAVILSHFFRHPNITYTWTFTVG<br>SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNLFAGAVRGLN<br>YLHQNGCIHRISIKASHILISGDLVTLGSLSHLSLVKHGQRHR<br>AVYDFPQFSTSVQPLSPPELLRQDLHGYNVKSIDIYSGITACEL<br>ASGOVPFQDMHRTQMLLQKLKGPYPSPLDISIFPQSESRMKNSQ<br>SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC<br>LQODPEKRPASASSLLSHVFFKQMKKEESQDSILSLPPAYNKPSI<br>SLPPVLPTWTEPECDFPEKDSYNEF |
| 5477       | 3  | 1044   | RCNSRLRYSHDELQPLRPLPELFETGRQLLDEVEVATEPAGSRI<br>VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDELEIASTDLKYLLV<br>PAFQGALTMKQVNPFSKRLDHLQRAHEFINYLTCCHCYHVAEF3<br>LPKTMNNSAENHTANSSMAYPSLVAMASQRAKIQRKQKKELE<br>HRLSAMKSAVESGQADDERVREYLLHLQRWIDISLEETESIDQ<br>EIKILRERDSSREASTSNSSRQERPPVKPFIILTRNMAQAKVFGA<br>GYPSLPTMTVSDWYEQHRKYGALPDQGIKAAPPEFRKAAQQE<br>EQEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG   |
| 5478       | 2  | 835  | KTVRIWVPNVKGESTVFRAHTATVRSVHFCSGQSFTASDDKT<br>VKVWATHRQKFLFSLSQHINWVRCAKFS PDGRLIVSASDDKT<br>LWDKSSRECVHSYCEHGGFVTVDFHPSGTCIAAAGMDNTVKVW<br>DVRTHRLQLHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILD<br>MEGRLLYTLHGQGPATTVAFSRTGEYFASGGSDEQVMVKS NF<br>DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC<br>LENQQLIMQRATP   |
| 5479       | 2  | 835  | KTVRIWVPNVKGESTVFRAHTATVRSVHFCSGQSFTASDDKT<br>VKVWATHRQKFLFSLSQHINWVRCAKFS PDGRLIVSASDDKT<br>LWDKSSRECVHSYCEHGGFVTVDFHPSGTCIAAAGMDNTVKVW<br>DVRTHRLQLHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILD<br>MEGRLLYTLHGQGPATTVAFSRTGEYFASGGSDEQVMVKS NF<br>DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC<br>LENQQLIMQRATP   |
| 5480       | 444  | 1952   | LSLTSRMEEAEVLVKGRLQAITDKRKIQEERISQKRLKIEEDKLKH<br>QHKKKALREKWLDDGISSCKEQEEMKKQNDQDQHQIQVLEQSI<br>LRLEKEIQDLEKAEQISTKEEAALKKLSIERTTEDIIRSVKV<br>EREERAEESIEDIYANIPDLPKSYIPSRRLKEINEEKEDDEQNR<br>KALYAMEIKVEKDLKTGESTVLSSIPSPDDFKGTGKIKVYDDGQ<br>KSVYAVSSNHSAAAYNGTDGLAPVEVEELLRQASERNKSPTEYH<br>EPYANPFYRPTTPQRETVPGPFPQERIKIKTNGLGIGVNESI<br>HNMGNGLSEERGNFNHISPIPPVPHPRSVIQAEEKLHTPQKR   |

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|------------|--|--|--|
|            |  |  | LMTFWHEESNVMDKAPSPKPRLSPRETIFGKSEHQNSSPTCQE<br>DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDEEDKKFLT<br>GYDGIHAELVVIDDEEEDEGEAEKPSYHPIAPHSQVYQPAKP<br>TPLPRKRSEASPHEKHKS   |
| 5481       | 3  | 1422   | NSPGSVCLCQCVCPSLLHCLPPLLLLLLPLLLHESPOPPALRV<br>VATSSDRNFMNKHQKPVLTGQRFKTRKDEKEKFEPTVFRDITLV<br>QGLNEAGDDLEAVAKFLDSTGSRIDYRRYADTLFDILVAGSMLA<br>PGGTRIDGDKTKMTNHCVSANEDHETIRNYAQVENKLIRRYK<br>YLEKAFEDEMKLLLLFLKAPSETEQTKLAMLGILLNGTLPAT<br>ILTSLEFDSLVEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN<br>LDKRLLELPVNRQSVDFAKYFTDAGLKELSDFLRVQSLGTR<br>KELQKELQERLSQECPIKEVVLYVKEEMKRNLDLPETAVIGLLLT<br>CIMNAVEWNKKEELVAEQALKHLKOYAPLLAVFSSQGSSELILL<br>QKVQECYDNIHFMAKQKIVVLFYKADVLSEEAILKWKYEAHV<br>AKGKSVFLDQMKKFVFNWLNAREESESSEGEEN  |
| 5482       | 1492   | 528  | THVMTGHCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSRL<br>EGLQEKDSGPYSCSVNVQDKQKSRGHSIKTLELNVLPVPAPPS<br>CRLQGVPHVGANVTLSQSPRSKPAVQYQWDRQLPSFQTFPAPA<br>LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTELVSTGP<br>GAAVAVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA<br>IAPRTLWPWKSSDTISKNGTLSSVTSARALRPPHGPYPGALTP<br>TPSLSSQALPSRLPTTDGAHPQPIPIPGGVSSSGLSRMGAVP<br>VMVPAQSQAQSLV  |
| 5483       | 1  | 788  | FFPFKGCRAGRGNESEDYRKLEEMHQRFVLSERSKDDLQRLRLTRA<br>ENRIKQLEBDSSEEISRYQEMIQKLQNVLESERENCGLVSEORL<br>KLQENKQLRKETESLRKIALEAQKAKVKISTMEHEFSIKERG<br>FEVQLREMEDSNRNSIVELRHLLATQKKAANRWKEETKKLTESA<br>RIRNNLKSLSRQKLHTQELLQLEMANEKVAENEKLIILEHQB<br>KANRLQRRLSQAEERAASASQQLSVITVQRKAASLMNLENI  |
| 5484       | 3  | 1997   | IMADMEDLFGSDADSEAEKRSKDSGSDSDSDOENAAAGSNAGS<br>ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDN<br>SEASERSDHEDNDPSDQHSSEAPNDDEDEGHRSDGSHHSE<br>AEGSEKASDDEKKGREDKSDQSDDEKIQNSDDEERAQGSDEDK<br>LQNSDDDEKMQNTDDEERPQLSDDERQQLSEEEKANSDDERPA<br>SDNDEKQNSDDEEQQLSDDEKMQNSDDEPQASDEEHRHSD<br>EERQDHKSESARGSDSEVLRMKRNVAIASDSEADSDTEVPKD<br>NSGTMDLFGGADDISSGSDGDKPPTPGQPVDEGLPDQDQEE<br>PIPETRIEVEIPKVTDLGNDLYFVKLPNFLSVPRPFPDQYYE<br>DEFEDEMLDEEGRTLRKLKVENTIRWRIRRDEEGNEIKESNAR<br>IVKWSGMSLSHLGNEVFDVYKAPLQGDHNLHFIHQGTGLQQA<br>VFKTKLTFRPKSTDSATHRKMTLSLADRCSTQKIRILPMAGRD<br>PECQRTMIKKEERLRASIRRESQQRMRREKQHQGLSASYLE<br>PDYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE<br>EDKAQRLKAKKLTSDVRPNLFNSRGLSCTQBPETALNEELTDQ<br>AGTN |
| 5485       | 161  | 1074   | KRKILSSMMDSEAEKRPPILTSSKQDISPHITNVGEMKHLYCG<br>CCAAFNVAITFPQKVLFRQQLYGIKTRDAILQLRRDGFRLNLY<br>RGILPPLMQKTTTLALMFLGYEDLSCLLHKHVSAPFATSGVAA<br>VLAGTTEAIFTPLERVQTLQDHKHDKFTNTYQAFKALKCHGI<br>GEYRGLVPIILFRNGLSNVLFGLRGPIKEHLPTATTHSAHLN<br>DPICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFQKVFQKI<br>WLERDRKILNIFRGAHLNHYHRSLSWGIINATYEFLLKVI  |
| 5486       | 1404   | 142  | IPGSTISWSPAAAGRLSVCCRLHPASAMDLFGLDPEPERSPR<br>PAAGKEAQKGLPFLDPPASSTDSGSGGPLFDLPPASSGDS<br>GSLATISQMVKTEGKAKRKTSEEEKNGSEELVEKKVCKASSV<br>IFGLKGYVAERKGEREMQDAHVILNDITECRPPSSLITRVSY<br>FAVFDGHGGIRASKFAAQNHLQNLIRKFPKGDVISVEKTVKRC<br>LDTFKHTDEEFLQASSQKPAWKDGSTATCVLAVDNILYIANLG<br>DSRAILCRYNEBSQKHAALSLSKEHNPTQYEERMRIQKAGGNVR<br>DGRVLGVLEVSRSIGDQYKRCGVTSVPDIRRCQLTPNDRFILL  |

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|------------|--|--|--|
|            |  |  | ACDGLFKVFTPEEAVNFILSCLEDEKIQTREKSAADARVEAAC<br>NRLANKAVQQRGSADNVTVMVVRIGH  |
| 5487       | 535  | 182  | AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERTVLALLLAGLTA<br>LEANDPFANKDDPFYDWKNLQSLGICGGLLAAGIAAVLSGK<br>CKCKSSQKQHSPPVEKAIPITPGSATTG   |
| 5488       | 1072   | 259  | AMAAAGBPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETH<br>GHKFFIFGGGKGANQCVQAARLGAMTSMVKVGDSPGNDYIEN<br>LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL<br>NTEDLRAAANVISRAKVMVCQLEITPATSLAALTMARRSGVKTL<br>FNPAPAIADLPQFYTLSDVFCNESEASILTGLTVGSAADAGE<br>AALVLLKRGCCQVVIITLGAEGCVVLSQTEPEPKHIPTKVKAVD<br>TTVSPKI   |
| 5489       | 81   | 893  | GKGPVAAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK<br>LERDCRSPVEPWAAASPDALACLCHCQDLSSGAFPNRGVLGGV<br>LFPTVMVVIKVFVATSSGSIARKKQEEVVGFLANKIDFKELD<br>IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF<br>FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEEDVG<br>NLPEAQEKNEEGETATBETETIAMEGAEGEAEETAEGETE<br>GEDEDS  |
| 5490       | 81   | 893  | GKGPVAAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK<br>LERDCRSPVEPWAAASPDALACLCHCQDLSSGAFPNRGVLGGV<br>LFPTVMVVIKVFVATSSGSIARKKQEEVVGFLANKIDFKELD<br>IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF<br>FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEEDVG<br>NLPEAQEKNEEGETATEETEAMEGAEGEAEETAEGETE<br>GEDEDS  |
| 5491       | 204  | 1194   | GSAPRLSLGPTGAQARDPDWWARPPSRPYTOSKEDRPDTEGRSE<br>QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPSPHSEIETSC<br>LAELFEKAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP<br>SFFDFEGKQKWEAWKALGDSSPSQAMQEIYIAVVKLDPGWNFQI<br>PEKKKGAEANTGFGGPISSLYHEETIREEDKNIYDYCRENNIDH<br>ITKAISKNNVDVNVKDEEGRALLHWACDRGHKELTVLLQHRAD<br>INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDGLCP<br>EEVTGCKTVSLVLQRHTTGKA  |
| 5492       | 3  | 1896   | ASKNPLSAVCTTGIMSSLAVRDPAMDRLSLRVFVGNIPYEATEE<br>QLKDI FSEVGSVVSFRLVYDRETGKPKGYGFCYQDQETALSAM<br>RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIDSPYGD<br>IDPEDAPESI TRAVASLPPEQMFELMKQMKLCVQNSHQEARNML<br>LQNPQLAYALLQAQVVMRIMDPFIALKILHRKHIVTPLIPGKSO<br>SVSVSOPGPGPGPLCPGFNVLLNQNPAPQPQHLARRPVDKI<br>PPLMQTFPIQGGIPAPGPIPAAPVPGAGPGSLTPGGAMQPQLGMPG<br>VGPVPLERGVQMSDPRAPIPRGVTPGGLPPRGLGDAPNDPR<br>GGTLLSVTGEVEPRGYLGPPHQGPPMHASGHDTRGPSSEMERG<br>GPLGDPRLIGEPGPMDQGRPLPMDGRGGRDSRAMETRAMETE<br>VLETRVMERRGMETCAMETRGMEARGMDARGLEMGPVPSRGP<br>MTGGIQQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ<br>GTGMQAGIQGGGMQAGIQGVSIQGGGIQGGGIQAGSKQGGSQ<br>PSSFSFGQSQVTPQDQEKAAALIMQVLQTLADQIAMLPPEQRQSI<br>LILKEQIQKSTGAS |
| 5493       | 1  | 1876   | RAPMMTKAVPEZFRKPGRLTOALNSPLTWEHVWICVPGGTPDC<br>LTDTRVVRKPHLRRSASNGHVPGTPVYREKEDMYDEIIEKKSLH<br>VQKSDVDLMRTKLRLREENSRRKDRQIEQLLDPSSRGTDVFRILA<br>EKRPDASWVINGLKQRIKLLEQQCKEKDGTISKLQTDKMTTNLE<br>EMRIAMETYYEEVHRLQTLASSETTGKKPLGEKKTGAKRQKKM<br>GSALLSLRSVQELTEENQSLKEDLDRLVSTSPITSKTQGYVEW<br>SKPRLRLRIVELEKKLSVMESKSHAAEPVRSHPACLAASSAL<br>HRQPRGDRNDKHERLRGAVRDLKEERTALQEQLLQRLDLEVKQLL<br>QAKADLEKLEKAREGEEREREVLRERIQTLSKLQELQEM<br>KKBEKEDCEVPHKAQELPAPTSSRHCEDWPPDSSBEGLPFP<br>RSPCSDGRRDAAARVLQAQNVKYKHKKKAVLDEAAVVLQAARF   |

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|------------|--|--|--|
|            |  |  | GHLTRTKLLASKAHGSEPPSVFGLPDQSSPVPRVPSPIAQTGS<br>PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASRRRSASAT<br>HGDASSPPFLAALPDPSGPGQAVAPLPGDDVNSDDSDDIVIAP<br>SLPTKNFPV   |
| 5494       | 71   | 536  | RSKAKIGTPTREVPSTDMKVRRESSSSSLTHRPAPSPATPRLLGT<br>RRVLLGVSEGTGCADAMELVFLCSSLAPMVLASAAEKEKEMD<br>PFHYDYQTLRIGGLVFAVVLFSVGILLILSRCKCSFNQKPRAP<br>GDEEAQVENLITANATEPQKAEN  |
| 5495       | 273  | 2168   | DSLILLIQVDTMPFTLHLRSRLFSAIRSLILQKKPNIRNTSSMAG<br>ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLEPP<br>QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL<br>GCSFSLEEALAKAGLPRRDPAHSGAGAYKTTVPVTHAGFCCP<br>LVVTMRPIPKDKLEGLVRACCSLGGEGQGPVHMGDPBELLGKEL<br>SKPAYGDAMVCPGGEVPVFWPSPILSLGAVSSCETPLAFASIPG<br>CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ<br>KIRELESMIGIDPGNRGIGHLLCKDELKASLSLHARSVLIIT<br>GFPTHFNHEPPEETDGPQAVLVAFLQALEKEVAIIVDQRAWN<br>LHQKIVEDAVEQGVLTQIPILTYQGGSVEAAQAFCKNGDQPT<br>PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAK<br>IPGISSTGVGDGNGELGMGKVKAEVRRHRRHGDVIACDVEADFA<br>VIAGVSNWGGYALACALYILYSCAVHSQYLKAVGPSRAPGDOA<br>WTQALPSVIKBEKMLGILVQHKVRSVSGIVGMEVDGLPFHNT<br>AEMIQKLVDTTAQV   |
| 5496       | 3  | 2408   | QDTKMHETLYKGNITPOLNKNLTLSAATDVWAVYFSQFWIDYEG<br>MKSQKGRPISPVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT<br>SQSESSDLAGRLKRLKLLKEYYSTESEPLTNGGQKPSSTDFFR<br>FSPSSSEADHLLVHVHVKHVSQINHYQYLLLLFLHESLILSE<br>NLRKDVEAVTCSPASQTSICIGILLRSALALLHPVDQANTLK<br>SPVSESVSPVVDYLPTENGDFLSSKRRQTSRDINRIRSVTVNH<br>MSDNRSMSVDLSHIPKDPPLFKASDNTLQKGISFMDYLSDKH<br>LGKISEDESSGLVYKSGSGEIGSETSDKDSFYTDSSSVLNYRE<br>DSNILSFDSDGNQNILSSTLTSKNETIESIFKAEDLLPEAASL<br>SENLDISKEETPPVRTLSQSSLSGKPKERCPPNLAPLCVSYKN<br>MKRSSSQMSLDTISLDSMILEEQLES DGS DSHMFLEKGNKKNS<br>TNYRGTAESVNAAGANLQNYGETSPDAISTNSEGAQENHDDLMS<br>VVVFKITGVNGEIDIRGEDTEICLQVNVTPDQLGNISLRHYLC<br>NRPVGSQDKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ<br>CHIKNPFSTFLTSSLMNIQHFEDETATVMPMKIQVSNNTKINL<br>KDDSPRSSTVSLPAPVTVHIDHLVVERSDDGSFHIRDHMLNT<br>GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTS PGVPWPVSQS<br>ANFPPEFSDFTREQLMBENESLQELAKAKMALAEAHLEKDALL<br>HHIKKMTVE |
| 5497       | 1821   | 3308   | SISKLLKRRSNIDAYLLSNSCAFFAPRLFLSLASQIIREQQSPNV<br>CFIYKYSGFPSLECCQCHFVSPHSSCYINFFSPFPFVFCQLSN<br>GFSHYLSLSESHVGPPTGAGLFPCHLPASRLLPRTSVHLPDYAH<br>YTTIGPGMFPSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREP<br>PNGGGPTTASGPFAAAEEAQRPRSMTVSAATRPGEEMEACEELA<br>LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSOVS<br>DYDYFSVSGDQEQEFDKSSSTIPRNSDISQSYRRMFQAKRPA<br>STAGLPPTLGPAMVTPGVATIRRTPTSTKPSVRRGTIGAGPIPIK<br>TPVIPVKTPTPVDPGLPGVLPAPPDGPEERGEHSPESPSVGEPPQC<br>VTSMPSSMWSGQASVNPPLPGPKPSIPBEHRQAIPSEAEQDER<br>EPPSATVSPGGIPESDPAADLSPRDTTPQGEDMLNARRGVKLKKT<br>TTNDRSAPRFS   |
| 5498       | 2434   | 1492   | ILTHQEIFTGEXPCCEGKASIQMSHLSQKQIYSGENPFACKVCG<br>KVFSHKSNLTHEHFHTREKPFECNECGKAFSQKQYVIKHQNT<br>TGEKLFECNECGKFSQKENLLTHQKIHTGEKPFECDCGKAFI<br>QKSNLIRHQRTHTEKPFVCKEKGKTFSGKSNLTHEKIHIGEK<br>PFKCEGCTAFGQKKYLIKQNIHTGEKPYECNECGKAFSQRTS<br>LIVHVRHSGDKPYECNVCCKAFSQSSSLTVHVRSHTEKPKYGC<br>NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHIRH   |

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|------------|--|--|--|
| 5499       | 324  | 926  | QKITH<br>GFGQIGRGHKIITYPFSPRKSGRKGMAQSOGWVKRYIKAFCKGF<br>FVAVPVAVTFLDRVACVARVEGASMQPSLNPQGSQSSDVLLNH<br>WKVRNFEVHRGDIVSLVSPKNPEQKIKRVIALEGDIVRTIGHK<br>NRYVKVPRGHIWVEGDHGHGSHFSDNSFGPVSGLLHAHATHILW<br>PPERWQKLESVLPPELPPVQREEE  |
| 5500       | 1978   | 1286   | KPDWRLQNLFPRLYLWSSRFSGFGLKKRLQMDFKIEHTWDGFP<br>VKHEPVFIRLNPGRGVMMDISAFFRDPAPLGEFGKPFNELW<br>DYEVVEAFFLNDITEQYLEVELCPHGQHLVLLSGRNRVWQKEL<br>PLSPRVSRGETKWEKGAYLPWSYFPNNVTKFNSFAIHGSKDKS<br>YEALYPVPQHLQOQKPDFHCLEYFKSFNFNTLLGEEWKQPS<br>DLWLIKCDI   |
| 5501       | 2927   | 2226   | CRPPVSARVAPGHQGAAGSGRRPARVEVVDAAARPSSRPFLP<br>AAILMALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFFNVIA<br>SQQFSEDMIPTVCGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY<br>CRGVNAIVYMIDAADREKIEASRNELHNLDDKPOLQIGIPVLVGL<br>NKRDLNALDEKQLEKMNLSAIQDREICCYISCKEKNIDIT<br>LQWLIIHQSKSRRS   |
| 5502       | 3  | 824  | NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL<br>GKFFKGGSSSKSRAAPSQOEALVRLRETEEMLGKKQVEYLENRIQ<br>REIALAKKHGTQNKRAALQALKRKRFEKQLTQIDGLSTIEFQ<br>REALNSHTNTEVLNRNMGFAAKAMKSVHENMDLNKIDDLMEQIT<br>EQDIAQEISEAFSQRVGFGDDFDELMABELELEQEELNKKM<br>TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEDDD<br>IKQLAAWAT   |
| 5503       | 216  | 654  | KGVRRRGRVRSDESLSHLYFKMSFLLPKLTSKKEVDQAIKSTA<br>EKVLVLRFRGDEDPVCLQDDILSKTSSDLKMAIYLVDDVDT<br>AVYTQYFDISYIPSTVFFFGQHMKVVDYGGEDPALRSIKAVRRT<br>SPAGTLGSKPVNS  |
| 5504       | 58   | 3563   | QLSFSQAPVTFDDITVYLLQEEWVLLSQQKELCGSNKLVAPL<br>GPTVANPELFRKFRGPEPWLGSVOGQRSLLHHHPGKKQMGYMG<br>EMEVOGPTRESGQSLPPQKKAYLSHLSTSGHIEGDWAGNRKRL<br>LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL<br>IEGYTGPFKVELKYHAKSKAHMPCVNALAADPIWAARFRSIR<br>DPPGDVLASPELFTADCPFIYPGPGPLGGFDSMAELLPSRAEL<br>EDPGDGAIPAMVLDICISDLRQKEITDGIHSSSDINILYNDAVE<br>SCIQDPSAEGLESEVPVVFELPVVFEVAVYFTREEWGLDKR<br>QKELYRDMRMNYELLASLGPAAPKPDLSKLERRAAPWIKDPN<br>GPKWKGCRPPGNKKMVAVREADTQASADSALLPGSPVEARASC<br>CSSSICEEGDGPRIKRTYRPRSIQSWFGQFPWLVIDPKETKL<br>FCSACIERPNLHDKSSRLVRGYTGPFKVELKYHEVSKAHLRCV<br>NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYS IAYHSRPLN<br>DFEKILQLLQSTGTIVLGKYNRTACTQFIKYISETLKRILED<br>VRNSPCVSVLLDSSDASEQACVGIYIRYFKQMEVKESYITLAP<br>LYSETADGYFETIVSALDELDIFFRKPGWVVLGTDGSAMLSCR<br>GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLKVKCDRH<br>IRTVFKFYQSSNKRNLNELQEGAAPLEQEIIRLKDNLAVRWVASR<br>RRTLHALLVSWPALARHLQVAAEGGQIGHRAKGMKLKMRGFHF<br>VKFCHFLDPLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES<br>LRHQAGPKKEEFNASFKDGRHLGICLDKLEVAEQRFQADRERTV<br>LTGIEYLQQRFDADRPQLKQMEVFDTMAWPSGIELASFGNDDI<br>LNLARYFECSLPTGYSEEALLEEWLGLKTIQHLPPSMLCKNAL<br>AQHCRFPLLSKLMVAVVVCPISTSCCERGFKAMNRI RTDERTKL<br>SNEVLNMLMTAVNGVAVTEYDPPQAIQHWYLTSSGRRFSSHVYT<br>KACQVPARSPASARLKEEMGALYVEEPTQKPPILPSREAAEVL<br>KDCIMEPPERLLYPHTSQEAPGMS |
| 5505       | 3312   | 1219   | NCSPRSLSAAKMSNRNNKLPNLQNLQNLKRDPPAYIEEFLQ<br>QYNHYKSNEIFKLQPNKPSKELAEVLMFAQISHCYPEYLSNF<br>PQEVKDLLSCNHTVLDPLRMTFCKALILLRNKNLINPSSSLEL<br>FFELFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVVVNLQNF  |

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|------------|--|--|--|
|            |  |  | YTMRLRDSNATAAKMSLDVMIELRYRRNIWDAKTVNVITTACFSK<br>VTKILVAALTFFLGKDEDEKQSDSESEDDGPTARDLLVQYATG<br>KKSSKNKKLEKAMKVLKHKRKKKPEVFNFSAILIHDPODFA<br>EKLLKQLECKKERFEVKMMLNLSRLVGIHELFLFNFPFLQR<br>FLQPHQREVTKILLFAAQASHHLVPPEIIQSLMTVANNPVTDK<br>NSGEVMTVGINAIKEITARCPAMTEELLQDLAQYKTHKDKNVM<br>MSARTLIHLFRTLNPQMLQKKFRGKPTASIEARVQEYGEDAK<br>DYIPGARVLEVEKEBNAENDEGDWESTSLSEEDADGEWIDVQH<br>SSDEEQEISKKLNSMPBERKAKAAAAISTSRVLTQEDFQKIRM<br>AQMREKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK<br>PKSDKETRLATAMAGKTRKEFVRKKTNTNPFSSSTNKEKKKQK<br>NFMMMRYSONVRSKNRSFREKQALALRDALLKKKRMK  |
| 5506       | 1  | 1531   | FRGDLCCGQGGGAPGEGGSAWPAHPLPEREREREALCPGRS<br>CSGGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFPYRWAVV<br>LAAPPSLGAGGETPEAPPESWTQLWFFRPVVAAGYASFMVPGY<br>LLVQYFRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT<br>EAAETTPMWQALKLLFCATGLQVSYLTWGLQERVMTRSYGATA<br>TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCCKQPRHGAPMYRY<br>SFASLSNVLSNWCQYEALEKFSVFTQVLAKASKVIPVMLMGKLV<br>SRRSYEHWEYLTATLISIGVSMPLSSGPEPRSSPATTLSGLIL<br>LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNVFFSCLFTVGS<br>LEQGALLEGTRFMGRHSFAAHALLLSICSACGQLFIYFTIGQF<br>GAAVFTIIMTLRQAFAILLSCLLYGHTVTTVVGGLGAVVFAALL<br>LRVYARGRLKQRGKKAVPVSPVQKV   |
| 5507       | 3704   | 1271   | PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK<br>VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGKF<br>CTVTKEAQAVALACFLDKHDIIDHRNPRQLDAZALCRSIRSS<br>KISENTVIVGVVRRVDRELSVMPFISAGPTRRYVENPNIMACY<br>NELQLQLEFGEVRSQKLKLRACNSVFTALENSEDAIEITSEDRFIQ<br>YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI<br>GKEWQGIYYAKKNGDNIQONVKIIPVIGQGGKIRHYVSIIRVC<br>NGNNKAEKISECVQSDTHDNQTKHKKDRRGLDVKAVASRAT<br>EVSSQRRHSSMARISMTIEAPITKVINIINAAQESSMPVTEA<br>LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGMSDGLRRLSG<br>NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDIFI<br>FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIE<br>ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDVVAAL<br>IAATIHDDVDFGRTNSFLCNAAGSELAILEYNDTAVLESHHAALAF<br>QLTTGDDKCNIFKNMERNDYRTLROQIDMVLAITEMTKHFEHVN<br>KEVNSINKPLATLENGETDKNQEVINTMLRTPENRTLIKRMLI<br>KCADVSNPCRPLQYCIWAARISEEYFSQTDEBKQOGLPVVMPV<br>FDRNTCSIPKSQISFIDYFITDMFDAWDAFVOLDPDLMOHLDNNE<br>KYWKGLDEMCLRNLRPPE |
| 5508       | 1151   | 691  | LSSVPSRRSASMFAVGCSMGPFLLHYWYLSLDRLFPAAGLGRFPN<br>VLKKVLVDQLVASPLLGVWYFLGLGCGLEGQTVGESQELREKFW<br>EFYKADWCWPAAQFVNFLFVPPQFRVTYINGLTGLGWDYLSYL<br>KYRSPVPLTPPGCVALDTRAD  |
| 5509       | 1238   | 619  | RKSRGQNALASAGPAAAAAAMVRKLKFHEQKLLKQVDFLNWE<br>VTDHNLHELRLVRLRRYRLQRRREDYTRYNQLSRAVRELARRLDLP<br>ERDQFRVRASAALLDKLYALGLVPTRGSLLELDFVTASSFCRRR<br>LPTVLLKLMAQHLQAAPAFVEQGHVRVGPDDVDTDPALVTRSM<br>EDFVTWVDSSKIKRHVLEYNEERDDFDLEA  |
| 5510       | 96   | 1195   | PAGAHLSGSSSEPLVEPGRGRVGRVKGGERLQASGSAPGRSKM<br>AEGERQPPPSSEAPPAQNFIIIPKKEIHTVPDMGKWKRSQAY<br>ADYIGFIIITLNEGKVGKLTFFEYRVSEAEIKLVALNLTLDRWID<br>ETPPVDQPSRFGNKAYRTWYAKLDEENENLVATVPTHAAAVP<br>EVAVYLKESVGNSTRIDYGTGHEAFAAFLCCLCKIGVLRVDDQ<br>IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI<br>WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLCILFITEMKT<br>GPFAEHSNQLWNIISAVPSWSKVNQGLIRMYKAECLEKFPVIOHF<br>KFGSLLPPIHPVTSG   |

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|------------|--|--|---|
| 5511       | 276  | 1980   | <p>KLRLVNLPPENLITISAVPISQKEEVADFQLSVDSLLEKDND<br/> HSRPDIQVQAKRLAEKLRCDTVVSBISTGQRTVNFKINRELLTK<br/> TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKFHVG<br/> HLRSTIIGNFLANLKEALGHQVIRINYLGDNGMQFGLLGTGFQL<br/> FGYEEKLQSNPLQHLFEVYVQVNKEAADKSVAKAAQEFFQRLE<br/> LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK<br/> SQEVLKLLSKGLLLKTIKGTAVVDLSGNGDPSSICTVMSRSDGT<br/> SLYATRDLAADIRMDKYNPDITMIYVTDKQKGFQVQFQMLKI<br/> MGYDWAERCQHVPGVVGQMKTRRGDVTFLVDLNEIQRLMLQN<br/> MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR<br/> VFQSRGDTGVFLQYTHARLESLEETFGCGYLNDFNTACLOEPQS<br/> VSILQHLRLRFDEVLYKSSQDFQPRHIVSYLLTSLHAAVAHKTL<br/> QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITVPCRM</p> |
| 5512       | 120  | 1015   | <p>DPSLLLTITVTGTVLVVLKSMNSRRREPITLQDPEAKYPLPL<br/> IEKEKISHNTRFRFGLPSPDHVLGLPVGNVYQLLAKIDNELVV<br/> RAYTPVSSDDDRGFVDLIKIYFKNVHPQYPEGGMKTQYLENMK<br/> IGETIFFRGPGRFLFYHGPGLNLRIPDQTSKPKTLADHLGMIA<br/> GGTGITPMLQIRHITKDPDSRTRMSLI FANQTEEDILVRKELE<br/> BIARTHDPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK<br/> STLILVCGPPP LIQTAHPNLEKLGITQDMIFTY</p>   |
| 5513       | 2  | 837  | <p>ARWRLPSDSPRIIPAGAETPGRGSCRNYLPSSSPPPPESSSFP<br/> PPTSRGGPGSRDMSDEESQDRQLKIVVLGDGASGKTSLTTC<br/> FAQETFGKQYKQTIGLDFLRRLITLPGNLNVTLQIWDIGGQTIG<br/> GKMLDKIYGAQGVLLVYDITNYQSFENLEDWYTVVKKVSESE<br/> TQPLVALVGNKIDLEHMRITKPKHLRFCEQNGFSSHFVSAKTG<br/> DSVFLCFQVAAEILGKLNKABIEQSORVVKADIVNYNQEPMS<br/> RTVNPRESSMCAVQ</p>  |
| 5514       | 1295   | 449  | <p>VNRPSWIMGNFRGHALPGTFFF IIGLWWTCKSILKYICKKQKRT<br/> CYLGSKTIFYRLEILEGITIVGMALTMAGEQFIPCCPHMLLYD<br/> YKQCHWNQLLGWHFTMYFFFGLLGVADILCFTISSLPVSLTKL<br/> MLSNALFVBAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAF<br/> EPLVRNNVLELLRSLIILQGSWFFQIGFVLYPPSGGPANDLM<br/> DHENILFLTICFCWHYAVTIVIGMNYAFITWLKSRKRLCSCS<br/> EVGLLKNAREQESEEBM</p>  |
| 5515       | 1572   | 260  | <p>FVRLVGRGDCDPLLSVCLTTPLYEGLSGGERTAVVIDLGEAF<br/> TKCGFAGETGPRCIIPSVIKRAGMPKPVVVQYNINTEELYSYL<br/> KEFIHILYFRHLLVNPRDRRVVIESVLCPSHFRETTLRVLFKY<br/> FEVPSVLLAPSHLMALLTLGINSAMVLDGQYRSLVLPIYEGIP<br/> VLNCWALPLGGKALHKELETQLEQCTVDTSVAKEQSLPSVMG<br/> SVPEGVLEDIKARTCFVSDLRGLKIQAAKFNDGNNERPSPPP<br/> NVDYPLDGEKILHILGSIKDSVVEILFEQDNEFQSVATLILDSL<br/> IQCFIDTRKQLAENLVVIGGTSMLPGFLHRLLAIRYLVEPKPY<br/> KKALGTKTFRHTPPAKANCVAWLGAIFGALQDILGSRSVSKE<br/> YYNQTRIPDWCSLNNPPEMMFDVGKTPPLMKRAFSTK</p>  |
| 5516       | 3  | 735  | <p>NSREPPQAGPQSPRKSPTASSFLFPWRPLASSFWMGAAQGAQES<br/> IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLTALLGGPTWAG<br/> KMYGPGGGKYFSTEDYDHEITGLRVSVGLLVKSVQVVKLGDSW<br/> DVKLGALGGNTQEVTLQPGEYITKVFAFAFLRGMVMTYSKDR<br/> YFYFGKLDGQISSAYPSQEGQVLVGIYQYQLLGKISIGFEWNY<br/> PLEEPTTEPPVNLTYSANSPVGR</p>  |
| 5517       | 246  | 499  | <p>SEIYVAMRTDSSKMTDVESGVANFASSARAGRRLNLPDIQSSAA<br/> TDGTSDDLPLKLEALS VKEDAKEKDEKTTQDQLEKPNQNEEK</p>  |
| 5518       | 3  | 1375   | <p>DAWADAWVRAWDLNMDPCLWLGLLLPLVAALDFNVHRQEGMEA<br/> FLKTVANQYSSVTHLSIGKSVKGRNLVVLVGRFPKKEHRIGIP<br/> EFKYVANMHGDETVGRELLHLIDYLVTSDDGKDPETINLINSR<br/> IHIMPMNPDGFEAVKPCDCYYSIGRENNYQYDLNRNPPDAFEBY<br/> NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA<br/> TGALYSRSLTPDDDDVQYLAHTYASRNPNMKKGDECKNMNFPN<br/> GVNNGYSWYPLQGGMQDYNIIWAQCFEITLSELSCCKYPREEKLP<br/> SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK</p>  |



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|------------|--|--|---|
|            |  |  | HICPYRTNKYGEYLLLLPGSYIINVTVPGHDPHTKVIPEKS QNFSALKKIDILLPFGQLDSIPVSNPSCPMIPLYRNLPHDSAAT KPSLFLFLVSLHIFFK   |
| 5519       | 87   | 477  | IKSKLNQQVEVQSEWRLEAKGPTMGKESGWDSGRAVAAVVG GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA AGSLVAILQSVGAAGLSVTSKVIIGGFAGTALGAWLGSPSS  |
| 5520       | 117  | 943  | PTEGRQKVLKFTVPRSALAMTKTSTCIYHFLVLSWYTFINYYI SQEGKDEVKPKILANGARWYMTLLNLLQTFYGVTCCLDDVLK RTKGGKDIKFLTAFRDLLFTLAFVSTFVFLAFWILFLYNRDL IYKVLDTVIPVWLNHAMHTFIPFITLAEVVLRPHSYPSKKTGL TLLAAASIAIYISIRILWLYFETGTWVYPVFAKLSLLGLAFAFFSLS YVFIASIIYLGEKLNHWKNSVQILQRWRLESVGICFQWPDWKS PAKHQLVKNIR   |
| 5521       | 546  | 911  | KILNMQKSCSENEGKPNMPKAEEDRPLEDPQEAEGNPQPSEE GVSQEAEGNPRGGPNQPGQFKEDTPVRHLDPEEMIRGVDELER LREIRIRVRNKFVMMHWKQRHSRSPYPVCFRP   |
| 5522       | 1224   | 637  | GSRPLGQRSREKMWVFGYGLIWKVDFPYQDKLVGYITNYSRRF WQGSTDHGVPKPGRVVTVLVEDPAGCVWGVAYRLPVGKEEVK AYLDFREKGGYRTTTFYIFPKDPTTKPFSVLLYIGTCNPDYLG PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEADEHL FALEKLVKERLEGKQNLNCI   |
| 5523       | 3  | 1280   | SKGKKRMGSSMSAATARRPVFDDKEDVNFDFQILRAIGKGSFG KVCIVQKRDTEKMYANKYMNKQCCIERDEVNRVPRELBILQBE HVFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVQFSEDTV RLYCEMALALDYLGRQHIHRDVKPDNILLDERGHAHLTDFNI ATIIKGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSQYVPTWSKEM VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLEKRVPEG FVPNKGRLHCDPTFELEEMILESRLPHKKKRLAKNKS RDNSSD SSQSENDYLDCLDAIQDFVIFNREKLKRSQDLPREPLPAPES RDAAPVEDEAERSALPMCGPICPSAGSG  |
| 5524       | 85   | 2318   | RERERDHRPGESSQSGAGGCFSPTEMLRCGGLLFSSRFDSG NLAHVEKVESLSSDGEVGGGASALTSGIASSPDYEPNVWTRPD CAETEFENGNSWFYFSVRGGMPGKLIKINIMNMKQSKLYSQG MAPFVTRLTPRPRWERIRDPTFEMTETQFVLVSVHREVEGRGA TTFEAFICYPSYSDCQELLNQLDQRFENPHHTSSPLDTIYYHR ELLCYSLDGLRVLDLLTITSCHGLREDREPRLEQLFPDTSTPRPF RFAGKRIFLSSRVHPGETPSSFVNGFLDFILRPDDPRAQTLR RLFVFKLIPMLNPDGVVRGHRVTDTRGVNLRQYKLPDAVLHPA IYGAVALLYHVVHSLNSQSSSEHQPSCLPPDAVPSDLEKAN NLQNEAQCCHSADRHNABAWKQTEPAEQKLSNVWIMPQOSAGLE ESAPDTIPPKESGVAYYVDLGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHDFDQGCNFKSEKNMYARDRRDQSGKEGSGRV AIYKASGIIHSYTLNNTYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVLFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAKMLKHVRNSRGLSSTLVGVNKKRGLRTPPKSHNGLPVSCSE NTLRSARSFSTGTSAGGSSSSQNSPQMKNSPSFFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK |
| 5525       | 105  | 834  | SNLDFERHLFIMGQISDQTLVINKLPEKVAKHVTLVRESGS LTYEFLGRVAELNDVTAKVASGQEKHLFEVQPGSDSSAPWKV VVRVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEBCCICMDGRAD LILCAHSFCQKCIDKWSDRHNCPICRQMTOANESWVVSADP TEDDMANYILNMADEAGQPHRP  |
| 5526       | 3  | 853  | RRPCNPVRAAKRTGAARAPRGLEVTMLRVAVRTLSLIRTRAVT QVLVPLPGGGSAKFPFNQWGLQPSRLLLQAAGYVVRKPAQSR LDDDDPPSTLLKDYQNVPGIEKVDVVKRLLSLEMANKKEMKTI KQEQFMKKIVANPEDTRSLEARIALS VKIRSYEBHLEKHKRDK AHKRYLLMSIDQRKKMLKNLRNTYDVEKICWGLGIEYTFPPL YYRAHRRFVTKKALCIRVQETQKLKRRRALKAAAAAQKQAK  |

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|------------|--|--|---|
| 5527       | 3225   | 565  | RRNPDSPAKAIPTLKDSQ<br>LLRKYLHQNPLLRHQPNNRTCSFSATMKLKDTSRPKQSSCG<br>KFQTKGIKVVGKWKVKIDPNMPADGQMDLVCFEELTDYQLVS<br>PAKNPSSLSFKEAPKRKAQAVSEEEEEEGKSSSPKKIKLKKS<br>KNVATEGSTSQKEFEVKDPELEAQDDMVCDPEAGEMTSNENLV<br>QTAPKKKKKNGKKGLEPSQSTAQVKKAKTWIPEVHDQKADVS<br>AWKDLFVPRPVLRLSPFGFSAPTPIQALTLPAPIRDKLDILGA<br>AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE<br>AGATRS PGKAEASDALPDDTVIESEALPSDIAAEARAKTGGT<br>VSDQALLFGDDDAGEGPSSLIREFKVPKQNEEENLDKEQTGN<br>LKQELDDKSATCKAYPKRPLGLVLTPTRELAVQVQKHIDAVAR<br>FTGIKTALVGGMSTQKQORMLNRRPEIVVATPGRWLWELIKEKH<br>YHLRNLRLRCLVVD EADRMVEKGHFAELSQLEMLNDSQYNPK<br>RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLMMQKIGM<br>RGKPKVIDLTRNEATVETLTETKIHCTEDEKDFLYYFLMQYPC<br>RSLVFANSISCIKRLSGLLKVLDDIMPLTLHACMHQKQRLNLEQ<br>FARLEDCVLLATDVAARGLDIPKQVHIHQVPTSEIYVHRSG<br>RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK<br>YMDVVKERIRLARQIEKSEYRNFOACLHNSWIEQAAAALEIELE<br>EDMYKGGKADQGEERRRQKQMKVLKELRHLLSQPLFTESQKTK<br>YPTQSGKPPLLVSAPSSEALSCLSKQKKKKTKKPKPEQPEQP<br>QPSTAN |
| 5528       | 3  | 895  | GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFB<br>YVRDPEADDTCLAHCVVVRLDGRNFHFAEKHFAKPNDSRAL<br>QLMCKCAQTMEELEDIVIAYGQSDSEYFVKRKTNWFKRRASK<br>FMTHVASQFASSYVFYWRDYFEDQPLLYPPGDFGRVVVYPSNQT<br>LKDYLSWRQADCHINLYNTVFVALIQQSGLTPVQAQGRLLQGT<br>AADKNEILFSEPNINYNNEPFPYRKGTVLWQKVDEVMTKEIKL<br>PTENEGKKMAVTRTRTKPKCPSHLPAPCLRWL   |
| 5529       | 48   | 640  | TFRLVSAHLKTRKLI NFEAAERRWRDWSRQGWLSVKMQRVSG<br>LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTDPE<br>KPTLEELEVSESCVEVQEINEEYLVIRFTPTVPHCSLATL<br>IGLCLRVKLQRCPLPKHKL EYISEGTHSTEEDINKQINDKERV<br>AAAMENPNLREIVEQCVPLEPD   |
| 5530       | 4541   | 2606   | AQIVHAISYCHKLHVHGRDLKPENVVFFKQGLVKLTDGFGSNK<br>FOPGKKLTSCGSLAYSAP EILLGDEYDAPVDINSLGVILFML<br>VCCQPPFOEANDSETLTMIMDKYTPSHVSKECKDLITRMLQR<br>DPKRRASLEEBIENHPWLQGVDPSPATKYNIPLVSYKNLSBEEHN<br>SIIQRMVLGDIADRD AIVEALETNRYNHITATYFLAERILREK<br>QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDL TATPLSH<br>ATVPQS PARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP<br>PASLKPTASGRKCLFRVEEED EEDKKPMSLSTQVVLRRKPS<br>VTNRLTSRKSA PVLNQIFEEGESDDEFMDENLPPKLSRLKMNI<br>ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF<br>TYSWHRRDSSSGPPGSEGGGQSKPSNASGGVDKASPSENNAG<br>GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK<br>LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKQVEKSTWKMCI SST<br>GNAGQVPVAGGKIFPSDHMA DTTTBLERIKSKNLKNNVLQPLFC<br>EKTISVNIQRNPK ELLCASSPASCCHVI  |
| 5531       | 24   | 515  | GSQPRAPRPRDSMERPEPELIROSRAVRSRSPLEHGTVLFARLF<br>ALEPDLPLFQYNCQFSSPEDCISSEFLDHIRKVMLVIDAAV<br>TNVEDLSSLEEYLASLGRKHRAVGKLS SFSTVGESLLYMLEKC<br>LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE  |
| 5532       | 3395   | 1402   | SDWMVVGKRRMIETEDEFCEELHLSVLQCKSVFVDL DGEEMR<br>RARTRANPYEMIRGVFFLNRAAMKMANMDFVDMFTNPRDSYG<br>KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK<br>GNPDFKLEDFYSASSELFPYEGEGIDGDDITRPNISAFRN<br>FVLNDRKGVHFLMADGGFVVEGQENLQEI LSQQLLQCFLMA<br>LSIVRTGGHFICKTFDLFTFVSVGLVYLLYCCFERVCLFKPITS<br>RPANSERYVCKGLKVGIDDDVLDYFAVNIKLNQLRNTDSDVNL  |

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|------------|--|--|--|
|            |  |  | VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL<br>SEPRQAEIRKECLRLWGIPOQARVAPSSDPKSKPFELIQGTETI<br>DIFSYKPTLLTSKTEKIRPVFDYRCMVSGSEQKFLIGLGKSKI<br>YTDWGRQSDRWIKLDLKTLPDRTLLSVEIVHELKGEKGAQRKI<br>SAIHILDVLVNGTDVREQHFNQRIQLAEKFVKAWSKPSRPMN<br>PIRVKEVYRLEEMEKIFVRLEMKIIKGSSTPKLSYTGRRDRHF<br>VPMGLYIVRTVNEPWTMGFSKSPKKKFFYNKKTOSTFDLPADS<br>IAPFHICYGRLFWEWGDGIRVHDSQKPDQDKLSKEDVLSFIQ<br>MIRA   |
| 5533       | 94   | 789  | MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLANDCYPETYVP<br>TVFENYACLETTEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV<br>LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD<br>LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI<br>HSIFRTASMLCLNKPSPLPKSPVRSLSKRLHLPSRSELISPT<br>FKKEKAKKCSIM   |
| 5534       | 3  | 605  | LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK<br>TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK<br>AIESPSKDDDTVWLTYWVYALFGLAEFFSDLLSWFPFYVVGK<br>CAFLFLFCMAPRPWNGALMLYQVRVPLFLRHGGAVDRIIMNDLSG<br>RALDAAAGITRNVKPSQTPQPKDK  |
| 5535       | 1029   | 332  | KSFMDSEARLCSLVESLSDTQDETQKSDSENEEDLKIDCLQESQEL<br>NLQKLKNSERILTEAKQKMRRLTVNIKMKBDLIKELIKTGNDAK<br>SVSKQYTLKVTKLEHDAEQAKVELTETQKQLQELNKLSDVAM<br>KVLQKQEFKRVDAKLRVQVLQKKQODSKKLASLSIQNEKRAN<br>ELEQSVDMKYQKIQLOKRLQEBENKRRQLDAVIKRDQKIKVI<br>LSYIPAKYNNMKC  |
| 5536       | 942  | 282  | AAATAASLSPRGCLRLTPSSDVSFSPRAFPSPAAPLPTGRAQMSD<br>SGRLCLLTIVGLILPTRGQTLKDTTSSSADATIMDIQVPTRAP<br>DAVYTELQPTSPPTWFADETPQPTQTQQLBGTGDLVTDPT<br>HKSTKAAHPTDDTTLSERPSPSTDVQTDPTLKPSTGFHEDDPF<br>FYDEHTLRKGLLVAALFTIGIILTSKCRQLSRLCRNHC  |
| 5537       | 3  | 2391   | RARVSSPOLRVRFSRGRPRRLRVLRINRTSVALRIAGTRFVAKT<br>PGHFGSWEMGLLTFRDVAVEFSLEWEHLEPAQKNLYQDVMLEN<br>YRNLVSLGLVVSXPDILTFLQKKEPWNVKSEETVAIQPDVFSH<br>YKDLLEHCTEASFQKVISRRHGSCLDENLHLRKRWKRECEG<br>HNGCYDEKTFKYDQFDESSVESLFHQQLSSCAKSYNFDQYRKV<br>PTHSSLLNQOBEIDIWGHKHIYDKTSVLFQVSTLNSYRNVFIG<br>EKNYHCNNSEKTLNQSSSPKNHQENYFLEKQYKCKEFEEVFLQS<br>MHGQEKQEQSYKCNKCVBCTQSLKHIOHTIHIENSYSYNKY<br>DKDLSQSSNLKQIINHNEKPKCKEKGDSLNLHSLHLTQHIIIP<br>TEEPYKWKCEGKVFNLCNSLYLTQKQIDTGENLYKCKACSKS<br>PTRSSNLIVHQRHTGKPYKCKEKGKAFRCSSYLTKHRIHTG<br>EKPYKCKEKGKAFNRSSCLTQHQTHTGKLYKCKVCSKSYARS<br>SNLIMHQRVHTGKPYKCKEKGKAFNRSSCLTQHRIHTGENLY<br>KCKVCAKPFTCFNSNLIVHERIHTGKPYKCKEKGKAFPYSSHLI<br>RHHRIHTGKPYKCKACSKSFSDSSGLTVHRRHTGKPYTCCKE<br>CGKAFSYSSDVIQHRRHTGORPYKCECGKAFNYRSYLTTHOR<br>SHTGERPYKCECGKAFNSRSYLTTHRRHTGERPYKCECGKA<br>FSYRSYLTTHRRSHSGERPYKCECGKAFNSRSYLIHQRSHTR<br>EKL |
| 5538       | 926  | 161  | HSMMMKIPWGSIPVLMLLLLGLIDISQAQLSCTGPPAIPGIFG<br>IPGTPGPDGQGTGPIKGEKGLPGLAGDHGEFGKGDPIGPNP<br>GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI<br>NVPLRRDQTI RFDHVTNMNNYEPKSGKFTCKVPGLYFTYHA<br>SSRGNLCVNLMRGRERAQKVTFCDYAYNTFQVTTGGMVLKLEQ<br>GENVFLQATDKNSLLGMEGANSIFSGLLFPDMEA  |
| 5539       | 38   | 1258   | HRGPGSAAAPGALPRGQALEGPRSCRPPQPMARRYDELPHYPG<br>IVDGPAAALASFPETVPAVPGPYGPHRPPQLPPLDSDGLKRREK<br>DEIYGHPLFPLALVFEKCELATCSPRDGAGAGLTPPGGOVCS<br>SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIAIQVLRFHLL   |

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|------------|--|--|---|
|            |  |  | ELEKVDLDCDNFCHRYITCLKGKMPIDLVIIDRDGGCREDFEDY<br>PASCPSLPDQNNMWRDHEDSGSVHLGTGPSSGGLASQSGDNS<br>SDQGDGLDTSVASPSSGGEDLDQERRRNKKRGIFPKVATNIM<br>RAWLFQHLSHYPSEEQKKQLAQDTGLTILQVNNWFNARRRIV<br>QPMIDQSNRTGQGAAPSPGQPIGGYTETQPHVAVRPPGSGVMS<br>LNLEGEWHYL   |
| 5540       | 148  | 1440   | PPLGAGAGVHARSHPHARRLPLTTAGVGGRAPDLLPTPWRQHRG<br>PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD<br>GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI<br>YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPGGDVCSSDS<br>FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLLLELE<br>KGMKPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWRDHED<br>SGSVHLGTGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED<br>EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHYPSEEQKKQ<br>LAQDTGLTILQVNNWFNARRRIVQPMIDQSNRTGQGAAPSPG<br>QPIGGYTETEPHVAFRAPASVGDEFGRKEEWHYL   |
| 5541       | 148  | 1440   | PPLGAGAGVHARSHPHARRLPLTTAGVGGRAPDLLPTPWRQHRG<br>PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD<br>GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI<br>YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPGGDVCSSDS<br>FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLLLELE<br>KGMKPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWRDHED<br>SGSVHLGTGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED<br>EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHYPSEEQKKQ<br>LAQDTGLTILQVNNWFNARRRIVQPMIDQSNRTGQGAAPSPG<br>QPIGGYTETEPHVAFRAPASVGDEFGRKEEWHYL   |
| 5542       | 148  | 1440   | PPLGAGAGVHARSHPHARRLPLTTAGVGGRAPDLLPTPWRQHRG<br>PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD<br>GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI<br>YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPGGDVCSSDS<br>FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLLLELE<br>KGMKPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWRDHED<br>SGSVHLGTGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED<br>EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHYPSEEQKKQ<br>LAQDTGLTILQVNNWFNARRRIVQPMIDQSNRTGQGAAPSPG<br>QPIGGYTETEPHVAFRAPASVGDEFGRKEEWHYL   |
| 5543       | 2405   | 665  | RWVREQPWFLRTSEAVKTPALRPFPGRGVSPFPKPDWKGSPAP<br>KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAPVPKPTRVHG<br>SSASRDRVLARTMIVADSECAELKDYLRFPAGGVGDSGPGEEQ<br>RESKARRGPRGPSAFIPVEEVLRGAESLEQHLGLEALMSSGRV<br>DNLAVVMGLHPDYFTSFWRLLHYLLHTDGPLASSWRHYIAIMAA<br>ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKLRKLSEINK<br>LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSL<br>SFVFGCILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF<br>ESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESL<br>VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQ<br>DYTWEDHGYSLIQRLYPEGGQLLDEKFOAAYSITYNTIAMHSGV<br>DTSVLRRAIWNYIHCVFIRYDDYDYGVEVNLERNLKVIYIKTV<br>ACYPEKTTTRMYNLFWRHFRHSEKVIIVNLLLEARMQAALLYAL<br>RAITRYMT |
| 5544       | 1895   | 514  | LGGLLGRQRLRLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD<br>PEGRRQEPRLRRASSASVPAVGASAEGRTRDRGLSYSGPTSVSR<br>QRVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAESEEEV<br>ESLSKIRKYLTSNVAYGSTGIRDVHLELKDLTLCCRKGNLHFIR<br>FPTHMPAFIQMRDKNPSSLHTVFCATGGGAYKFEQDFLTIGD<br>LQCKLDELCLIKGILYIDSVGFNGRSQCYYPENPADSEKCKQ<br>LPFDLKNPYPLLVNIGSGVSI LAVSKDNYKRVTGTSLGGGTF<br>FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRIYGGDYBERFG<br>LPGWAVASSFGNNMSKEKREAVSKEDLARATLITITNIGSIAR<br>MCALNENINQVVPVGNFLRINTIAMRLLAYALDYWSKQLKALF<br>SEHEGYFGAVGALLELLKIP  |

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|------------|--|--|---|
| 5545       | 802  | 131  | GAMWSAGRGGGAAPVLLGLLLALLVPGGGAAGTGA BLVTCGSVL<br>KLLNTHHRVRLHSIDI KYSGSGGQSVTVGEASDDANSYWRIRG<br>GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNQEV<br>SAFGEDGEGDDLDTVRCSGCHWEREA AVRFQHVGTSTVFLSVT<br>GEQYGSPIRGQHEVHGMP SANTHNTWKAMEGIFIKPSVEPSAGH<br>DEL   |
| 5546       | 1592   | 146  | FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYANPHSFVFT<br>RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKNSLKDCVAVAGP<br>LGVTHFLILSKTETNVYFKLMRLPGGP TLTFQVKKYS LVRDVVS<br>SLRRHRMHEQQFAHPPLLVLSFGPHGMHV KLMATMFQNLFPSI<br>NVHKVNLNTIKRCLLDYNDPSQELDFRHYSIKVVPVGASRGMK<br>KLLQEKFPNMSRLQDISELLATGAGLSESEAE PDGDHNITELPQ<br>AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEKVMFHS<br>FVSKTEELQAILAEKKEKRLKQAQQAQQAQNVQRKQEQREAH<br>RKKSLEGMKKARVGGSDDEASGIPSR TASLELGEDDDDEQEDDDI<br>EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGL<br>CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA  |
| 5547       | 1592   | 146  | FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYANPHSFVFT<br>RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKNSLKDCVAVAGP<br>LGVTHFLILSKTETNVYFKLMRLPGGP TLTFQVKKYS LVRDVVS<br>SLRRHRMHEQQFAHPPLLVLSFGPHGMHV KLMATMFQNLFPSI<br>NVHKVNLNTIKRCLLDYNDPSQELDFRHYSIKVVPVGASRGMK<br>KLLQEKFPNMSRLQDISELLATGAGLSESEAE PDGDHNITELPQ<br>AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEKVMFHS<br>FVSKTEELQAILAEKKEKRLKQAQQAQQAQNVQRKQEQREAH<br>RKKSLEGMKKARVGGSDDEASGIPSR TASLELGEDDDDEQEDDDI<br>EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGL<br>CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA  |
| 5548       | 1  | 2153   | DQTGPPETIAETFPFRSTMEPLCPLLVGFSLPLARALRGNETTA<br>DSNETTTTSGPPDPGASQPLLA WLLPLLLLLVLLAAYFFRF<br>RKQRKAVVSTSDKKMPNGILBEEQEQQRVMLLSRSPSGPKKYFPI<br>FVBHLEEEIRIRSADDCKQFREFNSLPSGHIQGT FELANKEEN<br>REKNRYPNILPNDHSRVLSQLDGI PCSDYINASYIDGYKEKNK<br>FIAAQGPQKETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY<br>WPDQGCWTYGNIRVCVEDCVVLVDYTIKFCIQPLPDGCKAPR<br>LVSQHLFTSWPDFGVPTPIGMLKFLKVKTLNPNVHAGPIVVC<br>SAGVGRGTGT FIVIDAMMAMHAEQKVDVFEFVSIRNRQRPQMVQ<br>TDMQYTFIYQALLEYYLYGDTLSDVSSLEKHLQTMHGTTTHFDK<br>IGLEEEFRKLTNVRIMKENMRTGNLPANMKARVIOIPIYDFNR<br>VILSMKRGQBYTDYINASFIDGYRQKDYFIATQGPLAHTVEDEFW<br>RMIWEWKSHITIVMLTEVQEREQDKCYQWPTTEG SVTHGEITIEI<br>KNDTLSEAISIRD FLVTLNQPOARQEQVRVVRQFHFHGWFEIG<br>IPAEGKGMIDLIAAVQKQQQTGNHPITVHCSAGAGRTGT FIAL<br>SNILERVKAEGLLDVFOAVKSLRLQRPIMVQTLQEQEFCKYKVQ<br>DFIDIFSDYANFK |
| 5549       | 915  | 256  | FEATGGKRLAFKMGATARHREMAIOAKKLLTATDPIERLRLO<br>CLARGSAGIKGLGRVFRIMDDDNRTLD FKEFMKGLNDYAVVME<br>KEEVBELFQRFDKDGNGTIDFNEFLT LRPPMSRARKEVIMQAF<br>RKLDKTGDGVITIEDLREVYNKHHPKYQNGEWS EEOVFRKFLD<br>NFDSPYDKDGLVTPPEFMNYYAGVSASIDTDVYFIIMMRTAWKL  |
| 5550       | 2364   | 1210   | RKRKVF LKMRRNLNRKKTLSLVKELDAFPKVPESYVETSASGGTV<br>SLIAFTTMALLTIMEFSVYQDTWMKYEYEVOKDFSSKLRLINIDI<br>TVAMKCQYVGADVLDIAETMVASADGLVYEPTVFDI SPQKQENQ<br>RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN<br>ACRIHGHLYVNKVAGNFHITVGKAI PHPRGHAHLAALVNHESYN<br>FSHRIDHLSFGBLVPAIINPLDQTEKIAIDHNQMFQYFTVVP<br>KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL<br>MVTVEEHMPFQFVRLCGIVGGIFSTGMLHGIGK FIVEIIC<br>CRFRLGSYKPVNSVPFEDGHTDNHLPLENNTH  |
| 5551       | 211  | 1700   | MQRDHTMDYKESCPSPVSI PSSDEHREKKRFTVYKVLVSVGRSE   |

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|------------|--|--|---|
|            |  |  | WVFRRYAEDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK<br>QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSDE<br>DERSSQKLHSTSQNINLGPSPGNPHAKPTDFDLKVIKGSFQKV<br>LLAKRKLQKPYAVKVLQKKIVLNKKEQKHMAERNVLLKNVKH<br>PFLVGLHYSFQTEKLYFVLDFVNGGELFFHLQERSFPFHRAR<br>FYAAEIASALQYLHSIKIVYRDLKPENILLDSVGHVLTDFGLC<br>KEGIAISDTTTTCGTPEYLAPEVIRKQPYDNTVDWVCLGAVLY<br>EMLYGLPPFYCRDVAEMYDNIHLKPLSLRPGVSLTANSILEELL<br>EKDRQNRLGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNPNV<br>AGPDDIRNFDATFTEETVPYSVCVSSDISVNASVLEADDAFVG<br>FSYAPPSDELFL   |
| 5552       | 2748   | 930  | LGPAAGAAMGKKHKKHKAERSSYEDYADKPLEKPLKLVKVG<br>SEVTLESGSGHDSYYDDRSHERERHKEKKKKKKKSEKHL<br>DDEERRRKEEKKRKRERHCDTEGEADDPDFGKKEVEPPPPDR<br>PVRACRTQPAENESTPIQQLLEHFLRQLQKOPHGFFAFPVTD<br>IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA<br>MTYNRPDVTYYKLAKKILHAGFKMMSKQAAALGNBDTAVEEPV<br>EVVPVQVETAKSKSPREVISCMFEPEGNACSLDSTASEHVL<br>ALVEHAADAEARDINRFLPGGKMGYKLRNGDGLSYSVNTAEP<br>DADEEETHPVDLSSSLSKLLPGFTTLGFKDERRNKVTLSSATT<br>ALSMQNNSVFGDLKSDMELLYSAYGDEBTGVCALSLQEFVKDA<br>GSYSKKVDDLLDQITGGHSTRFLQKQRRNVPMKPPDEAKVG<br>DTLGDSSSVLEFMSMKSYPDVSDISMLSSLGKVKKELDPDD<br>HLNLDETTLLQLDLHEAQAERGSRSSNLSLSNASERDQHHL<br>GSPRLSVGEQPDVTHDPVEFLQSPAPAASAKT   |
| 5553       | 74   | 1095   | LGREAVYLVSRMDCPVAEHAKQEPFHVVTPLESWALSQVAGMP<br>VFLKCNVQPSGSKIRGIGHFCQEMAKKGRHLVCSGGNAGI<br>AAAYAARKLGIPATIVLPSTSLQVQRLQGEAEVQLTGKWD<br>EANLRAQELAKRDGWENVPPFDHPLIWKGHASLVQELKAVLRTP<br>PGALVLAAGGGGLLAGVVGALLVGVQHVPIIAMETHGAHCFNA<br>AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE<br>DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGL<br>PPSLTSVVVIVCGGNNINSRELQALKTHLQV  |
| 5554       | 166  | 2318   | CSGRTGGGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKV<br>GRSFFWVLPVLPWAVQAVEHEEVAQRVILKLRGRGVAAMQSRQ<br>WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLQ<br>VHTFEIPQKFLNESENSVFQAVYGLQALQGDYKDVVMKESR<br>QRLEALREAAIKETEYMEELAAEKHQUEALXNMQHONQSLSM<br>DEILEDVRKAADRLEEBIEEHAFDDNKSXKGVNFEAVLRVEEB<br>ANSKQNIITKREVEDDLGLSMLIDSQNNQYILTTPRDSTIPRADH<br>HFIKDITVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN<br>SIKSIVQVETLGEFGVFFTLFLVGLFSPKLRKVVKISLQGPC<br>YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSTPLVSRFLM<br>GSARGDKEGDIDYSTVLLGLMLVTQDVQLGLFMVMPFLIQAGAS<br>ASSSIVVEVLRILVLIGQILFSLAAVFLCLVIKKYLIGPYRK<br>LHMESKGNKEILIGISAFIFMLTVTELLDVSMELGCFLAGAL<br>VSSQGPVVTEEIIATSIPIRDFLAIVFFASIGLHVFPTEVAYEL<br>TVLVPLTSLSVVMKFLAALVLSLILPRSSQYIKWIVSAGLAQV<br>S3FSPVLGSRARRAGVISREYVLLILSVTLTSLLLAPVLWRAAI<br>TRCVPRPERRSSL |
| 5555       | 212  | 1425   | LSLRTRTPAPPRCEAASQGRVGRADAAAEAVRSVMNRTRDR<br>GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDK<br>KAYRKALQLHFDNRNPDPAQAEKFDLGAAYEVLSDSEKQY<br>DTYGEGLKDGHQSSHGDI FSHFGDFGFMFGGTPRQDNRNIPR<br>GSDIIVDLVTLLEVYAGNFVVRNKPVARQAPGKRKCNCRQE<br>MRTTQLGPRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD<br>GMEYPPFIDGEPHVDGEPGLRFRIKVVVKHPIFERRGDDLYTNV<br>TISLVESLVGFEMDITHLDGHKVHISRDKITRPAKLNKKGEGL<br>PNFONNNIKGSLIITFDVDFPKEQLTEAREGKQLLQKGSQVK<br>VYNGLQGY   |
| 5556       | 5835   | 3346   | RTRGMSKNCVMEFEYLLRMFQGTFFYLQKITKDNNAHTVKS   |

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|------------|--|--|--|
|            |  |  | LEELDES YIEKFTDFLRLFSVHLRRIESYSQFPVVEFLTLLFK<br>YTFHQPTHEGYFSCLDIWTFLDYLTSKIKSRIGDKAEVLNRYE<br>DALVLLLTVEIANRIQFRYNQAQLEELDDDETLDQDQTEWQRYLR<br>QSLEVVAKVMELLPTHAFTSLFPVLQDNLEVYLGQQFIVTSGS<br>GHRNLITAENDCRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR<br>FNDALTVVERLVKVTLYGSOIKLYNIETAVPSVLKPDLDIVHAQ<br>SLAALQAYSHWLAQYCEVHRQNTQQFVTLISTTMDAITPLIST<br>KVQDKLLLSACHLLVSLATTVRPVLISIPAVQKVPNRI TDASA<br>LRLVDKAQVLVCRALSNILLPWPNLPENEQQWPVRS INHASLI<br>SALSRYRNLKPSAVAPQRKMPDCLKI IHQTL SVLEDIVENI<br>SGESTKSRQICYQSLQESVQVSLALFPFIHQSDVTDEMLSFLL<br>TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR<br>VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS<br>PDVKAELFELLFRTLHNNRYFFKSTVLASVQRGIAEQMENEP<br>QFSAIMQAFGQSFLQPDILHLFKQNLFPYLETLNTKQKLYHKKIFR<br>TAMLFQFQVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA<br>APLPEFLTSCDGV DANQKSVLGRNFKMDRVRREGRRAKRAEWA<br>RKPGTCAARRGHI EASGRGLCPPCSLAAAHMPADLVL |
| 5557       | 1712   | 491  | VILGAGLRDKDMWIPVVGLPRLRLSLALAGAGRFCLGSEAA TR<br>KHLPARNHCGSLDSSPQLWPEPDFRNP PRKASKASLDFKRYVTD<br>RRLAETLAQIYLGKPSRPPHLLLECNPGPGLTQALLEAGAKVV<br>ALES DKTFI PHLES LGKNLDGKLRVIHCDFKLPDRSGGVIKPP<br>AMSSRG LFKNLGIEAVPWTADI PLKVGMFSPRGKRALWKLAY<br>DLYSCTSIYKFGRIEVMNMFIGEKEFQKLMADPGNPDLYHVL SVI<br>WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQKQLY<br>LIQMI PRONLFTKNLTPMNYNIFPHLLKHC FGRRSATVIDHLRS<br>LTPLDARDILMQIGKQEDSKVVMHPQDFKTLFETIERSKDCAY<br>KNLYDETLEDR   |
| 5558       | 1509   | 96   | RAGCTHPOVPADLGAPAEPRRPQKTCVCLLPQPGGQRGPTTMI<br>TGVSFMR LWTVPVGLTSLAYCLHQRRVALAEQADGQCPVD RS<br>LLKLMQVQVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD<br>YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQMF A<br>LGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLA<br>GLFQCQKEGPII IHTDEADSEVLYPNYQSCWSLRQRTGRRRQTA<br>SLQPGISED LKKVDRMGIDSSDKVDFFILLDNVAEQAHLNPS<br>CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPPFLHILES<br>NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTGLIFDHKNPP<br>FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF<br>LNAMSVYTLSP EKYHALCSQTQVMEVGN E  |
| 5559       | 150  | 1983   | PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK<br>ELDVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFC EKETKK<br>LMQREMSMDESQVETKTDKNGEERGRDASKKALGPRRDS DLG<br>KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA<br>VDKKEAGKDGGRGEERAVATKKBEERKKS DRNTGLSRDKDKKREE<br>MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGNTDMKKEDEK<br>VKRGTGNTDTKKDDEKVKNEPLHEKEAKDSDSKTPEKQTPSG<br>PTKPSGPAKV EEEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC<br>ITNEILVRFTEALEFNTVVKL FALANTRADHDHVAFAIAMLKAN<br>KTITSLNLD SNHITGKGI LAIFRALLQNNTLTELRFHNQRHICG<br>GKTEMEIAKLLKENTTLKLG YHFELAGPRMTVTNLLSRNMDKQ<br>RQKRLQEQRQAQEAKEKKDLLEVPKAGAVAKGSPKPSQPSPK<br>PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNLSLSPATQRKM<br>GDKVLPAQEKN SRDQLLAAIRSSNLKQLKKVEVPKLLQ   |
| 5560       | 9  | 921  | SSVVEFSALSVSMACLSPSQLQKQFQDGLVLBGLSAEBCVAM<br>QQRIGEIVAE MDPVPLHCRTEFSTQEEELRAQGSTDYFLSSGDK<br>IRFPFEKG VDEKGNFLVPPEKSINKIGHALHAHDVPFKSITHS<br>FKVQTLARSIGLQMPVVVQSMYIFKQPHFGGEVS PHQDASFLYT<br>EPLGRVLGVWIAVEDATLENGCLWFI PGSHTSGVSRMVRAPVG<br>SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVHVHKSQNL<br>SDRSRQAYTFHLM EASGTTWSPENWLQPTAELEFPQLYT   |
| 5561       | 2175   | 1775   | CYFIFQFFSSPYGLHHPQTAPLPNPGLYPPFVMSMSPGQPPPO  |

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|------------|--|--|---|
|            |  |  | QLLAPTYFSAPGVNFGNPSYPYAPGALPPPPPHLYPNTQAPS QVYGVVYYNPAQQQVQPKSPRRTPQPVVT:KPPPEVVSRS S   |
| 5562       | 342  | 1385   | SSGKNDMAAGAAGLVRLKAGVLSQADYLNVLQCELTEDLKLH LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP LASPLDFITYSYMIDNVILLITGTLHQRSAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAPPQDCISEQDLDEMNIET IRNTLYKAYLESFYKFTLLGGTTADAMCPILFEADRRAFIT INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF   |
| 5563       | 342  | 1385   | SSGKNDMAAGAAGLVRLKAGVLSQADYLNVLQCELTEDLKLH LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP LASPLDFITYSYMIDNVILLITGTLHQRSAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAPPQDCISEQDLDEMNIET IRNTLYKAYLESFYKFTLLGGTTADAMCPILFEADRRAFIT INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF   |
| 5564       | 3  | 914  | RVRDRKRAVWTAARGRRRCGDSMSGGWAQVGAWRTGALGLALL LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC VTLTWRCDRDLDCSDGSEEBECRIEPTQKQCPFPPLGPCPT GVSDCSGGTDKLRNCSRLACLAGELRCTLSDDCIPLTWRCDSGH PDCPDSSDELGCCTNEILPEGDATTMGPPVTLESVTSLRNATTM GPPVTLESVPSVGNATSSSAGDQSGSPAYGVIAAAVLSASLV TATLLLSWLAQERLRPLGLLVAMKESLLSBOKTSLP  |
| 5565       | 993  | 138  | RWNSPNPARAGSISRPPQAPGSVSAVAMTAAVFFGCAFIAGGPA LALYVFTIATEPLRIIPLIAGAFFWLVSLLISSLVWFMARVIID NKDQPTQKYLIFGAFVSYYIQEMPRFAYYKLLKASEGLKSLN PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLPGPTVGIH GDSPPQFLYSAMTLVILLHVFWGIVFFDGCCKKKGILILVL LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS LKLCCLLQDKNFFLLYNQSR   |
| 5566       | 2043   | 1232   | SHIQHHGRGAQAPKVMVSWMISRAVVLVFGMLYPAYYSYKAVKT KNVKEYVRMMYWIVFALYTVIETVADQTVAMFPLYELKIAFV IWLLSPYTKGASLIYRKFLHPLLSSKEREIDYIVQAKERGYET MVNFGRLGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTITQG DEPVGQRPYQPLPEAKKSKPAPSESAGYGIPLKDGDEKTDDEEA BGPYSNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVKK RPQVYP  |
| 5567       | 1554   | 233  | EFLGSGVSPDLANEDGLTALHQCCTIDDFREMVOQLLEAGANINA CDSECVTFLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSLQ AGADLHAPLDHGATLLHVAANGFSEAAALLLEHRASLSAKDQD GNEPLHAAAYWQVPLVELLVAHGADLNALSMDETPLDVCGBE EVRAKLLLELKHHDALLRAQSRORSLLRRRTSSAGSRGKVVRV SLTQRTDLVRKQHAQEAIWQQPPPTSPEPPEDNDRQTGAELR PPPPEEDNPEVVRPHNGRVGGSVVRHLYSKRLDRSVSYQLSPLD STTPHTLVHDKAHTLADLKRQAAAKLQRPPEGPESPETABP GLPGDTVTTPQDCGFRAGGDPPLKLTAPAVEAPVERRPCCLLM |
| 5568       | 1731   | 587  | AEDRQPASRRGAGTTAAMAASGPGCRSWCLCEVFSATFFTALL SLLVSGPRLFLLOQLAPSGLTALKSEALRNQVYRLVTYIFVYE NPISELLCGAIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL SFEAVSSLSKLGVEDARGPTPVAFAMLGVTTVRSRMRRALVFG MVVPSVLVPWLLGASWLIPTSFSLNVCGLSIGLAYGLTYCYS IDLSERVALKLDQTFPFLMRRISVFYVSGSSAERRAAQSRKL NPVPGSYPTQSCPHLSPSHPVSOTQHASGQKLASWPSTCPGHM PTLPPYQASGLCYQNHFGPNPTSSSVYPASAGTSLGIQPTTP VNSPGTVYSGALGTGAAGSKESSRVMP   |
| 5569       | 2  | 835  | QTPCPLAWERGSSEDISVPGQKPPCTCSSFSGMDVGPSSLPHLG  |



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|------------|--|--|--|
|            |  |  | LKLLLLLLLLPLRQANTGCGIFGMPGLPGAPGKDGYPGLPGP<br>KGEPIPAIPGIRGPKGQKGEPLGHPGKNGPMGPPGMPGVPG<br>PMGIPGEPGEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL<br>TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK<br>VVTFCGHTSKTNQVNSGGVLLRLQVGEVWLAVNDYDMVGIQ<br>SDSVFSGFLFPD  |
| 5570       | 264  | 946  | RDRDRGGVATSTEEPAPRAPQSRGPGPVSTQGRGRERGGGDT<br>MSSSPSGKRRMDTGVVKLIESKHEVTILGGLNEFVVKFYGPQGT<br>PYEGGVKVRVDLPDKYFPKSPSIGFMNKIFHPNIDEASGTVCL<br>DVINQNTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH<br>RPEBYKQIKIKEYIQYATEEALKEQEETGDSSESSMSDFSED<br>EAQDMEL  |
| 5571       | 264  | 946  | RDRDRGGVATSTEEPAPRAPQSRGPGPVSTQGRGRERGGGDT<br>MSSSPSGKRRMDTGVVKLIESKHEVTILGGLNEFVVKFYGPQGT<br>PYEGGVKVRVDLPDKYFPKSPSIGFMNKIFHPNIDEASGTVCL<br>DVINQNTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH<br>RPEBYKQIKIKEYIQYATEEALKEQEETGDSSESSMSDFSED<br>EAQDMEL  |
| 5572       | 2802   | 2085   | RTDYRTGIPGRFRVMAAGDGVKLGTLGSGSESSNDGSES<br>DAGAAEGGGWAAAALALLTGGEMLLNVALVALVLLGAYRLWV<br>RWGRRGLGAGAGAGEESPATSLPRMKRDFSLEQLRQYDGS<br>RNP<br>RILLAVNGKVFDVTGSKFYGPAGPYGIFAGRDA<br>SRLATFCLD<br>KDALRDEYDDLNAVQMESVREWEMQFKEKYDYVGRLLKPG<br>EPSEYTTDEEDTKDHNKOD  |
| 5573       | 2562   | 219  | VPARTPNAEDQGPAAATATPCQSGGRERAGEAAEDGVKMAAF<br>SEMGVMPETIAQAVEEMDWLLPTDIAESIPILGGGDVLMMAET<br>GSGKTGAFSIPVIVYETLKDQEQEGKKGKTTIKTGASVLNKWQ<br>MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE<br>VSCHDQGLCRVWSTMQASLDLGTDFGFGGTGKKSHNKQFD<br>NYGEFTMMDTIGCYLDIDKGHVKFSKNGKDLGLAFETPPHMK<br>NALFPACVLKNAELKFNFGEEEFKFPKDFGVALSKAPDGYIVK<br>SQHSGNAQVTOTKFLPNAPKALIVEPSRELAETLNNIKQFKKY<br>IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTGRLDDLVST<br>GKLNLSQVRLVLDEADGLSQGYSDFINRMHNQIPQVTS<br>DGKR<br>LQVIVCSATLHSDVKKLSEKIMHPTWVDLKGEDSVDPDTHHV<br>VFPVNPKTDRWLRLGKSHIRTDVHAKDNTRPGANSPENWSEA<br>IKILKGEYAVRAIKHKMDQAIIFCRTKIDCDNLEQYFIQGGG<br>PDKKGHQFSCVCLHGDRKPKHERKQNLERFKKGDVRFICTDVA<br>ALGDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA<br>TEKEKVYHVCSRGKGCYNTRLKEDGGCTIWNEMQLLSEIEE<br>HLNCTISQVEPDIKVPVDFDQKVTYQKRAAGGGSYKGHVDIL<br>APTVOELAALEKEAQTSEFLHLGYLPNQLFRTF |
| 5574       | 1731   | 952  | NEGLEVFEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG<br>LGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS<br>TGITQCDIYSTLLGLPADIAQAQAMMTSSAIISSSLACTIISVVG<br>M<br>RCTVFCQESRAKDRVAVAGGVFFILGGLGPIPVAWNHLGILRD<br>FYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCSCQRN<br>RSNYYDAYQAQPLATRSPRPGQPKVKSEFNSYSLTGYV  |
| 5575       | 456  | 766  | LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTAKADSPRTAL<br>LCSAWLLTASFSAQOHKGSLOKDPLLSQACVGCLEALLDYLDAR<br>SPDIGRNSPHYLMFP   |
| 5576       | 249  | 2146   | RSWGAFWFRMRLLRRRHMPRLRLAMVGCAPVLFLLHHRDVSSR<br>EATEKPKWLSLVSRLKDHVLDLMEAMNNLRDSMPKLQIRAPEA<br>QQTLPFINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK<br>SKWTPLETQEKEEGYKKHCFNAPASDRISLQRLGPDTRPPECV<br>DQKFRRCPLATTSVIVFHNEAWSTLLRTVYSVLHTTPAILLK<br>EIIIVDDASTEHLKEKLEQYVKQLQVVRVVRQBERKGLITARL<br>LGASVAQAEVLTFDLAHCECFHGWLEPLLARIAEDKTUVVSPDI<br>VTIDLNTFEFAKPVQGRVHSGNFDWSLTFGWETLPHEKQRR<br>KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEINGENVEM   |

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|------------|--|--|---|
|            |  |  | SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNQVR<br>LAEVWMDSYKKIFYRRNLQAAKMAQEKSEFGDISERLQRLREQLHC<br>HNFSWYLNHVYPFVFDLPTTFYGAIKNLGTNQCCLDVGENNRG<br>GKPLIMYSCHGLGGNQVFYETTQRDLRHNIQKQLCLHVSKGALG<br>LGSCHFTGKNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKKPA<br>MAPCNPSPDPHQLWLFV  |
| 5577       | 3  | 1275   | RNSDCSCGEISVHCLPWLFLDLKVESSMFCPLKLLPVLDD<br>YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKFKIDWTL<br>SPGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDLICNDGSLLL<br>QDVQEADQGTYYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV<br>GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRLM<br>SVEYSQSWGHFQNRVNLVGDIFRNDGSI MLQGVRESDDGGNYTCS<br>IHLGNLVFKKTIVLHVSPEEPRTLVTTPAALRPLVLGGNQLVIV<br>GIVCATILLPVLILIVKKTGCGNKSSVNSTVLVQNTKKTNPETK<br>EKPCHEFERCEGEKHIYSPPIIVREVIEEPEPEKSEATYMTMPHV<br>WPSLRSDRNNLEKSGGGMPKKTQAF   |
| 5578       | 3  | 783  | AVESMASFGACRAPPPELPERNCGYREVEYWDQRYQGAADSAPYD<br>WFGDFSSFRALLEPELRLPEDRILVLGCGNSALSVELFLGGFPNV<br>TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFFSASFDVVL<br>EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI<br>SMTSAAPHFRTRHYAQAYYGSLSRHATYGSGFHFLYLMHKGK<br>LSVAQLALGAQILSPRPPTSPCFLQDSDHEDFLSAIQL  |
| 5579       | 3  | 1540   | RNSGLARGASALARHGGGLAGGVGWDCCACASRCQGVMEGLLTR<br>CRALPALATCSRLSGYVPCRFHHCAPRRGRRLLSRVFQPNL<br>REDRVLSLQDKSDDLTKCSQRLMLQVGLIYPASPGCYHLLPYTV<br>RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK<br>ELLRLDRRHGKSYCLGPTHEEATL IASQKLSYKQLPFLLYQ<br>VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSILVC<br>DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA<br>ICPRCSFSANMETLDSQMNCPCACQGPLTKTKGIEVGHTFYLG<br>KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAI EVLSTED<br>CVRWPSLLAPYQACLIIPKKGSKQAASELIGQLYDHITEAVPQ<br>LHGEVLLDDRTHLTIGNRLKDANKFGYFPFV I IAGKRALEDPAHF<br>EVWCQNTGEVAFLLTKDGVMDLLTPVQTV |
| 5580       | 1681   | 450  | ADAGTRCIPGFVPPSGAGYSAPAQGRSSGGRMAAAAPGLTAP<br>WRLQLCCLEAGELGMVPAAMGPSALGQSGPGSMAPWCVSVSS<br>GPSRYVLGMQELFRGHSKTREFLAHSAKVHSAVNSCDGRRLASG<br>SPDKTASVFLLEKDRLVKENNYRGHGDSDVQLCWHIPSNPDLFVT<br>ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDQGTIAVGNK<br>DDVVT FIDAKTHRSKABEQKFEEVNEISWNNDNMFFLTNGNGC<br>INILSYPELKPVSINAHPSNCICIKFDPMGKYFATGSADALVS<br>LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA<br>EVEGTGDKLWEVQCESPTFTVAWHPKRPLLAFAACDDKDGKYDSSR<br>EAGTVKLFGLPDS   |
| 5581       | 54   | 947  | GGSGGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVAFACS<br>CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTYPTAYPAAAPA<br>YNPSLYPTNSPSYAPFQFLHSAYATLLMKQAWPONSSSCGTG<br>TFHLPVDGTENRTYQASSAIFYTAGTPYKVPPTQNSNTAPPPY<br>SPSPNPYQTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPHVHH<br>TTVVQPNISPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL<br>TTPQHTAIGAHVPVSMPTYRAQGTTPAYSYPVPHW  |
| 5582       | 5775   | 2739   | IITNNNNV IIPLVIAVHLSGSAQARGERSPAERLMERQKRKADI<br>EKGLQFIQSTLPLKQEEYEAFLKLVLQNLFAEGNDLFREKDYKQ<br>ALVQYMEGLNVADYASDOVALPRELLCKLHVNRACFYTMGLY<br>EKALEDSEKALGDSSESIRALFRKARALNELGRHKEAYECSSRC<br>SLALPHDESVTQLGQELAQKLGRLVRKAYKRPQELETFSLLSNG<br>TAAGVADQGTSNGLGSIIDDIETDCYVDPGRGPALLPSTPTMPLF<br>PHVLDLLAPLSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL<br>VQGLSGSGVPSLPQLIPVFPGGTFLPFPVVGGSIPVSSPLPF<br>ASFGVLMDPSKKLAASVLDALDPGPTLDPDLLPYSETRLDAL   |

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|------------|--|--|--|
|            |  |  | DSFGSTRGSLDKPDSFMEETNSQDHRFPSSGAQKPAFSPPEPCMPN<br>TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKKC<br>RDILGRLRSSDQTWKRI RPRPTKTSFVGSYYLCKDMINKQDC<br>KYGDNCTFAYHQEEIDVWTEERKGT LNRD LLDPLGGVKRGS LT<br>IAKLLKBHQGIFTPLCEICFDSKPRIISKGT KDSPSVCSNLAPK<br>HSPYNNKCLVHIVRSTSLKYSKIRQFQEHFQFDVCRHEVRYGCL<br>REDSCHFAHSFIELKVWLLQOYSGMTHEDIVQESKKYQQMEAH<br>AGKASSSMGAPRTHGPTFDLQMKFVCGQCWRNGQVVEPDKDLK<br>YCSAKARHCWT KERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD<br>LCIHAQNGRKQCYVGNCSFAHSPEERDMWTFMKNKILDMQQTY<br>DMWLKKNHNGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL<br>CGKNSNSKKQWQHIIQSEKHKEKVFTSDSDASGWAFRPFMPGEFR<br>LCDRLQKQKACPDGDKCRCAHGQEELENEWLDRREVLKQKLAKAR<br>KDMLLCPRDDDFGKYNFLQEDGLAGATPEAPAAAAATATTGE |
| 5583       | 3  | 1265   | SSGCRQGRPRGSDRPPRRHMKVETRYDILGVKPSASPEE<br>IKKAYRKALALYHPDKNPDEGEKFKLISQAYEVLSDPKRDRVDY<br>QGGEQAIKEGSGSPSPSPMDIFDMFFGGGGRMARERRGKNVV<br>HQLSVTLEDLYNGVTKKLALQKNVICCKCEGVGGKKGVSVEKCP<br>CKGRGMHIHQIGPGMVQIQTVCI ECKQGGERINPKDRCESC<br>SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPLEPGDVI<br>IVLDQKDHSVFORRGHDLIMMKIQLSEALCGFKKTIKTLDNRI<br>LVITSKAGEVIKHGDLRCVRDEGMPYKAPLEKGIILIIQFLVIF<br>PEKHWSLEKLPQLEALLP2RQKVRITDDMDQVELKEFCPNEQN<br>WRQHREAYEEDDGPQAGVQCQTA  |
| 5584       | 3  | 1265   | SSGCRQGRPRGSDRPPRRHMKVETRYDILGVKPSASPEE<br>IKKAYRKALALYHPDKNPDEGEKFKLISQAYEVLSDPKRDRVDY<br>QGGEQAIKEGSGSPSPSPMDIFDMFFGGGGRMARERRGKNVV<br>HQLSVTLEDLYNGVTKKLALQKNVICCKCEGVGGKKGVSVEKCP<br>CKGRGMHIHQIGPGMVQIQTVCI ECKQGGERINPKDRCESC<br>SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPLEPGDVI<br>IVLDQKDHSVFORRGHDLIMMKIQLSEALCGFKKTIKTLDNRI<br>LVITSKAGEVIKHGDLRCVRDEGMPYKAPLEKGIILIIQFLVIF<br>PEKHWSLEKLPQLEALLP2RQKVRITDDMDQVELKEFCPNEQN<br>WRQHREAYEEDDGPQAGVQCQTA  |
| 5585       | 2619   | 915  | LPAGTPESSLHEALDQCM TALD LFLTNQFSEALS YLKPRTKESM<br>YHSLTYATILEMQAMMTFDPQDILLAGNMMEQAQMLCQRHRRKS<br>SVTDSFSSLVNRPTLGQFTEEEIHA EVCYAKCLLQRAALTFLQD<br>ENMVSF IKGKIKVRNSYQTYKELDSLVSQSYCKGENHPHFEGG<br>VKLGVGAFNLTL SMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS<br>GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNI EAEKLLKPYLNR<br>YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECC EAQHQHWKQFHMM<br>CYWELMWCFTYKQGWKMSYFYADLLSKENCWSKATYIYMKAAYL<br>SMFGKEDHKPFGDDEVELFRAVPGLK LKIAGKSLPTEKFAIRKS<br>RRYFSSNPISLPVPALEMMYIWN GYAVIGKQPKLTDGILEIITX<br>AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEA EENFRS<br>ISANEKKIKYDHYLIPNALLELALLMEQDRNEEA IKLLES AKQ<br>NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL   |
| 5586       | 2619   | 915  | LPAGTPESSLHEALDQCM TALD LFLTNQFSEALS YLKPRTKESM<br>YHSLTYATILEMQAMMTFDPQDILLAGNMMEQAQMLCQRHRRKS<br>SVTDSFSSLVNRPTLGQFTEEEIHA EVCYAKCLLQRAALTFLQD<br>ENMVSF IKGKIKVRNSYQTYKELDSLVSQSYCKGENHPHFEGG<br>VKLGVGAFNLTL SMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS<br>GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNI EAEKLLKPYLNR<br>YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECC EAQHQHWKQFHMM<br>CYWELMWCFTYKQGWKMSYFYADLLSKENCWSKATYIYMKAAYL<br>SMFGKEDHKPFGDDEVELFRAVPGLK LKIAGKSLPTEKFAIRKS<br>RRYFSSNPISLPVPALEMMYIWN GYAVIGKQPKLTDGILEIITX<br>AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEA EENFRS<br>ISANEKKIKYDHYLIPNALLELALLMEQDRNEEA IKLLES AKQ<br>NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL   |
| 5587       | 1768   | 148  | SSAVPDGAVGRPVAVAVGGPFHSCRCRCPCLMAAIGVHLGCTSA   |

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|------------|--|--|--|
|            |  |  | CVA VYK DGRAGV VANDAGDRVTPAVVAYSENEEIVGLAAKQSRI<br>RNISNTVMKVQILGRSSSDPQAQKYIAESKCLVIEKNGKLRVE<br>IDTGEETKFVNPEDVARLIFSMMKETAHSVLGSDANDVVITVFP<br>DFGKQKQNALGEAARAAGFNVRLIHEPSAALLAYGIGQDSPTG<br>KSNILVFKLGTSLSLSVMEVNSGIYRVLSNTDDNIGGAHFTS<br>TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS<br>ANCFDLSLYEQDFDCNVSRARFELLCSPLFNKCIERGLLDQ<br>NGFTADDINKVVLGCGSSRI PKLQQLIKDLFPVALLNSIPPDE<br>VIPGAATEAGILIGKENLLVEDSLMIECSARDILVKGVDESQA<br>SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLLEYSDGKNSAK<br>EETKFAQVVLQDLDDKENGRLDILAVLTMKRDGSLHVTCTDQET<br>GKCEAISIEIAS |
| 5588       | 3  | 589  | TPPPPEQAMVAATVAAWLLWAAACAQOEQDFYDFKAVNIRGK<br>LVSLEKYRGSVSLVNVASECGFTDQHYRALQQLQRLGPHHFN<br>VLAFFPCNQFGQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG<br>AHPAFKYLAQTSKGTEPTWFWKYLVPADGKVVGAWDPTVSVVEV<br>RPQITALVRKLI LKREDL  |
| 5589       | 1884   | 553  | LRQAWHEGGIGQTDKERGAAALPGEEDPTGRSLGRASWESGS<br>PRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS<br>GLNRSSGLWLGPDRCRPRSRCRCRVMENPSPAAALGKALCALLL<br>ATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAPFKQYPLF<br>RPPAQWSSLLGAHSSDYSMWRKNQYVNSGLRDFAEERGEAWALM<br>KETEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRLSLVSF<br>VVRIVPSPDWFGVDSLDLDCDGRWREQAALDLYPYDAGTDSG?<br>TFSSPNFATIPQDTVTEITSSSPSHPANSFYPRKLKALPPIARV<br>TLLRLRQSPRAFI PPAPVLP SRDNEIVDSASVPETPLDCEVSLW<br>SSWGLCGGHCGRLGTSRTRYVRVQPANNGSPCELEEEAECVP<br>DNCV  |
| 5590       | 72   | 896  | LCSSGALRLLPAMVAWRS AFLVCLAFSLATLVQRGSGDFDDFNL<br>EDAVKETSSVKQPDHDTT TTTTNRPGTTTRAPAKPGSGLDLADA<br>LDDQDDGRRKPGIGGRERNHVT TTTTKRPVTTTRAPANTLGNDFD<br>LADALDDRRDDGRRKPIAGGGGFSKDKLEDIVGGGEYKPDKG<br>KGDGRYGSNDPDSGMVAEPGTIAGVASALAMALIGAVSSYISY<br>QQKKFCFSIQQLNADYVKGENLEAVVCEBPQVKYSTLHTQSAE<br>PPPPPEPARI   |
| 5591       | 68   | 1494   | AGSSRRAAERLLVSAGCRSLAGRASGVLLP AELLPGEEAAMA<br>LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG<br>DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVEMLV<br>PVPVSEPVPEPEPEPEPEPVKEEKLSP EPI LVD TASPSMETSG<br>CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSBYVKDIYAYL<br>RQLEEEQAVRPKYLLGREVTGNMRAILIDWLQVQMKFRLQET<br>MYMTVSIIDRFMNNNCV PKMLQLVGVMTAMFIASKYEEMYPRI<br>GDFAFVTDNTYTKHQIRQMEMKILRALNFGLRPLPLHFLRRAS<br>KIGEV DVEQHTLAKYLMELTMDLYDMVHFPPSQIAGAFCLALK<br>ILDNGEWPTTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM<br>TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV                      |
| 5592       | 242  | 924  | YGESKDNQKDLLSALVLTIVNCLFTPIMAKSAEVKLAIFGRAG<br>VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMELD<br>TAGQEDTIQREGHMRWGEFVLVYDITDRGSFEEVLPLKNILDE<br>IKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYEC<br>ACTGEGNITEIFYELCREVRRRRMVQKTRRSSTTHVQAINK<br>MLTKISS  |
| 5593       | 3  | 1113   | HASGGRAANMAAERGAGQQSQEMMEVDRRVESEESGDEEGKKH<br>SSGIVADLSEQLKDGEERGEEDPEEEHEL PVDMETINLDRDAE<br>DVDLNHYRIGKIEGFVLKVKTLCLRONLIKCIENLEELQSLR<br>BLDLYDNQIKKIENLEALTELEILDISPNNLRNIEGVDKLTRLK<br>KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE<br>SLFLGKNKITKLQNLDAITNLTVLSMQSNRLTKIEGLQNLVNL<br>ELYLSHNGIEVIEGLENNKLTMLDIASNRICKIENISHLTELQ<br>EFWMDNLLLESWSDLELKGARSLETVYLERNPLOKDPQYRRKV   |

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|------------|--|--|--|
| 5594       | 3  | 1113   | MLALPSVRQIDATFVRP<br>HASGGRAANMAAERGAGCQQSQEMMEVDRRVESEESGDEEGKKH<br>SSGIVADLSEQLKDGEEERGEDPEEHELPMVDMETINLDRDAE<br>DVDLNHYRIGKIEGFEVLKKVKTLCRQNLKICENLEELQSLR<br>ELDLYDNQIKKIEENLEALTELEILDISFNLLRNIEGVDKLTRLK<br>KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE<br>SLFLGKNKITKLQNLDAITNLTVLSMQSNRLTKIEGLQNLVNL<br>ELYLSHNGIEVIEGLENNKLTMLDIASNRIKKIENISHLTELQ<br>EFWNNDNLLESWSLDELKGCARSLETVYLERPLQKDPQYRRKV<br>MLALPSVRQIDATFVRP  |
| 5595       | 3  | 1476   | ARWNGRWVQVPAWPGGCGTNASGERQRLPRAWRPVGRITLGE<br>PIALAWSPPLYLFPPIPLPSWAVSQPTPTLGTMTFADLDYDIEEDK<br>LGIPTVPGKVTLOKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP<br>AALDGTVAAGDEITGVNCRSIRKGTKEVAKMIEQEVKGEVTIHY<br>NKLQADPKQGSMLDIVLKKVKHRLVENMSSGTADALGLSRAILC<br>NDGLVKRLEBELRTAELYKGMTEHTKNLLRAFVYLSQTHRAFGD<br>VFSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLKTIKPMLT<br>DLNTYLNKAIPTDRLTIKKYLDVKFEYLSYCLVKEMDDEEYSC<br>IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKML<br>LDQKHVQDIVFQLQRLVSTMSKYNDYAVLRDADVPFPIEVDLA<br>HTTLAYGLNQBEFTDGESEEEEEEDTAAGEPSRDRGAAGPLDKG<br>GSWCDS   |
| 5596       | 698  | 219  | GAVALPSSSLPAAELAAQGESQSLDLNSTRPTSEVYKISFIFP<br>NGDKYDGDCTRTSSGIYERNIGIHTTPNGIVYTGSKWDDKMNG<br>FGRLEHFSGAVYEGQFKDNMFHGLGTTFPNGAKYTGNNFNENRV<br>KGEGEYTHIQGTRMDVVTFFHTSCSQT  |
| 5597       | 3  | 731  | ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP<br>VPVIVGFVTLIIFKRELHTISFLGGLAELNEGWNWLIKNIQEP<br>PCGGPHTAVGTYKGMPSHSSQPMWFFSVYSFLFLYLRMHQTNNA<br>RFLDLLWRHVLSLGLLAVAFVSYSRVYLLYHTWSQVLYGGIAG<br>GLMAIAWPIFTQEVLTPLFPRIAAWVSEFFLIRDTSLIPNVLW<br>FBYTVTRAEARNRQKLGTKLQ   |
| 5598       | 326  | 2440   | GIGPIAASFIFCKVASLYIFLSPPPSVSGVPYSPANSWSICAL<br>VPLLGSQVPPHPPAPSPCCSGQTMKMLSFKLLLLLAVAGFFEG<br>DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQLELLSGG<br>EMLCGGFYPRLSCLLRSDSPGLGRLENKIFSVTNTECGKLEE<br>IKCALCSPHSQSLFHSPPERVLRLDLVPLLCCKDYCKEFFYTCR<br>GHIPGFLQTTADEFCFYARKDGLCFDPFPRKQVRGPASNYLD<br>QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR<br>LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL<br>SLAFHPNYKNGKLYVSYTTNQRWAIGPHDHLRVVEYTVSRK<br>NPHQVDLRTARVFLVLAELHRKHLGGQLLFGPDGFLYIILGDGM<br>ITLDDMEEMDGLSDFTGSVLRDLVDTCMNVPSIPRSPHFN<br>TNQPPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS<br>SARILQIIKGDYSESEPSLLEFKPFNSGPLVGGFVYRGCSBRL<br>YGSYVFGDRNGNFLTLLQSPVTKQWQEKPLCLGTSQSGCRGYFSG<br>HILGFEDELGEVYIILSSSKSMTQTHNGKLYKIVDPKRPLMPEE<br>CRATVQPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTG |
| 5599       | 326  | 2440   | GIGPIAASFIFCKVASLYIFLSPPPSVSGVPYSPANSWSICAL<br>VPLLGSQVPPHPPAPSPCCSGQTMKMLSFKLLLLLAVAGFFEG<br>DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQLELLSGG<br>EMLCGGFYPRLSCLLRSDSPGLGRLENKIFSVTNTECGKLEE<br>IKCALCSPHSQSLFHSPPERVLRLDLVPLLCCKDYCKEFFYTCR<br>GHIPGFLQTTADEFCFYARKDGLCFDPFPRKQVRGPASNYLD<br>QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR<br>LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL<br>SLAFHPNYKNGKLYVSYTTNQRWAIGPHDHLRVVEYTVSRK<br>NPHQVDLRTARVFLVLAELHRKHLGGQLLFGPDGFLYIILGDGM<br>ITLDDMEEMDGLSDFTGSVLRDLVDTCMNVPSIPRSPHFN<br>TNQPPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS  |

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|------------|--|--|---|
|            |  |  | SARILQIIKGDYSEPSLLEFKPFSNGPLVGGFVYRGQSERL YGSYVFGDRNGNFLTQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDLGEVYILSSSKSMTQTHNGKLYKIVDPKRLMPPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRGTG  |
| 5600       | 1977   | 1244   | SLRVLSGHLMQTRDLVQDPKSPKFIVTLTGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNNGSF SNAEMSELSVAQKPEKLLERCKYWPACNGDECAVHHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCTHVSRRIPVLSPKP AVAPPAPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC TFYHPTINVPRLHAKWIRPQTSE   |
| 5601       | 1977   | 1244   | SLRVLSGHLMQTRDLVQDPKSPKFIVTLTGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNNGSF SNAEMSELSVAQKPEKLLERCKYWPACNGDECAVHHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCTHVSRRIPVLSPKP AVAPPAPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC TFYHPTINVPRLHAKWIRPQTSE   |
| 5602       | 246  | 766  | YHTSCTVWRTAKEALENTEVPVGLMVYNNNEVVGKGRNEVNTK NATRHAEMVAIDQVLDWCROSGKSPSEVFEHTVLYVTVEPCIMC AAALRLMKIPLVVYGCNERFSGCGSVLNIAADLPNTGRPFQC IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECQILNMF  |
| 5603       | 1  | 565  | FRGRTPISSGGERGCAQYFIPATPARSGENRTMPGAGDGGKAPAR WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS CFGFBDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLLKDDRI TLVGSTKEKRNINISIVLRDLFSDTGKYTCHVKNPKENNLQHA TIFLQVVDRRMQ  |
| 5604       | 1  | 1506   | EDIFPAQLLKLQRHERVWQEPVDRHSWGGSGAGGVAGREWTDQGVVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GDFGCGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDGLGYKDLDLIFCADLRGEFQTVKDV VLDCLDLFPEGVNKEKITPLTLKEAYVQKMKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMETETFHPTIIGESVYGDQEAFFDHLCKNIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQKRL ESYLQNHVGLDRKYELMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCTYQAPYVADANFSNYIAQV QPVFTCQQQTYSTWLPNCN  |
| 5605       | 35   | 1821   | SQRSCPRSPSPAPPWARCSPDSRTGGVFPVPAWSAGGPALGL MAAPVRLGRKRPLPACPNLFVRWLTEWRDEATRSRHRTRFVQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMIDRLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNNGHFLTKEELLQRCQKS PRVAP GSARPPALRSLIIRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKPEPGEETA VPGAASAELASEAGVQQPLELRP GBYRVLLCVDIGETRGGGHRPELLRELQRLHVHTVRKLHVGF VVVAQETNPRDPANPGLVLDHIVERKRLDDLCSIIIDGRFREQ KFLRXRCGLERRVYLVEEHGSVHNLSPBSTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHITLRSRPWGTGPNPE SGAMTSPNPLCSLLTFSDFNAGAIKNAQSVREVFARQLMQVRG VSGEKAALVDRYSTPASLLAAYDACATPKQEETLLSTIKCGR LQRNLGPALSRITLSQLYCSYGPLT |
| 5606       | 3  | 1099   | GRSRCPGPGARGGTMSPRSCLSRLRLVFAVFAAASNWLYLAK LSSVGSISBEETCEKLGKLIQROVMCKRNLEVMDSVRRGAQLA IRECYQFRNRRNWCSTLDSLVPFGKVVTQGTREAAFYAISSA GVAFVTRACSSGELEKCGCDRTVHGVSPPQGFQWGSNDIAYG VAFSQSFVDVREKSGASSSRALMNLHNEAGRKAILTHMRVEC KCHGVSGSCEVKTCTWRAVPPFRQVGHALKEKFDGATEVEPRRVG SRRALVPRNAQFKPHTDEDLVYLEFSPDFCEQDMRSGVLGTRGR TCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCFKHWCFFVKC RQCQRLVELHTCR   |

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|------------|--|--|--|
| 5607       | 521  | 141  | PPVCNPAEAMPSPGTVCSSLLLLGMIWLDLAMAGSSFLSPEHQRV<br>QQRKESKKPPAKLQPRALAGWLRPEDGGQAECAEDELEVRFNAP<br>FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK  |
| 5608       | 2  | 983  | WFQSLRQADPGPPRHLLFMDFVAGAIIGVCGDAVGYPLDTVKV<br>RIQTEPKYTGIIWHCVRDYHRRBRVWGFYRGLLPVCTVSLVSSE<br>VFGTYRHCLAHICRLRFGNPDAPKPTKADITLSGCASGLVRVFLT<br>SPTEVAKVRLQTQTQAQKQRRLSASGPLAVPPMCPVPPACPEP<br>KYRGLPHCLATVAREEGLCGLYKGSALVLRDGHFSFATYFLSYA<br>VLCENLSPAGHSRDPDVGVLVAGGCAGVLAWAVATPMDVIKSL<br>QADGGQRRYRGLLHCVMTIVREEGPRVLFKGLVLNCCRAFPVN<br>MVFVAYEAVLRLARGLLT  |
| 5609       | 1628   | 304  | AKGVWVLPSPPPRPGRGALVSGSLRRGRSGTSWRPRRMNHSK<br>KRIRAKRSARPELKDSLDTWRHNYYESFSLSPAADVADNVERAD<br>ALQLSVEEFVERPERPKPVVLLNAQEGWSAQEKWTLERLKRKY<br>RNQFKCQGEDNDGYSVKMKYIYEMESTRDDSPLYIFDSSYG<br>EHPKRRKLEDDYKVPKFFTDLFQYAGEKRRPPYRWFMGPPRS<br>GTGIIHIDPLGTSANALVQGHKRWCLFPTSTPRELIKVTRDEGG<br>NQQDEAITWFNVIYPTQLPTWPEFKPLEILQKPGETVFPVGG<br>WNHVVNLDDTTIAITQNFASSTNFPVWHKTVRGRPKLSRKWYR<br>ILKQEHPELAVLADSVDLQESTGIASDSSSSSSSSSSSSSDSD<br>SECESSGEGDGTVHRRKKRRTCSMVGNDTTSQDDCVSKERSSS<br>R |
| 5610       | 54   | 1196   | LERTPASADMATKYQLFLAGLMLVTGSINTLSAKWADNFMAG<br>CGGSKESFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGQSDSS<br>VDPQQPFNPFLFLPPALCDMTGSLMYVALNMTSASSFQMLRGA<br>VIFTEGLFSVAFGRRLVLSQWLGLIATIGLVVVGADLLSKH<br>DSQKLESEVITGDLIIIMAQIIVAIQMVLEEFVYKHNVHPLRA<br>VGTEGLFGFVILSLLLVPMYIIPAGSFSGNPRGTLEDALDAFCQ<br>VGQPLIAVALGNISSIAFFNFAGISVTKELSATTRMVLDSLR<br>TVVIWALSALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR<br>LSRGRPLAESESEQRLLGGTRTPINDAS  |
| 5611       | 2  | 577  | FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG<br>ELSNRFQGGKAFGLLKAQERRLAEBINREFLCDQKYSDEENLPE<br>KLTAPEKBYMBFDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKM<br>ISEVTGGVSDTISYRDFVNMMLGKRSVAVLKLVMFEGKANESSP<br>KPVGPPPERDIASLP   |
| 5612       | 1  | 721  | ASRDGYMDATIAPHRIPEMPQYGEENHIFELMQAMWLCKHLNS<br>SLLTLENLILNEFSYTATERRLYLQKKTVPSSALLVQLIQRLE<br>EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDPTVL<br>IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET<br>AQKLLEYHRNIVRVIPIPKILKVISADQPCVDVFYQALTYVQS<br>NHRTNAPFTPRVLLGLGPVGS  |
| 5613       | 115  | 1279   | RGVDPALRRRAEKMLPLSLIKODEYKPKFNLFGKISGWFRSILSD<br>KTSRNLFFFLCLNLSFAPVELLYGIWSNCLGLISDSFHMFPDST<br>AILAGLAASVISKWRDNDAFSYGYVRAEVLAGEVNGFLFIPTAF<br>FIFSEGERALAPPDVHHERLLLSILGFVNVNLIGIFVFKHGGH<br>GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAHSHDH<br>AHGHGHFHSHDGP SLKETTGPSRQILQGVFLHILADTLGSGIVI<br>ASAIMMONGFLMIADPICSILIALIVSVIPLLRRESVGIIMQR<br>TPPLENSLPQCYQORVQQLQGVYSLQEQLFWTLCSDDVYVGTCLK<br>IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM   |
| 5614       | 3  | 1268   | LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER<br>APNGARQRLGVMAELQQLQEFPIPTGREALRGNHSAALLRVADYC<br>EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD<br>LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG<br>QKVIAPENLPLTPYCRRPLNFGCLDDIGHGKLDLSTQLSRTGT<br>LSRKSIIKAPATPASATLGRPPRIPEPVHLVVPVDPGRLSAASSA<br>SLASAGSAEGVGAPTPKGQAAPPAPPLPSSLDPPPPPAVEVF<br>QRPTLELSPPPPDEELPLPLDLPPLPDLGDELGLPPPPPGF<br>GPDEPSWVPASYLEKVVTLYPYTSQKONELSFSEGTVICVTRRY   |

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|------------|--|--|---|
| 5615       | 9  | 1558   | SDGWCEGVSEGTGFFPGNYVEPSC<br>ALGRRRPGDPRMEAAATPAAAGAAARREELDMVMRPLINEQNF<br>DGTSDDEEHEQEELLPVQKHVQLDDQEGISFVQTLMLHLKGNIGTG<br>LLGLPLAIKNAGIVLGPISLVFIGIISVHCHILVRCSHFLCLR<br>FKKSTLGYSDTVSFAMEVSPWSCLOKQAAWGRSVVDFFLVITQL<br>GFCSVYIVFLAENVKQVHEGFLESKVFISSNSTSSNPCERRSVD<br>LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMASLVIIYQ<br>YVVRNMPDPHNLPIVAGWKYPLFFGTAVFAFEGIGVVLPLENQ<br>MKESKRFPQALNIGMGIVTTLVTLATLGMYCFHDEIKGSITLN<br>LPQDVWLYQSVKILYSFGIFVTYSIQFYVPAEIIIPGITSKFHT<br>KWKQICEFGIRSFVLSITCAGAILIPRLDIVISFVGAVSSSTLA<br>LILPPLVEILTFSEKHYNIWMVLKNISIAFTGVVGFLLGTYYITV<br>EEIYPTPKVAVAGTPQSPFLNLNSTCLTSLGLK           |
| 5616       | 1  | 719  | DDFVRGQPSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE<br>LKLHSSGDLRLDNMLRGTEIGVLAKAFIDQGLIPDDVMTRLAL<br>HELKNLTQYSWLLDGFPTLPOAEALDRAYQIDTVINLVNPFV<br>IKQRLTARWIHPASGRVYNIENPPKTVGIDDLTGEPLIQREDD<br>KPETVIKRLKAYEDQTKPVEYYQKGVLETFSGTETNKIWPYV<br>YAFLOTKVPQRSQKASVTP  |
| 5617       | 176  | 765  | PWRGRGSRPRGAGAMAEQVNRSAAGLAPDCEASATAETTVSSVG<br>TCEAAGKSPKDYDSTCVFCRIAGRQDPGTELLHCENEDLICF<br>KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTL<br>ERNFTDFTNVRMGFHMPPFCSISHLHLVLAPODQLGFLSKLV<br>YRVNSYWFITADHLIEKLRT   |
| 5618       | 3  | 1692   | YLYNINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLRVPDES<br>LFLNSGGDSLKSIRLLSBIKLVGTSVPGLEIILSSSILEIYN<br>HILQTVVPDEDTVTRKSCATKRKLSNINQEEASGTSLHQKAIMT<br>FTCHNEINAFVVLRSQSILSLNSTRFLTGLHCSSACPSDSVS<br>QTNIQNLKGLNSPVLICKSKDPCVAKVSEEGKPAIGTQKMEH<br>VRWRSDTGKCVDAAPLVVPTFDKSTTVYIGSHSRMKAVDFY<br>SGVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVVVLKNSNG<br>EKYWMFTTEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKCK<br>VWKSCKGGTVFSSPCLNLI PHLYFATLGGLLAVNPATGNVW<br>KHSCGKPLFSSPQCCSQYICIGCVGNLLCFTHFGEQVWQFSTS<br>GPIFSSPCTSPSEQKIFFCSDHCFIYCCNMKGLQWKFETTSRV<br>YATPPFAFHNYNGSNEMLLAAASTDGKVVWILESQSGQLQSVYELP<br>GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK |
| 5619       | 2160   | 1477   | DSPVLPTSGNVISTAQPAQPSAVEAALRSLGSPPGAGRGCCPCP<br>AQLSHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR<br>RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGHCSVL<br>LWGTGRGSGSPSPGCLHPAQAHSQDLPLVHVDVGWQFPPLGP<br>TVGLRPLGLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA<br>ECSPPATP  |
| 5620       | 930  | 182  | PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAEIAIKLGST<br>AIGIQTSEGVCLAVEKRITSPLEPSSIEKIVEIDAHIHCAMSG<br>LIADAKTLIDKARVETQNHWFYNETMTVESVQAVSNLALQFC<br>EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR<br>AIGSASEGAQSSSQEVYHKSMTLKEAIKSSLIILKQVMBEKLNA<br>TNIELATVQPGQNFHMFTEKELEBEVIKDI   |
| 5621       | 3  | 819  | VVEFVEYTATDANVKNESLSSVQQLGIMTVRYGKFLSLLKDG<br>ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNAYAGHDWVSSLF<br>MIMLGDKEXTFQFLHQFSRLTSAFLWLPRLHISSYLPNDTVES<br>GIHPVYFCSTHYIEMLLKAEPLVFSFAHMSGFAPSQICLOWIT<br>QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQDDILQ<br>HTQTDLQVFLKEALHGFVSDYFEXMEILLEQNYRTVLLRDMR<br>NIRLQST   |
| 5622       | 1122   | 456  | AASTKDAVSRKRSHSASEKSGTGTSSIKRLNMNPNQIRNPMKAMY<br>PGTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTGVFERN<br>QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA<br>GEVAEFLARHSNNVNTIIFARLYYFQYPCYQEGELRSLSQEGVAV   |



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|------------|--|--|--|
|            |  |  | EIMDYEDFKYCWENFVYNDNEFFKPNKGLKTNFRLLKRRRLRESLQ   |
| 5623       | 3  | 954  | FLPFFIRAPKISRNGQWLF TTTT PPFANKALPGWEGIVPACFW<br>RKKILTPSTGTMLLQVTILFLLPSICSSNSTGVLEAANNLSLV<br>TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST<br>ATFLTSKDEGLKATTTDVRKNDISIISNVTVTSVTLPNVASTLQS<br>SKPKTETQSSIKITEIPGSVLQPDASPSKTGTLTSPVTPIPENT<br>SQSQVIGTEGGKNASTSATSRSYSSIIIPVIVIALIVITLSVFL<br>VGLYRMCWKADPGTPENGNDQPSQSKESVKLLTVKTISHESGEH<br>SAQGTKN   |
| 5624       | 159  | 898  | PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT<br>SSGSRKLYFDTHALVCLLEDNGFATQQAETIIVSALVKILEANMD<br>IVYKDMVTMKQOEITFQQVMSQIANVKKDMIIIEKSEFSALRAE<br>NEKIKLELHLKQVMDEVIKVRTDTKLDNFLEKSRVKELYSLN<br>EKKLELRTEIVALHAQQDRALTQTDRIETEVAGLKTMLLESHK<br>LDNIKYLASGIFTCLTVALGFYRLMI   |
| 5625       | 1  | 1180   | TIPSSAAARAGPAGALEALS PGCARAHAEERRGEMRATPLAAP<br>AGSLSRKKRLEDDNLDTERPVQKRARSGPQRLPPCLLPLSP<br>TAPDRATAVATASRLGPVVLLEPEEGGRAYQALHCPTGTETCR<br>VYPVQEAVALVEPYARLP PHKHVARPTEVLACTQLLYAFFTRTH<br>GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL<br>CRFVFADRERKKLVLENLEDS CVLTGPDSDLWDKHACPAYVGPE<br>ILSSRASYSKGAADVWSLGVALFTMLAGHYPFQDSEPVLLPGKI<br>RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ<br>DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLVG  |
| 5626       | 3123   | 2011   | PPRALGSAVAMENQVLT PHVYWAQRHRELYLRVELSDVQNPATSI<br>TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN<br>ITVQKKVSQWWRRLTKQEKRLFLAPDFDRWLDES DAEMELRAK<br>EERLNLKRLSESGSPETLTNLKGYLFMYNLVQFLGFSWIFVN<br>LTVRFICILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT<br>SPVLP SLIQLLGRNFILFII FGTMEEMQNKAVVFFVYLWSAIE<br>IFRYSFYMLT CIDMDWKVLTWLR YTLWIPLYPLGCLAEAVSVIQ<br>SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIIMIFLGLYINF<br>RHLYKQRRRRYGQKKKKIH   |
| 5627       | 3123   | 2011   | PPRALGSAVAMENQVLT PHVYWAQRHRELYLRVELSDVQNPATSI<br>TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN<br>ITVQKKVSQWWRRLTKQEKRLFLAPDFDRWLDES DAEMELRAK<br>EERLNLKRLSESGSPETLTNLKGYLFMYNLVQFLGFSWIFVN<br>LTVRFICILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT<br>SPVLP SLIQLLGRNFILFII FGTMEEMQNKAVVFFVYLWSAIE<br>IFRYSFYMLT CIDMDWKVLTWLR YTLWIPLYPLGCLAEAVSVIQ<br>SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIIMIFLGLYINF<br>RHLYKQRRRRYGQKKKKIH   |
| 5628       | 75   | 1455   | VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYS SSPCKLP<br>SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG<br>GGWFGEGILTGNKEKTMQSLNDRLAGYLEKVRQLEQENASLESR<br>IREWCEQQVPYMC PDYQSYFRTIEELQKKTLCSKAENARLVVEI<br>DNAKLAADDFTKYETEVSRLQLVESDINGLRRILDDLTLCKSD<br>LEAQVESLKEELLCLKNHEEVNSLRCLQGLDRNLNVEVDAAPV<br>DLNRVLEEMRCQYETLVENNRDAEDWLDTQSEELNQQVVSSE<br>QLQSCQAEIIE LRRTVNALEIELQAQHS MRDALESTLAETEAR<br>SSQLAQMQCMITNVEAQLAEIRADLERQNGEQVLLDVRARLEC<br>EINTYRGLLESEDSKLP CNPCADYSPSKSCLPLPAASCGPSA<br>ARTNCSARPICVPCPGGRF |
| 5629       | 2287   | 938  | GRPRSSSDNRNFRLE RAGLSSAAVQTRIGNSAASRRSPAA RPPV<br>PAPPALPRGRPGTEGSTSL SAPAVLVAVAVVVVVV SAVANAMA<br>NIYHVPPGSP EVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP<br>QEVTLQLFTDGI TNKLIGCYVGN TMEDVVLVRIYGNKTELLVDR<br>DBEVKSRVLAHGCA PQLYCTFNNGLCYEFIQGEALDPKHVCN<br>PAIFRLIARQLAXIHAHNGWIPKSNLWLKNGKYFSLIPTGF   |

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|------------|--|--|--|
|            |  |  | <p>ADEDINKRFLSDIPSSQILQEEMTWKEILSNLGSPPVVLCHNDL</p> <p>LCKNIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNFAVGSVDV</p> <p>DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV</p> <p>NQFALASHFFWGLWALIQAKYSTIEFDLGYAIVRFNQYFKMKP</p> <p>BVTALKVPE</p>   |
| 5630       | 1194   | 278  | <p>GFWAIATCAHHLPPGSPWLVFASPWRLPEMSSFGYRTLTVALF</p> <p>TLICCPGSEKVFVHVRPKLAVEPKGSLEVNCSSTCNQPEVG</p> <p>GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM</p> <p>NSNVSVYQPPRQVILTLPQTLVAVGKSFTEICRVPTVEPLDLSLT</p> <p>LFLFRGNETHYETFGKAAPAPQEAATATFNSTADREDGHRNFSC</p> <p>LAVLDMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL</p> <p>LSLFTSVLLCFIFGQHLRQRMGTGVRAAWRRLLPOAFRP</p>   |
| 5631       | 1053   | 290  | <p>SRVDDFVRPEPSRAEPSRSGRRRPARAATMSVFGKLFAGAGGGK</p> <p>AGKGGPTPQEAIRLRDTEMLSKKQEFLEKKIEQELTAACKHG</p> <p>TKNKRAALQALKRKKRYEKQLAQIDGTLSTIBFQREALBNANTN</p> <p>TEVLKNMGYAAKAMKAHNDMDIDKVDLMQDIADQQLAEIEIS</p> <p>TAISKPVGFGEFDEDELMAELELEQEEELDKNLEISGPETVP</p> <p>LPNVPSIALPSKPAKKKEEDDDMKELNWAWSM</p>  |
| 5632       | 3  | 952  | <p>VVLGWSPPRRLLWWSLGAARPAVPVSGLARSLHVETRRPHRRRA</p> <p>SVRVARGRLGVWAQPOPLPRPVGSRREMPPGPPPAYAPTNGD</p> <p>FTFVSSADAEDLSGSIASPDVKLNLGDFIKESTATTFLRQRGY</p> <p>GWLLEVEDDDPEDNKPLLEELDIDLDIYYKIRCVLMPMPSLGF</p> <p>NRQVVRDNPDFWGPLAVVLFSSMISLYGQFRVWSWIIITWIFGS</p> <p>LTIFLLARVLGGEVAYGQVLGVIGYSLPLIIVAPVLLVVGSEF</p> <p>VVSTLIKLFVFWAAYSAAASLLVGEFPKTKKPLLIYPIFLLYIY</p> <p>FLSLYTGTV</p>  |
| 5633       | 771  | 460  | <p>QGCSKTMSVGRPFYRSSEFMEQLLSSHQVPPFFCCFTVVCLCN</p> <p>CLFENSVSPLYMLCFNFFMSIFFYSLITKLNLIYLGWSYQSL</p> <p>LLLLSGHRPWGSSMV</p>  |
| 5634       | 1446   | 855  | <p>PRATGRIRSRVAASRPAGAGASGAEPFRSGRERSRLSGRRAPAM</p> <p>ARNTLSSRRFRVDIDFDENKFVDEQEAAAAAAEPGDPSEVD</p> <p>GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK</p> <p>SSEIEQAVQSLDRNGVDLLMKYIYKGFKEKPTENSSAVLLQWHEK</p> <p>ALAVGGLGSIIRVLTARKTV</p>  |
| 5635       | 3  | 943  | <p>DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL</p> <p>RSLFHPPFVTRSGAPRAVLVGSWSWPAKMVAAPVAVARGWSGLAL</p> <p>GVRRAVLQPLGTQVRWSRYSPFKDPLIDKEYRKPVHEELTEE</p> <p>EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMIGGNRV</p> <p>LARSLMIQTLEAVKRKQFEKYHAASAEQATIERNPYTIFFHOAL</p> <p>KNCEPMIGLVPILKGRFYQVPVPLPDRRRRFLAMKWMITECRD</p> <p>KKHQRITLMPEKLSHKLLEAFHNQGPVIRKXDLHKMAEANRALA</p> <p>HYRWW</p>  |
| 5636       | 2253   | 1143   | <p>LEDITICQHPPEAKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG</p> <p>LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI</p> <p>ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFGSSPK</p> <p>YGSEEDCSSATSGSVGANSTGGIAGVASSSKNTLDMQSSGFD</p> <p>ALLHEIQEIRETOARLEESFETLKEHYQRDYSILMQTLQEERYR</p> <p>CERLBEQLNDLTTELHQNEILNLKQELASMEEKIAYQSYERARDI</p> <p>QEALEACQTRISKMELOQQQQQVQVQLEGLENATARNLLGKLINI</p> <p>LLAVMAVLLVVFSTVANCVVPLMKTRNRFTSTLFLVVFIAFLWK</p> <p>HWDALFSYVERFFSSPR</p>              |
| 5637       | 948  | 2532   | <p>MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHLLPHLPPPHLH</p> <p>HHHHQHHLHPGSAAAVHPVQOHTSAAAAAAMNLPNG</p> <p>QQQYFSPAPGOAPGPAAPAAQVQAAAAATVKAHHHQHSHHP</p> <p>QQQLDIEPDRPIGYGAFGVVSVTDPRDGKRVALKKMPNVFQNL</p> <p>VSCRKRVRELKMLCFPKHDNVLSALDILQPPHIDYFEEIYVVT</p> <p>LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD</p> <p>IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTOYYRA</p> <p>PEILMGRSHYSNAIDWSVGCIFAEELLGRRILFQAQSPQQQLDL</p> <p>ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA</p> |

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|------------|--|--|---|
| 5638       | 125  | 1155   | THEAVHLLCRMLVFDPYKRISAKDALAHPYLDDEGRRLRYHTCMCK<br>CCFSTSTGRVYTSDFEPVTNPKFDDTTEKNLSSVRQVKEIIHQF<br>ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPSPPLVWE<br>DRKMSELDQLRQAEQLKNQIRDARKACADATLSQITNNIDPVG<br>RIQMTRRRLRGLHLAKIYAMHWGTD SRLLVASQDGKLIWDSY<br>TTNKVHAIPLRSSWMTCAYPAGSNYVACGGLDNICSIYNLKTR<br>EGNVRVRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET<br>GQQTTFGTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM<br>CROTFTGHESDINAICFFPNGNATGSDDATCRFLDLRADQEL<br>MTYSHDNIIICGITSVSFSKSGRLLLAGYDDPNCNVWDALKADRA<br>GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN |
| 5639       | 125  | 1155   | DRKMSELDQLRQAEQLKNQIRDARKACADATLSQITNNIDPVG<br>RIQMTRRRLRGLHLAKIYAMHWGTD SRLLVASQDGKLIWDSY<br>TTNKVHAIPLRSSWMTCAYPAGSNYVACGGLDNICSIYNLKTR<br>EGNVRVRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET<br>GQQTTFGTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM<br>CROTFTGHESDINAICFFPNGNATGSDDATCRFLDLRADQEL<br>MTYSHDNIIICGITSVSFSKSGRLLLAGYDDPNCNVWDALKADRA<br>GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN  |
| 5640       | 280  | 1092   | QQGNKKTMLSHNTMMKQKQKQATAIMKEVHNDVDGMDLGGKVS<br>IPRDIMLEELSHLSNRGRLFKMRQRSDKYTFENFQYQSRQAQ<br>NHSIAMQNGKVDGNSLEGGSQAPLTPNTPDPRSPNPDPNIAP<br>GYSQPLKEIPPEKFNNTAVPKYQSPWEQAISNDPELLEALYPK<br>LPKPEGKAEPLDYRSFN RVATPFGGFEKASRMVKFKVPDFELL<br>LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT<br>VPESDIL   |
| 5641       | 27   | 332  | CRHNCNGDVKLLSNQMDKLFAPHLFTFHGLLHFLDGSIQKLIQA<br>EILSDNSSLVLENNFLFKVSKQFIHLIAKKFYISITIVSAS<br>NGESFVLSMIVTG  |
| 5642       | 199  | 1247   | ITPCRMDFLVFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ<br>IFSCIPECLQRAMHGLLHLYLFHTRNHTFIVLHLVQGMVYTEY<br>TWEVFGYCOELELSLHYLLLPYLLGVNLFFFTLCGTNPGIIT<br>KANELLFLHVFYFDEVMPFKNVRCSTCDLRKPARSKHCSVCNWC<br>VHRFDHHCWVNNCIGAWNIRYFLIYVLTASAATVAIVSTTF<br>LVHLVMSDLYQETYIDDLGHLHVM DTVFLIQYFLTFPRIVFM<br>LGFVVVLSFLGGYLLFVLYLAATNQTTNEWYRGDWANCRCPL<br>VAVPSPAEPQVHRNIHSHGLRSNLQEIFLPAPFCHERKKQB   |
| 5643       | 1  | 847  | PSGGVRDVETRGPSRAARGPRVVMERRGVGAGAIKKKLAERK<br>YKERGTVLAEDQLAQMSKQDMFTNLEEFASKHKQEIIRKNPEF<br>RVQFQDMCATIGVDPLASGKGFWEMLGVGDFYELGVQIIEVC<br>LALKHRNGGLITLEELHQOVLKGRGKFAQDVSDDLITRAIKKLK<br>ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVVLQLAENGYVTVS<br>EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALE<br>TDLYSQEITAEAREALP  |
| 5644       | 83   | 1138   | PRRMGSWVQLITSVGQQNHPGWTVAGQFQEKRFTEEVIIEYFQ<br>KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP<br>YVAIEDKDMQKQEQQFREWFLKEFPQIRWKIQESIERLRVIANE<br>IEKVHRGCVIANVVGSTGILSVIGVMLAPFTAGLSLSITAAGV<br>GLGIASATAGIASSIVENTYTRSALSTASRLTATSTDQLEALRD<br>ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW<br>RYVPINNVETLRTRGAPTRIVRKVARNLGKATSGVLVLDVNL<br>VQDSLHLHKGESSEAEELLRQWAQEEENLNELTHIHQSLKAG  |
| 5645       | 537  | 799  | VQSVRLKRLSPDTPPGDSGNRDVTRDPVTGPLNSASSQVPTL<br>YLCQLNSLLGHSSVEDARATMELYQISQIRARRGLPRLAVSD  |
| 5646       | 3745   | 3328   | AEQVGTSPHLLPTMLSSCLPPANVTTKAATPPPLVLSLTTADP<br>AGKPAPCRVTLTLRLASIPATKRASFLSSFIKMFBELEYILGF<br>LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL<br>RAEGGAQ   |
| 5647       | 288  | 800  | GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPREGCSLH<br>EEDTORHETYHQGGCQVLRQSPWLMMRMGLGRGLQEQYQLPY  |

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|------------|--|--|---|
| 5648       | 7  | 1518   | QRVLPPIFTPAKMGATKEEREDTPIQLQELLALLETALGGQCVD<br>RQEVAEITKQLPPVVPVSKPGALRRSLRSMSQEAQRG<br>VLSELGGRHEALREVGAEWPPPTCSFNICSGLQQAGNTDWSLTM<br>APQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPKEK<br>SSTKETERKETKAEELDAEVLEVFPHTHEWQALQPGQAVPAGS<br>HVRNLQGTGERAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS<br>ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV<br>IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYVYVHQM DNAQD<br>LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAPSSNPKVQVEAI<br>EGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK<br>LGGLQVLRTLVQEKGEVLAVRVVTLVLDVTEKMFABEEAEALT<br>QEMSPKQLQYRQVHLLPGLNBQGWCEITVHLLALPEHDAREKV<br>LQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLASLELQDGE<br>DEGYFQELGVSNSLLKELR                  |
| 5649       | 1172   | 3006   | MLQEQDLDAINEEIRMIQBEKESTELRAEEIETRVTSGSMEALNL<br>KQLRRKRSIPTSLTDLASLASAPPLSGRSTPKLTSRSAQDLDR<br>MGVMTLPDRLKRRKLLSPVSRREENREDKATIKCETSPSSPR<br>TLRLEKLGHPALSQEEGKSALEDQGSNPSSNSSQDSLHKGAKR<br>KGIKSSIGRLFGKKEKGRLIQLSRDGTGHVLLTDSEFSMQEPM<br>VPAKLGTAQAEKDRRLKKKHQLEDARRKGMPPAQWDGPTVVSWL<br>ELWVGMPAWYVAACRANVKSGAIMSALSDEIQREIGISNALHR<br>LKRLAIQEMVSLTSPSAPPTSRSSGNVWVTHEMETLETSTK<br>TDSSEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV<br>DARMLDHLTKKDLRVHLKMVDSFHRTSLQYIGIMCLKRLNYDRKE<br>LEKRREESQHEIKDVLVWTDQVHVWQSIGLRDYAGNLHESGV<br>HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNLLALG<br>TDRKLDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA<br>GFRVSTLGTLPFPAPPKKIMPEAHSHYLYGHMLSAFRD |
| 5650       | 1172   | 3006   | MLQEQDLDAINEEIRMIQBEKESTELRAEEIETRVTSGSMEALNL<br>KQLRRKRSIPTSLTDLASLASAPPLSGRSTPKLTSRSAQDLDR<br>MGVMTLPDRLKRRKLLSPVSRREENREDKATIKCETSPSSPR<br>TLRLEKLGHPALSQEEGKSALEDQGSNPSSNSSQDSLHKGAKR<br>KGIKSSIGRLFGKKEKGRLIQLSRDGTGHVLLTDSEFSMQEPM<br>VPAKLGTAQAEKDRRLKKKHQLEDARRKGMPPAQWDGPTVVSWL<br>ELWVGMPAWYVAACRANVKSGAIMSALSDEIQREIGISNALHR<br>LKRLAIQEMVSLTSPSAPPTSRSSGNVWVTHEMETLETSTK<br>TDSSEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV<br>DARMLDHLTKKDLRVHLKMVDSFHRTSLQYIGIMCLKRLNYDRKE<br>LEKRREESQHEIKDVLVWTDQVHVWQSIGLRDYAGNLHESGV<br>HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNLLALG<br>TDRKLDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA<br>GFRVSTLGTLPFPAPPKKIMPEAHSHYLYGHMLSAFRD |
| 5651       | 646  | 1869   | ARQGRQRPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL<br>AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP<br>WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAALSPASPAGP<br>ADP*LPGHSSQSPPRG*RWGRSRAPAPAHPEHPAPAGSASASQ<br>QTPGWPGSCCLAQGWQAEPLGAPGAEDG\VPVPPQRGFPLGTIGS<br>PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAAPNCRV*GSA<br>PALHRAPAAADPGSPLQAPPRAWASPAAGPGLSSSDYCGGLGA<br>GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA<br>CMPSPVVEGSLGLSRKGHGLPSQAR*GWHECRRARHLVPLPRL<br>LGPRGRTGRFPSSPS   |
| 5652       | 735  | 343  | HHKKYQHIIHQKFSFCEPACGKSFNFKKHLKEHMKLHSDTRDYI<br>CEFCARSFRTSSNLVIRRIHTGKPLQCEICGFTCROKASLNW<br>HQRKHAETVAALRFCEFCGKRFEKPDVSAHRSKSHPALLLA   |
| 5653       | 66   | 1401   | RGRQLSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL<br>CFPQPCQPGTRRRRRSLKEATEPQLAMAEFVTLKDVGMDFTL<br>GDWEQLGLEQGDFTWDALDNCQDLFLDDPPRPNTLSHPDGSBD<br>LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ<br>GWLLELQFRRSLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMQ   |

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|------------|--|--|---|
|            |  |  | ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF<br>SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTOHWITHTREK<br>PTVHQECEQGFDRKASHSGYPKTHGTGYKPYVCNEYGTPFSQSTY<br>LWHQKTHAGEKPKCSQSDSDHPPSHDTQSGEHQKTHTDKSYNCN<br>ECGKAFTIRIFHLTRHQKIHTRKRYSCSKCOATFNLKRLHIQHQK<br>THAANV  |
| 5554       | 3  | 598  | TLPLFPGRFRFRGWRRCGAVAAKKNSTGGNVSNQRRDSVRMSAL<br>NWKPFVYGGGLASITABCGTFPIDLTKTRFQIQGQTNDAKFKEII<br>YRGMHLALVRIGREGLKALYSG*VGLHAFCHCSLPHMGIDFR<br>PRLHRSQVKSRLCV*KEQIA**/MFSLLISTLISKYIYYAADVL<br>EKLFFYIQVQTDNNKKICLFKNI  |
| 5655       | 2  | 867  | RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP<br>PLSYPSVFFAVARVLPQRSQDYRAAGMPQLSGGGGGGGGDPCLC<br>ATDEMI PFKDEGDPQ\REKIFAEIVNPEEGDLADIKSSLVNES<br>EII PASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG<br>PSYSSYSYGYIMPMNMNDPYMSNGSLSPPI PRTSNKVPVQPSH<br>AVHPLTLITYSDEHFSPGSHPSHIPSDVNSKQMSRHPAPDI<br>PTFYPLSPGGGQITPPLGWQQP  |
| 5656       | 228  | 1066   | PRRVPLPEFASGPGAAFFHSGRLQSRSLTKDSAGCFSCQCRSAM<br>LVLRSGLTKALASRTLAPQVCSFATGPROYDGTFFYEFRTYYLK<br>PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVPHIWK<br>YDNFPHRAEVRKALANCKENQEQS IIPNIAIDKQETEITYLIP<br>WSKLQKPPKEGVYELAVFQMKPGGPALWGDFAFERAINAHVNLGY<br>TKVVGVFHTTEYGEINRVHVLWVWNSADSRAAVRHKSHEDPISWG<br>GVRESVNYL\VSQNM   |
| 5657       | 105  | 1052   | GQRLQSPRVQMPVQPPSKDTEEMEAEQDSAAEMNGEESEEEER<br>SGSQTESEEESEEMDEDEDYERRRSECVSEMLDLKQFSELKEXL<br>FRERLSQLRLRLLEVGAEARPEYTEPLGGLQSRSLKIRIQVAGIY<br>KGFCLDVIRNKYECLEQGAQHLESEKLLLYDTLQGELOERIOR<br>LEEDRQSLDLSEWDDKLHARGSSRSWDSLPPSKRKKAPLVSG<br>PYIVYMLQEI DILEDWTAIKKARAASVPOKRSD\LDPAVHSQ<br>GDPQSSWHCTQDSRLPPADRRTHRLRVCPARLLWCCWALPLHL<br>ALVWTPPL   |
| 5658       | 2346   | 3541   | TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK<br>NQLLALLKCTDTLQLRDAIFCQALVAACVTFSEQLLAALGY<br>RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE<br>RTMLIEDIWTLSLDNVTFSFKQLDENYVANTNVFYHIEGSRQA<br>LKVI FYLD SYHFSKLPSRLEGGASLRHLTALFTKVLENVEGLPS<br>PGSQAADLQDDINAQSLKVKQYRYRKLAPYRLERSNLPTDAST<br>TAVKIDQLIRPINALDELCLRMKSPVHPKPCAAGSVGAGLIPIS<br>SEL CYRLGACQVMCMGTGMQRSTLSVSLQQAAILARSHGLLPKC<br>IMQATDIMRKQGPVEILAKNLRVKDQMPQGAFLYRLCQPKMN<br>GDL |
| 5659       | 2  | 696  | WKRSGEVSPKGLGAWRGNSGRPKIIGRAAEAEENEDRTLGRLLP<br>GNERSQPRSPRLRLAPQLKAEAAADKGLAPVPPFPSSGHSGPC\<br>EREGEGQGRGRSRRGAHLELKPSPLRAGAPTDRGRGGPAEVA<br>AAGGRMVQKESQATLEERESELSNPAASAGASLEPPAAPAG<br>EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL<br>FRRLQKWELNTYL  |
| 5660       | 229  | 853  | PVTMAFSELPMEILLINLIVSLLGFVATVTLIPAPRGHFIAARL<br>CGQDLNKTSRQIPESQSVISGAVFLIILFCFIPFPFLNCFVKE<br>QRKAFPHHEFVALIGALLAICCMIFLGFADVLNLRWRHKL LLP<br>TAASLPLLMVYFTNFGNTTIVVPKFRPILGLHLDLGR*SYHCC<br>PYGYTFREPFLVHLHLLQVFLCLCVFDPFW  |
| 5661       | 2  | 473  | LNLYPSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL<br>AGMAVTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK<br>ADFVDTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP<br>SLAVHMERGMMDGEQKWYRGRT  |
| 5662       | 2  | 1318   | LRKEGRCRGRSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSA<br>FFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF   |

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|------------|--|--|---|
|            |  |  | LHVNDGSSLESQVVDASGLDSRELTFGSSVEVQGLIKSPSKR QNVELKAEKIKVIGNCDADKDFPIKYKERHPLEYLROYPHFR CRT NVLGSILRIRSEATAAHSFFKDSGFVHIHTPIITSNDSEGAGE LFOLEPSGKLKVPENFFNVPAFLTVSGQLHLEVMSGAFQVPT FGPTFRAENSQSRRLAEFYMIEABISFVDSLQDLMQVIEELFK ATTMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE AVELLKQASQNF TFTP EWGADLRTEHEKYL VKHCNIPV FVIN Y PLTLKPFYMRDNE DGPQLEGSVA*HSLGLMILLSIVVIGQP                                    |
| 5663       | 119  | 698  | PADTGRSTAKTGPFPRLSLEMDPRYGMCPKLGASGCPGAERSLL VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQGLYRKVMLENYR NLVFLGIALTKPDLITCLEQKKEPWNKRHEMVAKEPVCISHFP QDLWAEQDIKDSFQEA ILKKGKYGHANFQLQKGCKSVDECKVH KEHDNKLNQCLIPK KKK  |
| 5664       | 118  | 572  | SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGORKY G GPPPGWDAAPPERGCEIFIGKLPRLDFEDELIPCEKIGKIYEM RMMDFNNGNRGYAFVTFSNKVEAKNAIKQLNNYIEIRNGRL LGV CASVDNCRFLVGGIPKTKK   |
| 5665       | 347  | 702  | VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE ETEVKGKRRGRPGRPSPSTNKKPRKSPGEKSRIEAGIRGAGRGR ANGHPQQNGEGEPVTLFEVVKLGSAMQRC   |
| 5666       | 213  | 540  | VSLPTSCCKMITLNNQDQPVFPNSSHDEYKIAALVFYSCIPYI GLFVNITALWVFSCTTKKRTVTIYMMNVALVDLIFIMTLPPRM FYYAKDEWPFGEYFCQILGA  |
| 5667       | 1  | 695  | HPLPSASLGLPSVSLGVSLCVRSALEAVVPMLPKRRRARVGSF SGAASSTPPSTRFPGVAIYLVEPRMGRSRRRAFLTGLARSKGFR VLDACSSSEATHVMEETSAAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLAGQPPVPECHRLLEVAGPSKGPLSPAAMPAYACQR PTPLTHTHTGLSEALEILAEAAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQ  |
| 5668       | 691  | 894  | CSFLFCIPDLFLQLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ VLVRTAIRCAQAQTGIDLSGCTKW  |
| 5669       | 407  | 1  | DSGAPEGLSPLMSTQEGLSMAHPQAYTTFIYLHARKRRGEIGD ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK ARGAPT KYSGSPIGSPTTPPTRPPSFNLPAPHLASMLQKL NSQ  |
| 5670       | 3  | 373  | SSECLTMAWIPLLLPLLICTVSVASYELAQPSVSVSPFGQTA K ITCSDVLAKKYARWFQKPGQAPVLVIYKOTERPSGIPERFSG STSGTTVTLTISGAQVEDADYFCYSATDNFLWVF  |
| 5671       | 280  | 524  | KFPFKKTPPHLGMSAITLWQFLQLLQDQKHEHLICWTSNDGE FKLLKAKKVAKLWGLRKNKNTNMNYDKLSRALRLLFMT   |
| 5672       | 2  | 557  | FVPATPDGVLPPSRDPAMAKRSSIYIRIVEGKNLPAKDITGS SDPYCIVKVDNEPIIRTATVWKTLCFWGEEYQVHLPTTFHAVA FVVMDEALSRDDVIGKVCLTRDTIASHPKGKFSLPSTGLPSP WPPSHSETSPLGSVWSPAQKGPFLLSPEAGATFCTPGLCSAACS QAWLLPLP   |
| 5673       | 327  | 696  | ITVADQISHWSAGRIKNRTRIPECIHSSAATLAGPHTMEGESV KLSSQTLIQAGDDEKNQRTITVNPAMGKAFKVMNELRSKQLLC DVMIVAEDVEIEAHRVLAACSPYFCAMFTGDMS   |
| 5674       | 17   | 984  | GGGSMEGESTSAVLSGFVLGALAFQHLNLTDSDEGFLLEVKGE AKNSITDSQMDDEVVYTIIDIQYIPCYQLFSFYNSSGEVNEQA LKKILSNVKNVVGWYKFRHSDQIMTFRERLLHKNLQEHFSNQ DLVFLLLTPSIITESCSTHRLHSYLYKPKGLFHRVPLVAVNLG MSEQLGKTVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKIN EMYASLQELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRGA QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID MFLKAVTTTTISM  |
| 5675       | 80   | 753  | EGSRRGPTRLARLSARAORLHFPFGFSSRLIHFRGVSECRPPG KSGVPVSAPGSDGKWEERPOMFSLMASCCGWFKRWREPVRKVT LLMVGLDNAGKTATAKGIQGEYPEDVAPTGVGFSKINLRQGF EV TIFDLGGGIRIRGIWKNYAESYGVIFVVDSSDEERMEETKEAM   |

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|------------|--|--|---|
|            |  |  | SEMLRHRPRISGKPFILVLANKQDKGALGEADVIECLSLKLVNE HKCL   |
| 5676       | 2  | 930  | FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV RDLARNDGEESTDRTPLLPAPRAEAPVCCSARYNLAILAFFG FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH HNQTGKKYQWDAETQGNILGSFFYGYIITQIPGGYVASKIGCKM LLGFGILGTAVLTLFTPIAADLGVGLPLVRLALEGLGEGVTFFA MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYMN WTVYFYFFGTIGIPWFLWLVSDTPQXHKRISHYEKEYILSS L  |
| 5677       | 1  | 1028   | PFRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGELVAAARAA VTAETHPLPLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP GRSLPGLTAATMSSSFESALEKKLSELSNSQSVQTLSLWLIIH RHAGPIVSVWHRELKAKSNRKLTFLYLANDVIQNSKRKGPEF TREFESVLVDASHVAREADEGCKKPLERLLNIWQERSVYGGF IQQLKLSMEDSKSFPKATEEKKSLKRTFQIQEEDDDYPGSY SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ DVSLEKITDKZAAERLSKTVDACLNRNGPGTS  |
| 5678       | 3  | 593  | SSSPSSSTPSLPLPFYLLGQLRLQLLWGTALHSGAGEAAPCPG GSGRTAAPRTADPAQSLMIMNMKNFKRRFSLSVPRTETIEE SLAEFTEQFNQLHNRNENLQGLGRDPPQECSTFSPDTSGBE PGQLSPGVQFQRRQNRFRSMEVRASGALPRQVAGCTHKGVHR AALQDPDFDVS KRLSLPMDI  |
| 5679       | 2  | 623  | LNSRVDDFVAVVGAIMDEDDYGSAAEWGDEADGGQEDDSGEGE DDAEVQQECLHKFSTRDYIMEPSIPNTLKRYFQAGGSPENVIOQL LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLIKH FDPKADSI FTEGETPAWLEQMIHTTWRDLFYKLAEAHPDCL MLNFTVKVGRVLELRRKVFMMNVYFWLLVCL  |
| 5680       | 258  | 592  | RRLTSTSEKLNRRNSHTPLESLIHPQPSYKGFIMFGKKKKKIE ISGPSNFHRVHTGFPDQEQKFTGLPQQWHSLLADTANRPKPMV DPSCITPIQLAPMKTIVRGNKPC   |
| 5681       | 45   | 869  | LLCAKTLGVRTKESQAGYNRSGINNHQAEPRFCPSFCWMRSA RQTRPQRLRKEAARPTPGSCPGTGMDGKKCSVMFLPLVFTL FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAAGDDP PASCVFSQVMNMAAFLALVAVLRFYQLKPKVLNPNLNSGLVA LCLASFGMTLLGNFQLTNDDEIHNVTSLTFGFGTLTCWIIQAAL TLKVNINKNEGRRVGIPRVILSASITLCVGPLLHPGPKHPHVC S QSPVGPCHVL   |
| 5682       | 39   | 622  | PSRSLGTMRKWRHREVNLPVTTQDQAVCFAPISPGLSAQTGL QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLVPLLLPGSYGL PFYNGFYYSNSANDONLGNHGKDLLNGVKLVETPEETLFTYQ GASVILPCRYRYEPALVSPRRVRVKKWKLSENGAPEKDVLAIG LRHRSFGDYQGRVHLRQD   |
| 5683       | 89   | 778  | GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRKVASMAPVTAEGFQERVRQRAVAEEESKGS ATYCTVCSKKPFASFNAYENHLKSRRHVELEKKAVQAVNRKVEEM NEKNLEKGLGVDSVDKDAMNAAIQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEGQAKKLAKHSEDD SEDEEHDLC  |
| 5684       | 195  | 677  | TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDGDEKTLRRSSLCKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE  |
| 5685       | 779  | 1262   | LLLOQPVVHCFLFFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ VKQEPHTSDSLMHVKPQHEQRKEQEPKRPKPHIKPLNAPMLYMK EMRANVVAECTLKESAAINQILGRWHALSREEQAKYYELARKE RQLHMQLYPGWSARDNYVSPSSIPVALHS   |
| 5686       | 128  | 1181   | CTWQVNIITLLDINDNHPTWKDAPYIYNLVENTPPDSVDTTVVA VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD PHEAELMRKIVSVTDCGRPPLKATSSATVFVNLLDNDNDPTF  |

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|------------|--|--|--|
|            |  |  | QNLFFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGM<br>RMDFLINSSSGVVTTTELDRERIAEYQLRVVASDAGTPTKSST<br>STLTIHVLVDVNDPTPTFFPAVYNVSSEDVPR\GSGWSG*AARN<br>NDVGLNABLSYFITGNNVDGKFSVGYRDAVVRTVVGDLRETTAA<br>YMLILEAIDNGPVGKRHTGTATVFTVLDVNDKRPILQSSYV  |
| 5687       | 17   | 917  | AAPPAPPDG/PPF/PPAPPT/PGPAA/APASSCQRLSAGRAA<br>QGDGGAAGVHVLVPAVGPRVNPGLQTPVPRPELLPGP/SSS<br>LHSDSSYPFDAGLSDDEPPDASLPDPPLTPV/ADA/PMPT<br>SGCRMPSTSAE/AAGGQGAETHAKGSETPPPASPTSEPA<br>LPPHLTGGPGMYSSEAKLPNSFSCIGLAGTGAGI*GTASAHGT<br>PPVLPHVCTPSLANPQP\AVGPEASSLPGLVSGIGMSA/SAPIS<br>SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGVPITTHGQEGQP<br>VLDI  |
| 5688       | 1  | 420  | LTKVDLFGNCYRLKLTGIEHGAMPEQGVVWYS/CLYDSRKLFF<br>*SHMIIRSL*KVIDSLGQLPLRELL*LNVIDRCIILAYV<br>LRVEKTFATYLNFTVKVDFSLGEBLISMAAILKLWIMKID<br>DGYIPAVF   |
| 5689       | 1504   | 3  | HELSGKHISMVSGNTCNWHPGGHSPGGGGQGEITSKDRGEIPAL<br>IWA/RKPIGTWTATKPTRHAG*GGAEEYQPPQCEGPRSTSRG<br>GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH<br>GSTARKPAPATPGTRHPTMETREVAQGWAPGRSQFWDQHPHS<br>PGEHRPSC/SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ<br>KLPRTRPEPLLAGWAVRKPWPSEAKEGLQAGRPSGMDSSAS\<br>PQTGGRGSLEWGLPLYLGPVHDK*RSRLG*PP*GGQGGGGH<br>GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCK<br>EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF<br>GQELKGPLDAGRLWPGAPSASSHR*GG*ERARAGAGHRGST*A<br>SSKIEQGRPRPGPTSDALADVEGGAES/GPHWPLPGLTPNR/P<br>GSEPPA*ASAGRKGTVSTLGGGLL |
| 5690       | 1424   | 58   | PSPAGVCAAPAPLPLALLARRDRRCPSPGAEAAPWTGGPAID<br>GAWRTSVSALLRRGATG/APCSFGAEAAPWTGGPAIDG/DGELP<br>*VRSEAPRGCGAEGGGPGSGPVRRPFCAGRGAGAHAGQGRQDPEP<br>DGLRHRQHGAASHARHLRLRPGHHQNRHVRDPQAPPGGPAP<br>GHAALPERTRGVAEPFAWAHAGSDAWRAGR*SQRT*ERARPRH<br>PTFQGRAGS\GQPGYQPPNHPGPPSPPAAP\GPRGA*GNPQLE<br>KAPSRDRNPSQGLRTRIRRPETPDGPPSPAGSSASASTFRCTS<br>SLSLGPG/PAHNLDTPAQDR*HGP*GDKRGAPGVAGEDPRPP*<br>GNFVR*LLMP/GVA*RHGTSPTFLGPSLGENGGQWDSGNLFGTP<br>KG*SHPAFTKST*SMEAEKSYWNHPR\DRGRQGVRIINCLRVGE<br>SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPPFPAG<br>PEGDPGLNSPGLLP       |
| 5691       | 107  | 550  | ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMVDSFSG=LSFYED<br>VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S<br>GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG<br>GVGVVVLLESVPLSYS   |
| 5692       | 1193   | 548  | TQAWTRAEDKRGSVRALRLHLERGPPT*RGSHPL\QSVPCIQK<br>PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSGCPASRMPL<br>TSRSVPPGRGALPPDLSLSTRKGLRPPSTAGHRVRESGHKVPVSQ<br>RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS<br>VPLASTQQTLPADSGPGTGGRDATRAGLPGVETMNGVD   |
| 5693       | 1258   | 1330   | ALTVPVRKGTIWWAQPHGCSNLVSRARLDLSSRPSONTEPQAP<br>*QAGPPSSLRPP\SRRR*APEWPKRATGSRRCGLSAPPWPWPA<br>RGE/PGSAPSHAP/PNSPSPSGTRHP/PGPSSRVLYSPSLPRNS<br>PEAIVWRSRFPPLWFLRCCFWVSGFKDPNPVLRFF  |
| 5694       | 3  | 1338   | GSKPARSLHRRSGHKSAGKWSVTLSAGALG*KQLHQ*WT<br>QRCL\NNLSSEEFNASSLSNLPSTPTASRRNSTIVLRDSEKR<br>SLAESGLSWFSESEBKAPKKLEYDSGLKMEPGTSKWRREPFES<br>CDDSSKGGELKKPISLGHPSLKKGKTPPVAVTSPITHTAQSAL<br>KVAGKPEGKATDKGLAVKNTGLQRSSSDAGRDRLSDAKKPPSG<br>LARPSTSGSGFYKKPPATGTATVMQTGGSATLSKIQKSSGIPV  |



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|------------|--|--|--|
|            |  |  | KPVNGRRTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGTTPSRLEKPTKVASGRTT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI  |
| 5695       | 3  | 1338   | GSKEPARSLHRRGSGHKSSAGKWSVTILSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEKAPKKLEYDSGLKMEPGTSKWRERPES CDDSSKGGELKKPISLGHGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQSSGIPV KPVNGRRTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGTTPSRLEKPTKVASGRTT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI   |
| 5696       | 3  | 1338   | GSKEPARSLHRRGSGHKSSAGKWSVTILSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEKAPKKLEYDSGLKMEPGTSKWRERPES CDDSSKGGELKKPISLGHGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQSSGIPV KPVNGRRTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGTTPSRLEKPTKVASGRTT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI   |
| 5697       | 1147   | 47   | PSEALSPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPA QGPATVQSVDFVDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEAEVAAPT KGPAPAPQCCSEPETKWSIIPAKPRRGTAPT RTAAPPPWGGVSVRTGPEKRSTRPFAEMEPGKEQASSSESDF EGIIAQMQLSFVMDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAPPPPPKLLPAPFRLKNSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKBEKEKAKKSKHKKSXKDEGKEKERR RRQRP RSRRTAA   |
| 5698       | 2  | 666  | GAEAAEPQEDLPPLSQSRFFQEQQKMNKSLGPVSFKDVAVDFT QBEKQQLDPEQKITRYRDMLENYSNLVSVGYHIKPDVISKLEQ GEEPWIVEGEFLQSYQDEVMQTDLLIERIQEENKPSRQTVPI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLHILKLEKTHPGDQAYE FNQ   |
| 5699       | 2  | 1448   | RVRQPPGLWVRTVPAMQCPAGLSRVPGVAG/DPSLPFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRINAPFPQGGKPAKAAAGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETVPVWS*AQPGWVSGLLLLGDPSPGPGSL*RS TWLVGGARGPEGSVVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTOKWTE/SPAPGEEG\VAPAPRGPTAEHGHCELTTEQYSNN VPILFQNPAGALRSRTEPAGWVPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQKPGCRPPCALPKPAGPERSA* CGSLGCR/SMLPASSGPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPSS*RELGLPGPGW*TLDPPLA HPAHPPGSAPPWALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG |
| 5700       | 923  | 597  | NGHKGVWEINII*RRSNIHKNKSSSEHLNQDHSFPPPTPNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRITICQEFSSCLQCAVLD E*CSIASSLIKAILRVSVLSE   |
| 5701       | 59   | 410  | IFEXICSDTQEFISPEINPOICSWLIFDKGAK/NHATGKDSLFN KWSKNWLSTCR*MRFGPYFTPYTKINSK*IK/DANIRCETVKL LEENTGENLHDTGLGNVFLDMTPKTQPTKQK   |

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|------------|--|--|--|
| 5702       | 3  | 1517   | ETFDVDSQCGGIPSDSPHPVITPSRAESSASSDGHGPVITPSRASESSASDGHGPVITPSRAESSASSDGHGPVITPSRAESSASSDGHGPVITPSRAESSASSDGHGPVITPSRAESSASSDGLHIEVINCSITEIETTSSIPGASDTDLIPTEGVKASSTSDPALPDSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSRNPLEETSALSSETPSYVKGAA PVSI EAGSAVGKTSFAGSSASSYSPEAALKNFPTSETLTMDITTKGPFPTSRDPLSPVPPTTNTSSRGTNSTLAKITTS AKTTMKP PTATPTTARTRP TT\A*VQVKN EVSSSCG* VWLPKRKTS LTPEWQ KG*CSSSTGNSTPTRLT SRSPYCVSGEANG/PSAARHV PYARK GCCP*PGPPPDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS LTSTGVYVWGASPVPRGVGLTLAHVLFCFSKEKT   |
| 5703       | 14   | 1117   | HHKDRSQGLPRTQECARPELRFLCPRALWPVTRL SYRCPWQA PKAGIGTKAKPSESHLKLHPGWPSLDROGE PATLTGTGHCSDS RILRNHP*HTAAR*PRWRRLPSSHRT RHLGVLRVODKS**VSL DPSCRPRFLRTC**YGMRSVASSSNPPGWSGPASVF PARPVS ALPTGPRCW*APRGRTQP CGWPRLS PHATA DWGPGCLSPSR GSWETA PGS*WCPWL*AARWTGWRTAS GASAGLGRAADRPSAWA RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC ACGRGP GSC*HPPFPVPSPSPVPCPSGR*HLRG PLLSAARPRA AGWPRHS PHDTQTPEP   |
| 5704       | 23   | 562  | GDYEFDSPYWDDISQA AKDLVTRLMEVEQDQRITAEAEISHEWI SGNAASDKNI KDGVCAQ IEKNFARAKWKAVRV TTLMKRLRAPE QSSTA AAQSASATDTATPGAAGGATAAAASGATS APEGDAARAA KSDNVAPRRP*LPPQPOMEVPPQPLMAVSPQPPMEASLQPLMGE SPQP  |
| 5705       | 23   | 562  | GDYEFDSPYWDDISQA AKDLVTRLMEVEQDQRITAEAEISHEWI SGNAASDKNI KDGVCAQ IEKNFARAKWKAVRV TTLMKRLRAPE QSSTA AAQSASATDTATPGAAGGATAAAASGATS APEGDAARAA KSDNVAPRRP*LPPQPOMEVPPQPLMAVSPQPPMEASLQPLMGE SPQP  |
| 5706       | 1161   | 610  | QLGRFXAQDTV AIRKV KEVFGTGAMRHVV ILFTHKED*GGQALD DYVANTDNCSLKDLVRECERRYCAFNNWGSVVEEQRQQOAE LLAV IERLGREREGSFHSNDLF LDAQLLQRTGAGACQBDYRQYQAKVE WQVEKHQELRENE SNWAYKALLRVKHLMLLHYEIFV FLLLC SI LFFIIIFLF  |
| 5707       | 28   | 609  | GSPAFTPGERRRPGRGTPSPGTRHHQGRAEPEDAPERAPLRR* MF AIQPG LAEGGQFLGDP PPGLCQPELQPDNSNFMASAKDANE NWHMGPRVPEPI LRSSSES PS DNQAFQAPGSPEEGVRSPPEGA EIPGAEP EKMGAGTVCS PL EDNGYASSSLSIDRSSSPBPACG TPRGP GPDPDLLPSVAQA  |
| 5708       | 44   | 1925   | SFSNEETIS PCFPKMP AEPPWWLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQARKPKP PRCPFTAMPSPRTKQKVRNKVCLLIARIYSDIPS DVSKAP/GPA GNPHDRSSTA*A LHRRAGAGSLCLSASLLPPPSFSLGAPGAPSPL RVSPASGGPRKEGRQSGG*AGGGGP\ARTHADLPCGVFCSSPP LLK*SDSPVKQLPA\SGQSGSGMPPVVGSSDILRPRPTS VS SGTG RAAG*CSWQPAACCTPRSQ*WAVARS PRCSRW*RQSGR*RG*S SRRRRGP*AAGRSTPA VP*PCS*GGAGRRAYACTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA** SRLCGTAGTG PLC SQSSRS* AG*RCCCTAASPCGGSGSPHGPS SAHCLSWSGGRTQPRAPSAH GRGRAMGSRVCVCTCTGLPCPGIPLSGASPGSGETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPP SAGHLLVGG*NS QRTSSDH*YTGTTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPPRPRLPAAS /SGGASGSPAASCSC SCRAPAKPASS/GEAPA PPPRPEPPPPPARRP |
| 5709       | 2  | 2031   | ITLCPLPQTEKCLNVVTEAAP TLGIYLKARVEAGGLKELEISWG LHQIVVRHGAVVMRAGMGCRC/GVMAPPAPR/NALS FLVNDCS LIHNVMCAA VFVD RAGEWKLGGDYMYSAQNGGGPPRKGI PE  |

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|------------|--|---|---|
|            |  | LEQYDPPPELADSSGRVVRKRSADMWRGLGLIWEVFNGLPRAA<br>ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFF<br>SNRFVETNLFLEEIQIKEPAEKQKFQELSKSLDAFFPEDFCRHK<br>VLPQLLTAPEFGNAGAVLTPLEFKVGKFLSAEEYQQKIIPVVVK<br>MPSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVHGFLOD<br>NPAIREQTIVKSMILLAPKLNANLNVELMKHFARLQAKDEQGPI<br>RCNNTVCLGKIGSYLSASTRHRVLTSAFSRATRDPPAPSRVAGV<br>LGFAATHNLYSMNDCAQKILPVLVCLGTVDPEKSVRDQAFKAIRS<br>FLSKLESVSEDPTQLEEEVEKDVHAASSPGMGGAASWAGWAVTG<br>VSSLTSLKIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT<br>TSGHWETQEEEDKDTAEDSDSTADRDDEDDWGSLEQEAESVLAQD<br>DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLTGLA<br>GAKLPGATS*RYTAGQVR |   |
| 5710       | 1  | 562   | IPGSTISCEVELMARMARKTIDSFTQNTQLRVVIIDGLDACEQOK<br>VLQMLDITVRVLFSGKGFIAIFASDPHIIKAINONLNSVPSGFK<br>\LNGHDMYMRNIVHLFVPLNSRGL/RQ/LOENFS*LQQQMETFHA<br>QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV<br>CIAIQFNNTNKDDAT   |
| 5711       | 1526   | 1130  | RRHPFQWTTVTQEAFFSHHDVAFTSTPVLFPYDPSAQPFIVKSESS<br>SQIAKAVLSQQRPSLFHECAFHFSS*SLQRHTINLDQGIPL*LM<br>LSEERQHLFESS/INTTPHNLK*/FEIHEHLGSHGHWTLFFLL<br>QIL  |
| 5712       | 3  | 1391  | GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEHGHCLDIKELP<br>ETVIDI.I.NKCLTFHPSKRPTPDELMKDKVFSEVSLYTPPTKPA<br>SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYVWLCL<br>AGGDLEKELVNKEIIRSKPPICTLPNLFLEDGESFGQGRDRSS/<br>TRF*YHWDIVVMPAKK*IERCWGRSILPITLKMSTLILPYSNSN<br>NELSAAATLPLIIREKDTYQLNRIILFDRLLKAYPYKKNQIWK<br>EARVDIPLMRGLTWAALLGVEGAITHAKYDAIDKDTPIPTDRQI<br>EVDIPRCHQYDELLSSPEGHAKFRVLKAWVSHDPLVYVWQGLD<br>SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIOEY<br>LTVFSQMIAPHDPPI.SNHLNEIGFIPLDYAIPFWLTMFTHVFL<br>HKIFHLW\DTLLLGEPLFPILYWE  |
| 5713       | 634  | 284   | PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH<br>TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWPLQPTSSATSP<br>*RAVLTSPCPSHLGSDAASSHWLGCVSFH   |
| 5714       | 212  | 613   | WGLGLPTMSSLGGGSGDAGGSSSSSTNGSGGGSGSGPKAGAAD<br>KSAVVAAPASVADDTPPPERNKSGIISEPLNKSRLRRSRPLS<br>HYSSFGSSGGSGGGSGMMGGESADKATAAAAAASLLANGHDLAAA<br>MA  |
| 5715       | 131  | 1979  | ESASQQRKRSKCLILTLKLELSGSAFKKTSARPGSSLWLPPHSQE<br>QTPPASKLQGGGGGLQTGWLHPVPVTAASPLPRWCLFGAVAK\<br>GLPGP*LCPSGAA/GGLQRGPGSLPLGAAGKVSCLHPPSMVENN<br>DSTCHEHHEGILARVTFVP\SGKPGRVLPKPPGRVCRPPHPAAS<br>PRPPGS/SDLDGPRPQMHLEAFPAAHGGPVNTPHGGEKTFMSS<br>QIRRKETPL*RKTPAG\NNYQNSIPVVSQSPQLTVDLLPSAGR<br>TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL<br>YPKTPKQRRWRRL/LLGPSQ*GSRQSTC*EV\GALGEPVRI PG<br>L*POLSCILSNGSKHRRREGLSFPRSLPGRRGPAGLQSLGCSPT<br>PKNTACHSSGHVALQAGHDSARDVGS GHVALQAGHDSTQDVGRP<br>VWRNIPLE*GLSRETQOATRRGLVWISPGRAAAACVACAQALE<br>EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DP<br>GLT/GVPGTDPKRGGRKPGQSGQETQGPVNSGPEPLQPKP*E<br>RQE/VGACASSGVGLSRGRAGCPSSAWEVAAMLLLLRHGSHSEL<br>DLTEAQTQSQ |
| 5716       | 1711   | 1370  | RVFSLLCGPGHCHYQGAVEREACAAASFGLDASAAEPHRLCEHTD<br>*LPK*GPYIQHFHCDSNILCILYNISFNLFSSYSF*GVARYAC*<br>RCPLVL*SGFFTIIIVGGYSCCMPLKT  |
| 5717       | 44   | 1489  | LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD<br>EGPGALVLESDLLLQDLEFEFEFEFEEDGNSDQLMGFERDSE  |

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|------------|--|--|---|
|            |  |  | <p>GDSLGRPGLPYGLSDDESGGRALSAESEEVEEPARGPGEARGE<br/> RPGPACQLCGGPTGEGPCCGAGGPGGGPLPPRLLYSCRLCTFV<br/> SHYSSHLKRHMQTHSGEKPFRCGRCPYASQALVNLTRHTRHTG<br/> EKPYRCPHCPFACSSSLNLRHQRTHAGPPTPPCPTCGFRCCTP<br/> RPARPSPTEQEGAVPRRPEDALLLPDLSLHVPGGASFLPDCG<br/> Q\CGVKGRASAGLDQNHQCS/SLFPWTCRGCGQEEEGESRLG<br/> AMCGRCMRGEAGGASGGPGQPSDKGFACSLCPFATHYPNHIA<br/> RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGKPKYKCLP<br/> CPYACGNLANLKRHGRHSGDKPFRCSLCNYSNQMNLIRHM</p>   |
| 5718       | 120  | 284  | VAHALSLPAESYGNVSMTHPQLPPTQLAWDLCTCLPLSYNET<br>S**STADPLHL   |
| 5719       | 48   | 428  | ELNNGPFCMPLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL<br>LSQGVNNAVTLDHVTPLEACGLGDHACAR\TLEAGANVNAIT<br>IDGVTPFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP  |
| 5720       | 1  | 1051   | <p>LQAFNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK<br/> \RCT\YYE\TCGGTYGLQMWVSFQDVAQKVVAL\RKQKQ\LA<br/> GPCK\SLPN\SPSH\SAVSAASIPARAPINQGH/SGGSAFSD<br/> Y\SSSVSPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS<br/> RKGADP\DREKKAAGCKVDSIGSGRAPIKQGIILKRSKSLNK<br/> EWKKKYVTLCDNGLLTYHPSLDHYMQNIHKEIDLRTTVKVP<br/> KRLPRATPATAPGTSPRANGLSVERSENTQLGGGTGAPHSASSA<br/> LHSEPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATSLPPGM<br/> QHPASG</p>  |
| 5721       | 97   | 492  | RHSSPCCSLRRTERSSNAVST/TTVQQFKRFIENYRRHIGCVA<br>VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI<br>SFMFSYILLTMCRLNITFLRETFLNRYVFPDAVDFHRLIASTA  |
| 5722       | 88   | 1043   | <p>VALDVLGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP<br/> GSLGVSHAAAPPARPQGAASPHRGRRHGGGAGLPPPRSPRFP<br/> QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRPGAGVAPRR<br/> GRARGQAGLLGRQGGGGAERERAAQARRGRRPGPEPDQSCG<br/> GRPRRAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA<br/> PPPPPHLGALTAGSGEERQSOPRAETLRLGRGAPLP\PRERGG<br/> RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT<br/> KSSTREIPEMI</p>  |
| 5723       | 88   | 1043   | <p>VALDVLGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP<br/> GSLGVSHAAAPPARPQGAASPHRGRRHGGGAGLPPPRSPRFP<br/> QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRPGAGVAPRR<br/> GRARGQAGLLGRQGGGGAERERAAQARRGRRPGPEPDQSCG<br/> GRPRRAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA<br/> PPPPPHLGALTAGSGEERQSOPRAETLRLGRGAPLP\PRERGG<br/> RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT<br/> KSSTREIPEMI</p>  |
| 5724       | 3  | 1841   | <p>FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK<br/> KGWLTQYEDGQWKHWFALADQSLRYRDSVAEBAADLDGEID<br/> LSACYDVTETPVQRYNQFIHTKEGEFTLSAMTSGIRRNWIQTI<br/> MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKQAEELGEP<br/> DPEQKRSRARE\RRREGSKTFDWAEPRIQQALAQERVGGVGP<br/> ADTH\DPWRPEAEHGELEERARRRREERRKRFGLDADTGPGETE<br/> DAALRMEVDRSPGLPMSDI.KTHNVHVEIEQRWHQVETTPLEEEK<br/> QVPIAPVHLSSEDDGDRSLTHELTSLEKELEQSQKEASDLLEQ<br/> NRLLDQLRVALGREQSAREGYVLQATCERGFPAAMEETHQKKIE<br/> DLQRQHORELEKLREKORLLAEETAATISAEAMKNAHREEME<br/> RELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSEQYS<br/> QKLENAHLAQALEAERQALRQCORENOELNAHQELNNRLAAE<br/> ITRRLTLLTGDDGGGATGSPLAQGKDAYELEVPSPGARPCLTQLC<br/> TQEPQGSAAANPLSYRVVGGTDLRQQESQGPGRSKSPGEGEEQ</p> |
| 5725       | 3  | 1049   | <p>VNGHSEETSQSNRTEPHSDSDSVLDGISKSTEDLSFPQKSGPVG<br/> SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVDG<br/> KNIVRSKAATLLYDQFLQVFTGSSSSDLSGTAKAIFKFDNHNH<br/> PB/GAKYNKRPHKWAHNLHLKYMVLHSIIISNTAV\RSQRHFVA</p>  |

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|------------|--|--|--|
|            |  |  | LQTKSPNRPQCFSSSAPS/VDQRAQ/INQSYAKHSANMNFNSHN<br>NVRANTAYHLHQLRGPARGEMWAISPNDRLIPAVTRSTIQRQS<br>SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMPMPG<br>SQRPLSARTYSIDGPNASRPQSARPSINIPERTMSVSDFNYSR<br>TSP   |
| 5726       | 2  | 486  | SRSLSMWNKSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP<br>TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVAGIPGPRAG<br>QGSPGSGEGPPLSSPSQPLPADLPATLPDVGLEVRPLAVT<br>GLIFHLGQARTPPYLQVTEKQVLLRADDG  |
| 5727       | 21   | 221  | RPILILKETRRLPWATGYAEVINAGKSTHNEQASCEVLTVKKK<br>AGAVTSTPNRNSKRRSSLPNGE  |
| 5728       | 2  | 877  | GTRNGQFEPRRGRWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG<br>NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAGAPDFPAVE<br>GR/PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSG<br>GGPAGAGGDAG/LPGRCPSPAPWRAGSRPAASCPDNI PGQGLWL<br>HRNPTS/GPPSQIGEGAEQDEGVADAPQIQCKN/GAEDPPAED<br>EPPQVPEAGEEDAVPAEPEGPGTPEQADQVRERPEAHLAEGGA<br>KGSRRRLADPQDLAPGOMSLAPFPFPVAAVIRSNK   |
| 5729       | 1  | 1525   | AGGAREVLTQLGHFAGFVGAHWNQQAALGRATDSKEPPGEL<br>CPDVLVYRTGRTLHGQETYPRLILMDLKGSLSSLEKEGGLYRDK<br>QLDAAIAWQGLTTHKBEVYKPNPYLQDFLSAEGVLSSDGVWRV<br>KSI PNGKGSPLPTATTPKPLIPTASIRVWSDFLRVHLHPRSI<br>CMIQKYNHDGEAGRLAEGQGESVLKEPKYQBELEDRLHFYVEE<br>CDYLQGFQILCDLHDGFSGVGAKAAELQDEYSGRGIITWGLLP<br>GPYHRGEAQRNIYRLNLTAFGLVHLTAHSSSLVCLSLGGSGLLR<br>PEPPVSFPYLHYDATLPFHCSAILATALTDTVCS/YRLCSSPVS<br>MVHL/ADMLSFCGKKVVTAGAIIPPLAPGQSLPDSLMOFGGAT<br>PWTPLSACGEPSTGTRCFAQSIVLRGIDRACHTSQLTPTGTPPPSA<br>LHACTTGEEILAQYLQQQQPGVMSSSHLLTTPCRVAPPYPHLPFS<br>SCSPPGMVLGSGPKGAIVESVPVFG |
| 5730       | 1258   | 1713   | KKFQAPARETCVECKTVPMERLLANQQVFHISCFRCSYCNK<br>LSLGTIYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT<br>KIBTEGFWERPRNFENCGRPLKSPGGEDCPC*GGCPSNY*AQ<br>GSSSREKGGQASWNPKLRA  |
| 5731       | 122  | 443  | RSHRGELIPKDS CYMRKPPRRPKRRQG/CALPQGCLTFKDVAI<br>EFSLEEWKCLNPAQALYRAVLENYRNLSVGLTSKDSWYMRK<br>KPGRGRGKQRRQEWFFLRVY  |
| 5732       | 226  | 772  | PPSRSCQSPRRKRRRAHVTVTLVCGFTSFSLSPLYLCCGLRF<br>PERTCSQLQADWAPDFGPFSSFPVSWGATATGARKFLIAPNI/N<br>LLGTKEQAHRIALNLRQGRGKDQPGRLKKVQIGWYLDENLA<br>QVSTNLDDFEVTALHTVYEETCREAQELSLPVVGSQVLVPLK<br>ALLDAA  |
| 5733       | 1  | 460  | PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES<br>MRTACS PDGLCS DGNGLKCPFTSRDFMKFRGGFEAIK SAYM<br>AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVIERDEKYM/AS<br>FDEI/VP/EFIGKMDEVLSRDP  |
| 5734       | 3  | 968  | RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFVFTVI<br>GSLFLMNLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS<br>SMVGEAGGAPPAQVGVKPNLLQVLQKVQLDSSHKQAMMEKVRSY<br>GSVLLSAEEFQKLFNELDERSVVKHPPRPEYQSPFLQSAQFLFG<br>HYFDYLGNI LIALANLVSICVFLVLDADVLPAERDDFILGILNC<br>VFIVYLLLEMLLKVFALGLRGYLSYPSNVFDGLLTVLLVLEIS<br>TL/VCTDCHTQAGGRNW/RLLSLWDMTRMLNMLIVFRFLRIIP<br>SMKPMMAVVASTVLGL   |
| 5735       | 2  | 540  | FTPCVARAFNFDQATVKKAAYSLPRVGGGTSCGLPOARRISL<br>ATPRLQYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ<br>YPVFPVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFAE<br>RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY<br>LKILT  |
| 5736       | 1  | 382  | GTRPSTKKS GYSPQQVAVIHCKGHQKENTAVAHSNQKADSAQV   |

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|------------|--|--|--|
| 5737       | 290  | 1041   | TARLSVTPPNLLPTVSFPQPDLPDNEVYSTTEKLASDLRANKN QES*ILPDSGIFIP*T*TSYLQSTTHLRRAKLPQLLRR<br>KACLHLSSFLTSNLFNPLLPDSLYSVEARSQRANLGPCCRKR LQTLMLAAGFYSSHKDPSLSAKEKTDYHNEARGPWPGWVG* RTADGSCGRPGDAHHPGPKSSSWRASRLPLGSGSHHLDAYVG RDLECGTPAPLQLEIPPQPRGHPAPIPTGOAGPRDSGPGASP*V ETRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW APSPTSQGCCEGRCDAPVKHRAWRTPLCSQ   |
| 5738       | 8  | 460  | DTLSLNLCTLPETLEMTPSF*LSFL*FPGGLARAKSIPTKTSNEV VTLWYRPPDILLGSTDYSTQIDMW*GOVEVWQGPCGKGGGLVTT ATQPAFLFTVPSLPRGVGCIIFYEMATGRPL*PGSTIVEQLHFI FRILSEEAWALCAVETHR   |
| 5739       | 1  | 1222   | SFQRRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC FPTLLEFLSLEPDLPALRAMGLHLWAAGPCTHPAGISDLLAEV SAEVDGPVPGYLSSPQSITDTCLYIFTSGETGLPKAARISHLKI LQCCGFYQLCGVHQEDVIYALPLHYHMSGSLGIVGCMGIGATV VLKSKFSAGQFWEDECQHRVTVFQYIGELCRYLVNQPPSKAERG HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY TGQRQAVGRASWLYKHIFPFLIRYDVTTEPIRDPOGHCMATS PGEPGLLVAPVSQQSPFLGYAGGPPELAQGLKLDVFRPGDVFFN TRDLLVCDQDQGLRFRHRTGDPFRWKGENVATTEVAEVFEALDP LQEVNVYGVTV |
| 5740       | 265  | 231  | PAYWLKVPTLCLESKTDLEKASHVSAQLQGEVRGLAGALWM*A YVYERVYN*NISRMVHALEQKQHPAGLSSSMALQLNFCGLMLMA LQSELHKLYDEETQSWVSGSACGGYP  |
| 5741       | 1  | 650  | PRKTMRRGVLMTLLQQSAMTLPWIGKPGDRPPPLCGAIPASGD YVARPGDKVAARVKAVDGDEQWILAEEVVSYSATNKYEVDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPOT TCFYRALIHAPPQRPQDDYSVLFEEDTSYADGYSPLNVAQRVYV ACKEPKKK*CRADSPSPNDTGQDSRGRAGIKHIPPLKKK  |
| 5742       | 2  | 362  | TQSVKEILKRNPNVNLTDKDGNTALMTASKEGHTETIVQDLLDAG TYVNIIPDRSGDTVLIGAVRGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDEICTKDG   |
| 5743       | 2  | 415  | GKTPEGIDATEEIEIDLEETEREISPOENGLLEVVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKLEETGRREISPEENGPEE VKPVDDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE  |
| 5744       | 3  | 703  | TRRTTTTSPITTRQMTTTPAALPTTVVTPDLTGTGFLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPESKEGPILTAESVTLV SDSWSSAESTSADTVLLTSKESKVDLPSTSHVSMNKTSDSVSS PQPGASDTAVPEONKTTKTGQMDGIPMSMKNEPISQLLMIAP SLGFVLFAFLFVAPLLRGKLMETCYCSQKHTRLDYIGDSKNVLDV QHGREDDEGLFTL  |
| 5745       | 1400   | 599  | GKSRFVNLKHSKKTVDVSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKVPVLFNFNQE YICGSHGVHRVYKHFSSDSTSTHQASHKQIHQKRKRHPPEEGR EKSEEBERSKHKKKSCCEIDLDKHKSIQRKKTEVEIETVHVSTE KLNKRKEKKS RDVVSKKEERKRTKKKKEQGQERTEEMLWDQSI LGF   |
| 5746       | 3  | 821  | SFASGRITPSSPAFDGELDLQRYSNNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLE LEERALREARLGRARSSGGMQATPATEGLARPOAPSSAPRCP YCKGKFR TSAERERHLHLRHPNWKGLCSFGSSQBEELLHHSIT AHGAPERPLAATSAPPPQPPQPPQPEPRSVQPEPEPEPPER EATPTPAPAPEEPAPPEFRCCVCGQSFTQSWFLKGHRKHKHA SFDHACPV  |
| 5747       | 2  | 1328   | DRHVETLCIHFLQPSGTGSAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKYSSNYRRSPERPTGDLRERIKNKRQDVTDEPQKRNTE BSSSPVRKESSRGRHREKEDIKITKERTPESEENVEWETNRDD   |

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|------------|--|--|--|
|            |  |  | SDNGDINYDYVHLSLEMKRQKIQRELMKLEQENMEKREETIIK KEVSPPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSASSKDRKTS AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE KYVKDRIIEKTRDQKDRGRDFERQREKRDKPRSTSPAGQHHSP ISSRHSSSSSQSGSSIQRHSPSPRRKRTSPSPYQRTLTTPPLRRS ASPYPSHSLSSPQRKQSPPRHRSMPREKGRHDHERTSQSHDRRH ERREDTRGKRDRKDSREEREYBQDQSSSRDHRDDREPRDGRDR RE  |
| 5748       | 934  | 473  | SEGPQVIFYKGLAPTIIAIFPYAGLQFSCVSSSLKHLWKWAI PAEG KKNENLQNLQCGSGAGVISKTLTYPLDLFKKRLQVGGPEHARAA FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM FFSYEPFCNVFHCMMNRITASQR  |
| 5749       | 552  | 1  | GPPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS SASSTYSSAEERMQSEQIRKLRRBLESSQEKVATLTSQLSANAN LVAAEFQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN SEAQAVIQALNASETTPKELRIKRONSSDSISSLSNITSHSSI GSSKDADA  |
| 5750       | 22   | 866  | IFISICLWNAHLCLLPLKDCIDQVMKLNQLFVDDSGRYLAIQF ILEWAYVFLYYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRE QENYVAQLILDVRREGDVLSNCEFTPAPTPOBHLTKNLELNDT ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ TQALADQFEDKTTSVLERLKIIFYCCQVPPHWAIRQLASLLFEL GCTSSALQIFFEKLEWME  |
| 5751       | 3  | 751  | SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA FPAGETFLVLRSSSAHWLAARARSGETGYVPPAYLRRLQGLQLE DVLOAIDRAIEAVHNTAMRDGGKYSLEQORGVLQKLIHHRKET: S RRGPSASSAVNTSSTSDHHLDAAAARQPNGVCRAFGERQHSLP SSEHLGADGGFLQIPLPSSQIPQPRRAAPTTPPPPVKRRDREA LMASGGGHNTMPSSGNSVSSGSSVSSCI  |
| 5752       | 3  | 471  | GPVCGVGLSVAWAGPWRGCPVHVSUGGGGRAALHGAELPCLSGAAT VEREMELRHKNEMLRVETEARAKAERENADIIREQIRLKASE HRQTVLESIRTAGTLPFEGEGRFVTDKVTATVNIIFIKQGWQV AERQHVGSWSPRSCPCRLCTAL   |
| 5753       | 34   | 483  | DDXAXIPGGVQAPFGAVRNITYTPRTGHRIRKLDQIQSGGNYVAG GQEAFFKKNLYLDIGEIKKRPMEVVNTVEKVPVIHSRINVSARFRK PLQEPCTIFLIANGDLINPASRLIIPRKTNLNQWDHVLQMVTEKI TLRSGAVHRLYLTLEGLRV   |
| 5754       | 14   | 331  | TLVHVVEPAGEHAEATASREQEVLGQWKELLSACEDARLHVSSST ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW WPTPATPSPLTAFFSME   |
| 5755       | 3  | 888  | LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI WMEKRRHGPGLAPGLQYTYPARCWRKKRRLHPPEDPKLRLEIK PEVELPLKKDGFTESTETLEALLRGEVGEKKVDAREEESIQEIQ RVLENDENVEEGNEEEDLEEDI PKRKNRTGRARGSGAGRRRHD AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEGDEAQ DQETRSPPNHRNENHRPQKGPDPGTVIPNNYCDFCLGGSNMNNKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA  |
| 5756       | 3  | 621  | SSKLQALFAHPLYNVPEEPPLGAEEDSLLASQEAALRYRRKVAR WNRHRMYREQMNLTSLDPPQLRLLEASWVQFHLGINRHGLYSR SSPVVSLLQDMRHFTTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFYFIDFQRHNAEI AAFHLDRILDFFRRVPPTVGRIVNVTEIL   |
| 5757       | 3  | 473  | YKDALLPFDNHRQVVFENGTLKLTLDVQKGMDEGEYLCSVLIQPO LSISSQSVHVAVKVPLIQPFEPFPPASIGQLLYIPCVVSSGDMPI RITWRKDGQVVISGSGVTIESKEFMSSSLQISSVSLKHNGNYTCI ASNAATAVSRRERQLIVRVPPRFVV  |
| 5758       | 1  | 474  | FRRGAGAERGEHREGERGAAGMGFEKVVHVRVFFNYVPSGIRCV A YNQSNRLAVSRDTGTVETIYNLSANYFOBKFFPGHESRATCALC WAEGQRLFSAGLNGEIMEYDQLALNIYKAMDAGGPIWMAAESP  |

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|------------|--|--|--|
| 5759       | 2  | 1240   | SGSQLVGCEDGSVKLFQITPDKIPV<br>GNAAFAGQGVVYETFFHMSDLPSYTTNGTVHVVNNQIGFTTDP<br>NARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAEWRNTF<br>NKDVGADLVCYRRRGHNEMDEPMFTQPLMYKQIHRQVPVLKKYA<br>DKLIAEGTVTLQEFEEIAYDRICEAYGRSKDKILHIKHWL<br>DSPWPGFFPNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF<br>KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL<br>NGQDVERGTFSHRHFVLDHDEVDRTCPMNLHLPDQAPYTVCN<br>SSLSEYGVLFGLGYAMASPINALVWEAQFGDFHNTAQCIIDQF<br>ISTGQAKWVRHNGIVLLPHGMEGMGPBHSARPERFLQMSNDD<br>SDAYPAFTKDFEVSQ |
| 5760       | 1  | 1221   | VRDITSDLSLSWTVPPEGQDFLFLVQFKNGDGQPKAVRVPGHED<br>GVTISGLEPDHXYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA<br>PASTEPTPEPPKPRLEELTVTDATPDSLSLSWTVPPEGQDFH<br>LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNXYKMNLYGFHGG<br>CRVGPVSAIGVTAEEETPTPTPEPSMEAPEPEPELLGELTVTG<br>SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPOVVRVGGESEVT<br>VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP<br>TEPGTEAPEPEPEPLGELTVTGSSPDSLSLSWTVPQGRFDSFT<br>VQYKDRDGRPOAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR<br>RLGPVSAIGVT                             |
| 5761       | 3  | 1275   | SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDN<br>VPVENFFVKCNGALINTSDTVQHGAVISLEPRLCGGKGGFGSML<br>RALGAQIEKTTNREACRDLGRRLRDVNHEKAMAENWKQAERE<br>AEKEQKRLERLQKLVKPKHCFTSPDYQQQCHEMAERLEDVVK<br>GMQAASSKMVSAEISENRKRWPTKSQTDRGASAGKRRCPWLGM<br>EGLETAEGSNSESSDDSEAPSTSGMGFHPKIGSNGVMAAK<br>FPSSGQRARVNTDHGSPBQLQIPVTDSGRHILEDSCAELGESK<br>EHMESRMVTETEETQEKKAESKEPIBEEPTGAGLNKDKETEERT<br>DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV<br>AELELLGLEKLKCELMALGLKCGGTLQ                   |
| 5762       | 2  | 344  | GSTGQTPLHSQGGGGGGGGRRRTPRGMPKEKEYEPDPRMYTI<br>MSSEEAANGKKSHWAELEISGKVRSLASLWSLTHLTALHLSDN<br>SLSRIPSDIAKLHNLVYLDLSSNKIR  |
| 5763       | 3  | 429  | LDKDTGLIMLIARLDYELIQRFLLTIARDGGGEETGVRVIRIN<br>LDVNDNVPTFQKDAYVGALENEPSVTQLVRLRATDEDSPPNNQ<br>ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL<br>TVMAMDAGN  |
| 5764       | 19   | 441  | VCARACGEMRQLLRPIDRQRYDENEDLSDBEIVSVRGFSLEEK<br>LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDLGLIK<br>MPDPDFTVRDVKLLVGSRRRLVDVMDVNTQKGTSMSSQFVRYYE<br>TPEAQDKL  |
| 5765       | 3  | 825  | QKILRLNNHQPTSSSSNSKDCGGPASSGAGATAALADGLKFPAS<br>VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS<br>STGKRQEVQGRPGATGMNSALGQSVSSGGSGNPNNSNSTSTST<br>AATAGAGSCGKSKEKPKGSQSSRGAKRDKDAGSRKDKHDLQ<br>GHONGSGSQAPSGGHLGYPGAKSNGGASPFHCGGTGSGSVAAA<br>GEVSKSAPDSGLMGNMMLVKKEEEESHRIKKLKEKVDPLF<br>TVFAPPPHV   |
| 5766       | 1608   | 663  | SGLFSVDPASSQAMELSDVTLIEGVGNEVMVAGVVVLLALVL<br>AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE<br>PTLPHPSEGNDKAEAGEGRDSTGEAGAGGGVEPSLEHLLD<br>IQGLPKRQAGAGSSSPAPLRSEDSTCLPPSPGLITVRLKFLND<br>TEELAVARPEDTVGALKSKYFPQGQESQMKLIYQGRLLQDPARTL<br>RSLNITDNCVICHRSPPGSAVPGPSASLAPSATEPPSLGVNVG<br>SLMVPVFVLLGVVWYFRINRYQFFTAATVSLVGVTVFVSFLV<br>FGMYGR  |
| 5767       | 2  | 892  | NFRATPRPPPTPELRTGTEVILWYLDWRALMKRKRKMKANIKLVG<br>SGFPLPSSDLDDSLTEEIDEKIGFRNDANFDWQNVADFRDAGGS<br>LTEVKVEEERDPQSPFEFIEEEEMLSVPIPSRRENELPDFP   |



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|------------|--|--|--|
|            |  |  | HIDEFTLNSTPSSAYDEPHLLVNIKQKLELEKRRLDIEAER LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV NSEKPSLENELGQGEKSMQPODIETELKLERERLQLEKDRLO FLKFESEKLQIEKERLQVEKDRRLRIQKEGHLQ  |
| 5768       | 3  | 476  | SSRSRLSVSVSPPEPGIVELGPPFAWEFC SRLGS AVTSQRAGPA AAMVAKDYP FYLTVKRANCSLELP PASGPAKDAE EPSNKRVKPL SRVTS LANLIPPVKATPLKRFSTLQRSISFRSES RPDILAPRP WSRNAAPSS TKRRDSKLWSETFDVC  |
| 5769       | 38   | 667  | TKTKKGVRKATDQSVKAFAEHCPELQYVGMGCSVTSKGVHIL TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSM TIETVDV GWCKEITDQATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY PHITFSTVLQDCKRTLERAYQMGTWTPNMSAASS   |
| 5770       | 1  | 484  | DSRRYDVKTRKNSFLEEHSKLIKVRCLPQVQDLPTLTLLA PASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFORAGVNF AI AKGGRLL LADDMGLGKTIQAICIAAFYRKEWPLL VVPSSVRFT WEQAFRLWLP SLSPDCINVVVTGKDR LTA   |
| 5771       | 168  | 741  | GLLPSACLRRASWREASEGPPSRACSNQSQTTFEACYS GTSTPS FHGSHCSGSDHSSIGLEQLQDYMTLSRSLGPLEIQQFAMLLRE YRLGLPIQDYCTGLLKYGDRRKFLLLGMRPFIPDQDIGYFEGF LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAQRPEAQ AFHRLADITHDIE  |
| 5772       | 148  | 383  | EPNLALVSPSHPOKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG ILTFSNLVTCSAIYHLPVFPEREFGCSMRDLRVA   |
| 5773       | 2  | 723  | PRVRSKHNFCFEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE KIPLSQEEITLQGHAFARIYAEDPSNNFMPVAGPLVHLSTPRA DPSTRIETGVROGDEVSVHYDPMIAKL VVWAADRQAALTKLRYS LRQYNI VGLHTNIDFLNLSGHPEFEAGNVHTDFIPQHHKQLL SRKAAAKESLQAAALGLILKEKAMTDTFTLQAHQDQFS PFSSSSG RRLNISYTRNMTLKDGNKSK  |
| 5774       | 2  | 592  | FVEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST VTEECVHILHGHRLNLTGILQNPNNHLQLYSCSLDGTIKLWDYI DGILIKTFIVGCKLHALFTLAQAE DSVFIVNKEKPDIFQLVSV KLPKSSSQEVEAKELSFVLDYINQSPKCI AFNGEVYVAAREF YLSVYFFKKETTSRVTLSSS   |
| 5775       | 3  | 538  | SSGCCDPAAPSSLAEAATMPVSKCPKKS ESLWKGWDRKAQRNGL RSQVYAVNGDYVVG EWKDNVKGKGTQVWKKGAIYEGDWKFGK RDGYGTLSLPDQQTGKCRRVYSGWNGDKKSGYGIQFFGPKEYY EGDWCGSQRS GWGRMYYSNGDIYEGQWENDKPNEGEMLRLSQNP RP   |
| 5776       | 2  | 484  | RLPQDCVCQNLSES LGTLCPSKGLLFVPPDIDRRTVELRLGGNF I IHSRQDFANMTGLVDLTL SRNTISHIQFFSFLDLESRLSLHL DSNRLPSLGEDTLRGLVNLQHLIVNNQLGGIADAEAFEDFLTL EDLDSYNNLHGPAVGLRGDAWVQPSTS  |
| 5777       | 2  | 949  | QODPEPGQDLFQPEREVDPSWGRGREPRLGKLRFPQNDHLSVLKQ VKLEQALKDGSAGLDPLPGTCYSPHCPPDKAEAGSTLPENLG GSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR NLPLPSLPPPLPSSPPSVNRLWTGRQKSSADHRKSYEFE DLQSSSESSRDVWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTQKSLSKPAFFRQ NSZRRNV   |
| 5778       | 1  | 1210   | QRRQSVSRLLLPVFLLEPPAEFGLPEPPEEEGEGEPAGVAEFGS GGPCWLQLEEVP GPGLGGGPLRSPSSSYSSDELSPGEPLTSP WAPLGA PERPEHLNRLVLERLAGGATRDSAASDILLDDIVLTHS LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHLQVE TVELKIPENQPPSKQVKPLFRHFRIDSCLOTRVAFRGSDEIF CRVYMPDHSYVTIRSLASVQDILGSVTEKLQYSEEPAGREDS LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV                                      |

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|------------|--|--|--|
|            |  |  | PLPEEIQVSPGDTETIHRVEPEDVANHLTAFHWELPRCVHLELFV DYVFHGE  |
| 5779       | 138  | 1571   | EAVQVLKHSADVNARDKNWQTPHVAANKAVKCAEVIPLLS SVNVSDRGRTALHHAALNGHVMVNL LAKGANINAFDKDRR ALHWAAYMGHLDVVALLINHGAEVTKDKKGYTPLHAAASNGQI NVVKHLNLGVEIDEINVYNTALHIACYNQGDVAVNELIDYGA NVNQPNNGFTPLHFAAASHTGALCLELLVNGADVNIQSKDGK SPLHMTAVHGRFTRSQTLIQNGGEIDCVKDGNTPLHVAARYGH ELLINTLITSGADTAKCGIHSMPFLHLAALNAHSDCCRKLSSG QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN ETDDWGR TALHYAAASDMDRNKTILGNAHDNSELERARELKEK EATLCLEFLQNDANPSIRDKGYNSIHYAAAYGHRQCLELLLE RTNSGFESDSGATKSPHLAVSEMP  |
| 5780       | 154  | 624  | QFRVITCLPFKGPYRLYKSEPELTVAEVDSENGEEKSEPVSEIETS VVKGSHPFVGVVPRAKSPTESSSTIASVYTLRKTCKMM DLRTERPRSAVEQLCLAESTRPMTEVEEQMERIRRHQOACLREK KKLNVIGASDQSPLOQSPNLNDP   |
| 5781       | 19   | 941  | RGSLGGHPWRPMPRAASQGLPVSFVTGPHQERAYGGRPGGAF PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQP PGERAAHRDGE QAPCRAGPTRKVA VAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ VQPHFTSQDAKSADEAPSRHLGKHQPRSAQVGSRLDALQGPKT QHSIHTVTCKSPRQKEDRS PKPPQAPKHPPEHGRQS\QAPPPLP VASRTCGGC*TWDPALLVSP/POGDSTPELPAP\QQFTGGPSR CQALPPQG*ROQPRQRPR/PTGASRSHPAKAKGCQGPPIRNY NIMD  |
| 5782       | 5176   | 1237   | DRSMMSMAADSYTDSYTDYTEAYMVPPLPPEEPPTMPPLPPEE PMPTPLPPEEPPEGPALPTEQSALTAENTWPTVEVPSLPSEESV SQPEPPVVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVEPP PEPESITLTPVESAVVABEHEVVPBPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLVPAVTTPLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPPEPPVVAEPDYVTIPVPVVSALEPSVPLEPAVSVLQ PSMIVSEPSVSQESTVTVSEPAVTVSEQTQVIPTVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAP EIGMQEIALHSGEEPFAE EHLKGDFYESEHGINIDLNNHLLIAKEMEHTVCAAGTSPVGE IGEKILPTSETKQRTVLDITYPGVSEADAGETLSSTGPFALPD ATG\TSKGI3FTTASTLSLVNKYDVLSTLTQDTEHMDLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKSSGGEKEVPFPPS*REHLPDSGFSANIEDINRAD LVPRVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLVSSPVV \SSMP\ERASGS\SSGEGKG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLSRSRKSRSSEHKSRLTSESRSRARKRSKSKS HRS\QTRSRRS/RDRRRSSRSRKSRRGRRSVSKEKRSRSPKH RSKSRERKRKRSRSDNRKTVRARSRTPSRRSRSHTPSRRRSR SVGRRRSFISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSPVRRRSFISIPVRLRRSRTPLRRRFS RSPIRRRKRSRSEGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEBLTECKQIAQSKE DDDVIVNKPVSDEBEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDNVFSSNLPSEPDISTAMSERALAKRLSENAFDLEAMSM LNAQERIDAWAQLNSIPQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMAVLMRKNGWREGEGLGKNKEGKPEILV DFKTDRKGLVAVGERAQKRSNFSAMKDLGSKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPCNMFLLNR Y |
| 5783       | 1693   | 698  | DSGLRVAFTMEGINSFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFTGVNVYLMKRSRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGEKSL NDLIEE/PI*SQ/PKILFQQP/LILKVALNMARGLKYLHQEKKL   |

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|------------|--|--|---|
|            |  |  | LHGDIKSSNVVIGKDFETIKICDVGVSLLDENMTVTDPEACYI<br>GTEPWKPKAVEENGVIDKADIFAFGLTLWEMMTLSIPHINLS<br>NDDDDDEKTFDESDFDEAYYALGTRPPINMEELDESQKQVIE<br>LFSVCTNEDPKDRPSAAHIVEALETDV  |
| 5784       | 2669   | 1388   | PRVRPRVRTDHNYYISRIYGPSDSASRDLVWNIDQMEKDKVKIH<br>GILSNTHRQAARVNLSPDFPFYGHFLREITVATGGFIYTGEVVH<br>RMLTATQYIAPLMANFDPVSRSNSTVRVFDNGTALVVQWDHVL<br>QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV<br>GLSDAFVHVHRIQQIPNVRRRTIYEYHVELQMSKITNISAVEM<br>TPLPTCLQFNRCGFCVSSQIGFNCSCWCSKLQRCSSGFDHRQDW<br>VDSGCFEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP<br>E/DAVTSQFPTSLPTEDDTKIALHLKDNASTDDSAAEKKGGL<br>HAGLIVGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSR<br>WPAMKFRRGSGHPAYAEVEPVGEKEGFIIVSEQC   |
| 5785       | 2669   | 1388   | PRVRPRVRTDHNYYISRIYGPSDSASRDLVWNIDQMEKDKVKIH<br>GILSNTHRQAARVNLSPDFPFYGHFLREITVATGGFIYTGEVVH<br>RMLTATQYIAPLMANFDPVSRSNSTVRVFDNGTALVVQWDHVL<br>QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV<br>GLSDAFVHVHRIQQIPNVRRRTIYEYHVELQMSKITNISAVEM<br>TPLPTCLQFNRCGFCVSSQIGFNCSCWCSKLQRCSSGFDHRQDW<br>VDSGCFEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP<br>E/DAVTSQFPTSLPTEDDTKIALHLKDNASTDDSAAEKKGGL<br>HAGLIVGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSR<br>WPAMKFRRGSGHPAYAEVEPVGEKEGFIIVSEQC   |
| 5786       | 2532   | 1674   | SYKLPAEERRASSCSQPPTPTRRRWPAFGRTSRGHRPQM*SGTP<br>APRPPARSTVSPASPLPKPRAGRCGRSRSACSTFRPC*SLN*M<br>S*H*KRNLSQRSSMSRRPLSCARPHR**RQGLTVAARLPWAK<br>SPPLACSFCAQAKSQSLSSGRSTR*PERMSFRP/SPFGNPAIP<br>SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTT*APTSSPGST<br>GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA<br>TGGSTATAPPKRFPNRNPNMMAE  |
| 5787       | 2  | 1460   | MASAASVTSLADEVNCP\ICQGTLEAGSLNCG/HKNFCRACL<br>T\RYCEIP/GPD\LEESP\TCP\LCKEPFRP/GSFRPNWQLANV<br>VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVR<br>EAGEHATHMTMFLEDA\APYREQIHKCLKLIKEREIEIQIS<br>RENKRMQVLLTQVSTKRQVISEFAHLRKFLQEQSILLAQLES<br>QDGDILRQRDEFDILLVAGEICRFSALIEELEEKNERPARELLTD<br>IRSTLIRCETRKCRKPVAVSPELGQRIROFPQALPLQREMKMF<br>LEKLCFELDYEPAHISLDPQTSHPKLLLEDHQRAQFSYKWQNS<br>PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLHAGGSCTVGVVS<br>EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLEQOP<br>RQVRVSLDYEVGWVFTNAVIREPIYTFTASFTRKVIPFFGLWG<br>RGSSFSLS  |
| 5788       | 2  | 6860   | EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTGHQEGDG<br>SEGEGETEGDVHTSNRLHMVRLMLLERILLQTLPLQLRNVGGVR<br>AIPYMQVILMLTTDLGDEKDKGALDNLSQLIAELGMDKKDV<br>SKKNERSALNEVHLVVMRLLSVFMSTKSGSKSSICESSSLISS<br>ATAAALLSGAVDYCLHVLKSLLEYWKSQONDEBPVATSQLLKP<br>HTTSSPPDMSPPFLRQYVKGHAADVFEAYTQLLTEMVLRPLFYI<br>KKITDTNSRIPPPVDHWSWFFLSEYLMIQQTPFVRQVRKLL<br>FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVT<br>SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDSDVLY<br>FLQVSVFLVDEGVSPVLLQLLSCALCGSKVLRLAASSGSSAS<br>SSPAPVAASSGQATTQSKSSTKSKKEEKEKEKGETSGSQBDQ<br>LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHLTLH<br>IYRNSKSKQELLLDLMSIWPPELPAYGKAAQFVDDLGYFSLK<br>TPQTEKKLKEYSOKAVEILRTONHILTNHPNSNIYNTLSGLVEF<br>DGYLSDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQVVKLI<br>GSHTISKVTIKIGDLKRTKMRVTINLYNNRTVQAIVELKNKPA<br>RWHKAKKVQLTPGQTEVKIDLPPIVASNLMIEFADFYENYQAS<br>TETLQCPRCASVPANPGVCGNCGENVYQCHKRSINYEKDPF |

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|------------|--|--|--|
|            |  |  | <p>LCNACGFCYARFDFMLYAKPCCAVDPIENEEDRKKAVSNINTL<br/> LDKADRVYHQLMGHRPQLENLLCKVNEAPEKQDDSGTAGGIS<br/> STSASVNRYYILQLAQEYCGDCKNSFDELSKIIQKVFASRKELLE<br/> YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG<br/> CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRRGA<br/> AAMREEVRQLMCLLTRDNPEATQOMNDLIIGXVSTALKGHWANP<br/> DLASSLQYEMLLLTDSISKEDSCWELRLRCLSLFLMAVNIKTP<br/> VVVENITLMCLRILOKLIKPPAPTSSKKNKDPVEALTTVKPYCN<br/> EIHQAQWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSELRH<br/> LYLTEKYVWRWKQFLSRRGKRTSPDLCLKGHNNWLRQVLFPTAT<br/> QAARQAACITVEALATIPSRKQQLDLLTSYLDLSIAGECAAE<br/> YLALYOKLTSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA<br/> TLSTDLQGGYALKSLTGLLSSFEVESIKRHPKSLVGTVLNGY<br/> LCRLKLVVQRTKLIDETQDMLEMLDMTGTGSETKAFMAVCI<br/> BTAKRYNLDDYRTPVFIERLCSIIPYEEBNEVTEFFVTLEKDPQ<br/> QEDFLQGRMPGNPYSSNEPQIGPLMRDINKNKICQDCDLVALLED<br/> DSGMELLVNKKIISLDLPVAEVYKVVCTTNEGEPMRIYVRMRG<br/> LLGDATBEFIESLDSTTDEEEDDEEVYKMGVMAQCGGLECMNL<br/> RLAGIRDQKGRHLLTVLLKLFYSYCVKVKVNRQQLVKLEMTLN<br/> VMLGTINLALVAEQESKDSGGAVAEQVLSIMEI\ICAEPNVPEP<br/> LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLLRIP<br/> YLSFGVEKMQILVERFKPYCNFDKYDEHSGDDKVFL\DCFCCK<br/> IAAGIK\NNSNGHQL\KDL\ILQGITQNALD\YMKKHIP\SAAR<br/> RIWDADI\WKSFLRPPALPFILRLRLGLAIQHPGTQVLIGTDSI<br/> PNLHKLEQVS\SDEGIGTLA\ENL\LESLEHDPVNKKIDA\AR<br/> RETRAEEKRMAMAMRQKALGTG\MTTNEKQGVVD\TRTALLEA<br/> DWEELIEEP\GLTCCICREGYKFQPTKVLGIYTFTRKRVLGQVW<br/> ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREWEESAA<br/> LQNANTKCNGLLPVWGPVPEAFATCLARHNTYLQECTGQREP<br/> TYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIHT<br/> GLYVLNTRATRSREEKNLQGFLEQPKKWWESAFEVDGPYYFTV<br/> LALHILPPEQWRATRVILRLRLVTSQARAVAPGGATRLTDKAV<br/> KOYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR<br/> HNDMPIYEAADKALKTKTQEEMFVETFSFELDVAGLLSEITDPE<br/> SFLKDLNLSVP</p> |
| 5789       | 1  | 2407   | <p>LPLHAVEKTGRPGQPALKMPGKLRS DAGLES DTAMKKGETLRKQ<br/> TEEEKKEPKSDKTEEIAEEETVFPKAKQVKKKAEPSVDMN<br/> SPKSKKAKK\KEEPSQNDISP KTKSLRKKKEPIEKKVVSSTKK<br/> VTKNEEPSEEEIDAPKPKMKKEKEMNETREKSPKLKNGFPHP<br/> EPDCNPSEAASEESNSEIEQEI PVEQKEG\AFSNFPISEETIKL<br/> LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL<br/> IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL<br/> SVACFYGGTPYGGQFERMRNGIDILVGTGRIKHQNGKLDLT<br/> KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDPQTLLFS<br/> ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAKCH<br/> WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSONSAIKQD<br/> AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD<br/> LVIOSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ<br/> VEQKAGIKFKRIGVPSATEI IKASSKDAIRLLDSVPPTAISHPK<br/> QSAEKLIEEKGAVEALAAALAHISGATSVDRSLINSNVGFVTM<br/> ILQCSIEMPNISYAWKELKEQLGEEIDS KVKGMVPLKGLGVCF<br/> DVPTASVTEIQEKWHSRRWQLSVATEQPELEGPREGYGGFRGQ<br/> REGSRGFRGQDGNRRFRGQREGSRGPRGQSGGNKSNRSQNK<br/> GQKRSFSKAFGQ</p>  |
| 5790       | 3786   | 1585   | <p>ARRQRDPLQALRRRNQELKQOVDSSLSESQLEALEPNKRQHIY<br/> QRCIQLKQAI DENKNALQKLSKADESAPVANYNQRKEEHTLLD<br/> KLTLQQLGLAVTISR ENITEVGAPTEEESESESEDSGGBEE<br/> DAEEEEBEKEENESHKWTGEEYI AVGDFTAQQVGDLT PKKGEI<br/> LLVIEKKPDGWWIAKDAKNEG LVPRTYLEPYSEEEEGQESSEE<br/> GSEEDVEAVDETADGAEVK\ORTDPHWSAVQKAI SEAGIFCLVN<br/> HVSFCYLIVLMRNRMETVEDTNGSETGFRAWNVQSRGRIFLVSK</p>   |

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|------------|--|--|--|
|            |  |  | PVLQQINTVDVLTMTGAIPAGFRPSTLSQLLEGNQFRANYFLQ<br>PELMPSQLAFRDLMDWDATEGTIRSRPSRISLILTLWSCKMIPLP<br>GMSIQVLSRHVRLCLFDGNKVLNSNIHTVRATWQPKPKTWTFSP<br>QVTRILPCLLDGDCFIRSNSASPDGILFELGISYIRNSTGERG<br>ELSCGWVFLKLFADASGVPIPAKTYELFLNGGTPYEKGI EVDPSI<br>SRRAHGSVFYQIMTMRQPQLLVKLRLNRRSRNVL SLLPETLI<br>GNMCSIHLILFYRQILGDVLLKDRMSLQSTDILISHPMLATFPML<br>LEQPDVMDALRSSWAGQES\TLKRSEKRPKEFLKVPFRLLVYH<br>\GCVLPPL/HTPTRLPPFRWAEETETARWKVITDFLKQKQENQ<br>GALQALLSPDGVHEPFDLSEQTYDFLGEHRKNAV  |
| 5791       | 3  | 1636   | LRVAEFACTSR/IGAGLIQPLHRAPARDHGLRGGAAPALSVSH<br>GN/GKQL/AMSSQGSDDDEQIKRENIRSLTMSGHVGFESLPDQLV<br>NRSIQQGFCEFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP<br>NVKLLKAQTYELQESNVQLKLTIVNTVGGDQINKESYQPIVDY<br>IDAQFEAYLQBELKIKRSLFTYHDSRIHVCLYFISPTGHSCLKTL<br>DLTMMKNLDSKVYIIPVIAKADTVSKTELQFKIKLMSSELVNSG<br>VOIQFPPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGKNMVKR<br>ROYPWGVQVENENHCDVFKLREMLICTNMEDLREQTHRIYEL<br>YRCKLEBMGFTDVGPEKPVSVQETYEAKRHEFHGBRQRKEEE<br>MKQMFVQRVKEKAILKEAERELQAKFEHLKRLHQEERMKLEEK<br>RRLLEEEIIAFSKKKATSEIFHSQSFLATGSNLRKDKDRKNSQF<br>FVKQKVPHEHRRSSSQANFIKKKLEVCDFAVICFITSIFGEQPO<br>LLIFMEKYFOVQGGYISQSE |
| 5792       | 2263   | 653  | AAAAPSPAWWCQGVFVVVYVHTCWVYGI VYTRPCSGDASCIQPY<br>LARRPKLQ/LRHSFTTTRSHLGAENNIDLVLNVEDFVSKFER<br>TVNVSVPKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPILT<br>YMPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL<br>NVMADNFVFDGSSLPADVHRVMKMIQLGKTVHYLPILFIDQLSN<br>RVKDLMVINRSTTELPLTVSYDKVSLGRRLFWIHMQDAVYSLQQ<br>FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLFLDFLAFKND<br>ISFWKKKSMIGMSTKAVLWRCFSTVVI FLFLDEQTSLLVLVP<br>AGVGAAIELWKVKALKMTIFWRGLMPEFQFGTYSESERKTEEY<br>DTQAMKYL SLYLLYPLCVGGAVYSLNLIKYSWYSLINSEFVNGV<br>YAFGFLFMLPQLFVNYKLKSAHLPWKAFTYKAFNTFIDDVFAF<br>IITMPTSHRLACFRDDVFLVYLYQRWLYPVDKRRVNEFGESYE<br>EKATRAPHTD            |
| 5793       | 2263   | 653  | AAAAPSPAWWCQGVFVVVYVHTCWVYGI VYTRPCSGDASCIQPY<br>LARRPKLQ/LRHSFTTTRSHLGAENNIDLVLNVEDFVSKFER<br>TVNVSVPKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPILT<br>YMPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL<br>NVMADNFVFDGSSLPADVHRVMKMIQLGKTVHYLPILFIDQLSN<br>RVKDLMVINRSTTELPLTVSYDKVSLGRRLFWIHMQDAVYSLQQ<br>FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLFLDFLAFKND<br>ISFWKKKSMIGMSTKAVLWRCFSTVVI FLFLDEQTSLLVLVP<br>AGVGAAIELWKVKALKMTIFWRGLMPEFQFGTYSESERKTEEY<br>DTQAMKYL SLYLLYPLCVGGAVYSLNLIKYSWYSLINSEFVNGV<br>YAFGFLFMLPQLFVNYKLKSAHLPWKAFTYKAFNTFIDDVFAF<br>IITMPTSHRLACFRDDVFLVYLYQRWLYPVDKRRVNEFGESYE<br>EKATRAPHTD            |
| 5794       | 1  | 5016   | MPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKDCDHGV<br>KGQKGERGLPGLQGVIGFPGMQGPEGPGPGQKGDGEPGLPG<br>TKGTRGPPGASGYPGNPGLPGIPGQDGP PGPPGIPGCNGTKGER<br>GPLGPPGLPFGAGNP GPGLPGMKGDGGEILGHVPGMLLKGERG<br>FPGIPGTPGPPGLPGLQGPVGPFGFTGPPGPPGPPGPPGEGQM<br>GLSPQGPKGDKGQGVSGPPGPVPGQAQVQEGDFATKGEKQKQ<br>EPFGQGMGPVGEKGEKGPFRGKPGKDGDKGEKSGPFPGEFG<br>YPGLIGRQGP/QGEKGEAGPPGPPIGIVGTGPLGEKGERGYPGT<br>PGRGEPGPKGFPGLPGQGPPLPVPGQAGAPGPPGERGEKGD<br>RGFPGTSLPGPSGRDGLPGPPGSGPPGPGPYTNGIVECQPGPP<br>GDQGPPIPGQPGFIGEIGEKQKGESCLICIDIGYRGPPGPGQ<br>PPGEIGFPQPGAKGDRGLPGRDGVAGVPGPQGTGPGIGQPGAK                                     |

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|------------|--|--|--|
|            |  |  | <p>GEPEFYFDLRLKGDGDPGFPQPGMPGRAGSPGRDGHFGLPG<br/>         PKGSPGSGVLKGERCPPGGVGFPGSRGDTGPPPGYGPAGPIG<br/>         DKQGAGFPGGPGSPGLPGPKGEPKIVPLPGPPGAEGLPSPGF<br/>         PGPGQDRGFPGTGPR\ PGL\ PGKGA VG\ QPGIGFPGPPGPKGV<br/>         DGLPGDMGPPGTGPRPGFNLPGNPGVQGGKGPVGLPGLKGL<br/>         PGLPGIPGTGPKGSGIGVGVPGEHGAIGPPGLQIRGEPGPPG<br/>         LPGSVGSPGVGPGPGARGPPGGQGGPGLSGPPGIGKEKGFPG<br/>         FPLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFP<br/>         SKGEMVMGTGPGPGSPGPNAGPLPGEKGD\HGFPSSGSPRGD<br/>         PSLKGDGKDVGLPGKPGSMKVMGSMKGQKGDQGEKQIGPIG<br/>         EKGSRGDPGTGPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGL<br/>         GPKGSVGMGLPGTPGEKGVPGIPGPGSPGLPGDKGAKGEKQ<br/>         AGPPGIGIPGLRGEKGDQGIAGFPSPGKEKGEKSGIPGMPGS<br/>         PGLKGSPPSVGYPGSPGLPGEKGDKGLPGLDGI PGVKGEAGLP<br/>         TPGPTGPAQKGEPSDGI PGSAKEKGPGLPGRGFPFGPAAG<br/>         DKGSKEGVFPGLAGSPGI PGSKGEQGFMPGPGQGGPGLPGSP<br/>         GHATEGPKGDRGPQGPGLPGLPGPMGPGLPGIDGVKDGKGNP<br/>         GWPAGPVPGPKGDPGFQGMPIGGSPGITGSKGDMGPPGVPGF<br/>         QGPKGLPGLQGIKGDQGDQGVPAKGLPGPPGPPGYDIKGE<br/>         GLPGPEGPPGLKGLQGLPGPKGQGVTLVGI PGPPGIPGFDGA<br/>         PGQKGE MPAGPTGPRGFPGPPGPDGLPGSMGPPTPSVDHGL<br/>         VTRHSQTIDDFQCPSGTKILYHGYSLLYVQGNRAHGQDLGTAG<br/>         SCLRKFSTMPFLFCNINNVCFASRNDYSYWLSTPEPMPMSAP<br/>         ITGFNIRPFISRCVCEAPAMVMAVHSQTIOIPPCPSGWSLWI<br/>         GYSFVMHTSAGAEGSGQALASPGSCLEEFPSAPFIECHGRGT<br/>         CNYYANAYFWLATIERSEMFKPTPSTLKAGELRTHVSRQCQCMR<br/>         RT</p> |
| 5795       | 1192   | 61   | <p>STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIH<br/>         PLAKIILFSNQPRDFFKYVELSTFDIASDAFATFKDLLTRHKVL<br/>         VADFLQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN<br/>         FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASH<br/>         KTQPIVEIILKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI<br/>         RDLKKTAP*RALRDSKR</p>   |
| 5796       | 2  | 1078   | <p>GRVGNELWCMYISPPKDWWDAGDPSLPRTAMIGCSFVUNRK<br/>         FGEIGLLDPGMDVYGGNIELGIKVLWLCGGSMEVLPCSRVAHIE<br/>         RKKKPYNSNIGFYTKRNALRAEVWMDYKSHVYIAWNLPLENP<br/>         GIDIGDVSERRALRSLKCKNFQWYLDHVYPEMRRYNNTVAYGE<br/>         LRNNKAKDVCLDQGPENHTAILYPCHGWGPQLARYTKEGFLHL<br/>         GALGTTTLLPDTRCLVDNSKSRLLQLLDCDKVKSSLYKRNFIQ<br/>         NGAIMNKGTRCLENRGLACIDLILRSCGTQQRWTIKNSIK*R<br/>         EGAGALEPGPDMAAPPNIWTSPPGETARGRQVLDGPPRASFG<br/>         QHRDPG</p>  |
| 5797       | 2  | 891  | <p>PRVRQKTLVDVTLSENSNIKDQIRNLQQTYEASMDKLREKQRQLE<br/>         VAQVENQLLKMKVESSEANAEVVMREMTKKLYSQYEEKLOEEQR<br/>         KHSAEKEALLEETNSFLKAIEBANKKMQAAEISLEEKDQRIGEL<br/>         DRLIERMEKERHQLQLLLEHETEMSGELTDSKERYQGLEEAS<br/>         ASLRERIRHLNDMVHCQKKVKQMVVEIESLKKKLQKQLLILQ<br/>         LLEKISFLEGENNELQSRDLTLTETQAKTEVETREIGVGC DLLP<br/>         SQTGRTREIVMPSRNYTPYTRVLELTMKKILT</p>  |
| 5798       | 644  | 115  | <p>KILGSRWKSNSNQEKOPYEEQARLSKIHLEKYPNYKYKPRPKR<br/>         TCIVDGKKLRIGYKQLMRSRQEMRQFFTVGQQQPIPIITGTG<br/>         VVYPGAI TMATTPSPQMTSDCSSTASPEPSLPVISTYGMKT<br/>         DGGSLAGNEMINGEDEMYYDDYEDDPKSDYSSENAEPAVSAN</p>   |
| 5799       | 2679   | 1435   | <p>LLSTYIKFINLFPETKATIQGLRAGSQLRNADVLELQRAVEYL<br/>         TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL<br/>         DDGRDPSSNDINGMEPTSTVSTPSADLLGLRAAPPAP<br/>         PASAGAGNLLVDVFDGPAAQPSLGTPPEEAPLSPGPEDIGPPI<br/>         EADLLNKFCVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN<br/>         KTSVQFQNFSPTVVHPGDLQTLAVQTKRVAQVDDGGAQVQVVL<br/>         NIECLRDFTLPPLLSVFRYGGAPQALTLKLPVTINKFPQPTM<br/>         AAQDFFQRWKQLSLPQQAQKIFKANHPMDAEVTKAKLLGFGSA</p>   |

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|------------|--|--|---|
|            |  |  | LLDNVDNPNFENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTLRTSKEPVSRLCELLAQGF   |
| 5800       | 2679   | 1435   | LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQORAVEYLTLSSVASTDVLATVLEEMPPFERESSILAKLRKKGPGAGSALDDGRDRPSSNDINGGMEPTSTVSTPSADLLGLRAAPPPAAPPASAGAGNLLVDVFDGPAAPSLGPTPEAFSPGDPEDIGPPPIPEADELLNKFVKQNGVLFENQLLQIGVKSEFRQNLGRMYLIFYGNKTSVQFQNFSPITVHPGDLQTLAVQTKRVAQVDGGAQVQQLNIECLRDFLTPPLSVRFYGGAPQALTLKLPVTINKFFQPTEMAAQDFFQRWKQLSLPQQEAQIFKANHPMDAETTKAKLLGFGSALLDNVDNPNFENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTLRTSKEPVSRLCELLAQGF   |
| 5801       | 3  | 1413   | FFRLVHLIPDGEITSIKINRVDPSSELSIRLVGGSETPLVHIIIIQHIVRQGVARDGRLLPGDIILKVNQMDISNVPHNYAVRLLRQPCQVLWLTVMREQFRSRNNGQAPDAYRPRDDSFHVLNKSSEPEQLGIKLVKRVDEPGVFI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRVQRSPDIFQAGWNNSWSVPGPGERNTPKPLHPTITCHEKVNNIQKDPGSLGMTVAGGASHREWDLPIYVISVEPGGVISRDGRIKYGDIILLNVGVELTBVSRSSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSPSWMWLELPRLCLYNCKDIVLRNTAGSLGFCIVGYEYNGNKPPFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL  |
| 5802       | 3  | 290  | CFSLYQIMERIMDLPTLLRHAFREMFVGGGLFWMFRIRIILCLMGAFFYLISPLDFVPEALFGILGFLDDFFVIFLLIYISIMYREVITQRLTR  |
| 5803       | 2234   | 1299   | BAQFGTTAEIYAYREEQDFCIBIVKVKAIGRQRFKVLRLTQSDGIQAKVQILPZCVLPSTMSAVQLESLNKCQIPPSKPVSRDQCSYKWNQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLREWDENLKDDSLSPNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQLRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSCGPMAYVNPBGVYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICASHIGWKFTATKXDMSPQKFWGLTRSAALLPTIPDTEDEISPDKVI LCL  |
| 5804       | 2  | 1707   | EMEKQRQEEQRKRTTEERKRRIEQDMLEKRRKIQRELAKRAEQIE DINNTGTESASEEGDDSLITVVPVSKYKTSKGMKNFEDLEKE REEKERIKYEEEDKRIRYEEQRP SLKEAKCLSLVMDDEIESEAKKESLSPGKLKLTFEELERQRQENRKKQAEERARKLEEKRAFEARRQMVNEDEENQDTAKIFKGYRPGKLKLSFEEMERQRREDEKRAEEEEARRRIEBEKKAFAEARRNMVDDDSPEMYKTISQEFITP GKLEINFEELLKQKMEEEKRTEERKHKLEMEKQEFQQLRQEMGEEEEENETFGLSREYEELIKLKRSGSIQAKNLKSKFEKIGQLSEKEIQKKIEERARRRAIDLEIKEREAFNEFHEEDDVDRPARKSEAPFTHKVNMKARFEQMAKAREEEEEQRRIEEQKLLRMQPEQREIDAAALQKKREEEEEEGSIMNGSTAEDDEQTRSGAPWFKPKLKNTSVVDSEPVRTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGETYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN |
| 5805       | 3  | 776  | YISDTLGQVYKSKIRWIEENGNGNISVDDLIALLDLAEHASSAFKESQQQSDREYEVKERLYPKSKRRYDTYNIAGVQGEIEVGLYTIQILQLIPFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA LKNYIPYLTKLKPSLKSFDFFDEYFVLLKPRNNIKQNEBAKTRRKVAGYFKKYVDIFCLLEESQNTGLGSKFSBPLQVERCRRNLV ALKADKFSGLLEYLIKQEDAISTMKCIVNEYTFLK   |
| 5806       | 1257   | 877  | AVFTFHNHGRRTANLYSLHSLGITTFFLFCORFLGFVAVLLPWASMWLRSLLPKIHVFFGAAILSLSIASVISGINEKLFSLKNTT RPYHSLPSEAVFANSTGMLVAFGLLVLYILLASSWKR  |
| 5807       | 2267   | 1302   | RFSKKTFRPMVADIQPACLGLYCGKTLFLKNGSTEIYGECGVC PRGRTNAQKYCQCTESPELYDWLYLGFMAHMLPLVHWFIEW YSGKKSSSALFQHITALFECSMAAIIITLVSDPVGVLYIRSCRVLMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYAFCLV   |

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|------------|--|--|---|
|            |  |  | LMMLLRPLLKVKIACGLGKSDRFKSIYAALYFPFILTTLVQLQAVGG<br>GLLYAFPIYIILVLSLVTAVYMSASBIENCYDLLVRKKRLIVL<br>FSHWLLHAYGIISIRVDKLEQDPLLLALVPTPALFYLFATAKFT<br>EPSRIILSEGANGH  |
| 5808       | 2  | 433  | SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS<br>EGRITHGFOLKSAYENNLMPYNTNYTFDFKGVIDYIFYSKTHMNV<br>LGVGLPDPQLVENNITGCPHPHIPSDHFSLLTQLELHPPPLLP<br>LVNGVHLPNRR   |
| 5809       | 464  | 2422   | ILVPGFQGLLHPGVYCALQSQHQAEVLADIDCEVSGLCREHGG<br>RCVNTHGSEFCYCMDGYLPRNGPEPFHTTDTATSCTEIDCGTTP<br>EVPDGYIIGNYTSSLSQVRYACREGFFSVPEDTVSSCTGLGTW<br>ESPKLHCQEINCGNPPMRHAILVGNHSSRLGGVARYVCQEGFE<br>SPGGKITSVCTEKGWTRESLTCTEILTINDVSLFNDTCVRWQ<br>INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVC<br>LALYPGTNYTVNISTAPPRRSMFAVIGFQTAEDVLEDDGGSFNI<br>SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSSHATSFN<br>FTTREQVPVCLDLYPTDVTNVNLTLLRSPKRHSVQITITATPPA<br>VKQITISNISGFNETCLRWRSIKTADMEEMYLFIHWQQRWYQKEF<br>AQEMTFNISSSSRDPEVCLDLRPGTNYNVSRLALSSBLPVVISL<br>TTQITEPPLPEVEFFTVHVGPLRLRLRKAKEKNGPISSYQVLV<br>LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM<br>HIPGDRLYYGEYYNAPLKRGSYCIILRITSEWNKVRHSCAV<br>WAQVKDSSLMLLMAGVGLSLAVVILTLTFLSFAV   |
| 5810       | 3  | 1641   | KVFGTHKDEHVEVSTLDTAISAVKVKLAEEFLENLQEKSLRIEAFVS<br>BIESFFNTIEENCCKNEKRLLEEQNEEMKKVLAQYDEKAQSFE<br>VKKKMEFLHEQMVFHLQSMDTAKDTLETIVREAEELDEAVFLT<br>SFEINERLLSAMESTASLEKMPAASFLEHYDDSSARSQDMLK<br>QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSPQVYCM<br>EPQDDQEVNELVEEYRLTVKESYCI FEDLEPDRCYQVWMAVNF<br>TGCSLPSERAI FRTAPSTPVIRAEDCTVCWNTATIRWRPTTPEA<br>TETYTLEYCRQHSPEGEGLRSPSGIKGLQLKVNLPNDNYFFVY<br>RAINAFGTSEQSEALISTRGTRFLLRETAHPALHISSSSGTVI<br>SFGERRRLTEIPSVLGEELPSCGQHYNETTVDPCPAYRLGICSS<br>SAVQAGALGQGETSWYMHCEPQRYTFFYSGIVSDVHVTERPAR<br>VGILLDYNQRLIFINAESQQLFIIRHRFNEGVHPAFALEKPG<br>KCTLHLGIEPPDSVRHK   |
| 5811       | 1918   | 851  | AAALADPLPEDKWSAEKRRPLKSSSLGYEITFSLNPDPKSHD<br>WDIEGAVRRYVQPFNLALGAAGNFVSQILYYAMLGVNPRFDS<br>ASSSYLDMHSLPHVINPVESRLGSSAASLYPVLNFFLYVPELA<br>HSPLYIQDKDGAPVATNAFHSRPGGIMVYNVDSKTYNASVLPV<br>RVEVDMVRVMEVFLAQLRLFLGIAQFQLPFPKLLSGPTSEGLMT<br>WELDRLLWARSVENLATATTTLSLAQLLGKISNIVIKDDVASE<br>VYKAAVAVQKSAEELASGHASAFVASQEAVTSSSELAFFDPSLL<br>HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETGRKSWRKPE<br>KTD   |
| 5812       | 5204   | 2744   | GGKQRCQGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT<br>LAEMGKNLKEAVKMLEDSQRRTEENGKKLISGDI PGPLQSGSQ<br>DMVSILQLVQNLMHGDEDEEPQSPRIQNIQEGQHALLGHSIGA<br>YISTLDKEKLRKLTTIRLSDTTLWLCRIFRYENGCAFYHREERE<br>GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ<br>YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKODIERG<br>RLPPLL VANAGTAAGHTDKIGRLKELCEQYGIWLHVEGVNLT<br>LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVFAVTLYKHDDPA<br>LTLVAGLTSNKPDKLRALPLWLSQYLGLDGFVERIKHACQLS<br>QLQESLKKVNYIKILVEDELSSPVVVFRRFQELPGSDPVFKAV<br>PVPNMTPSGVGRERHSCDALNRWLGEQLQLVPAASGLTVMDEA<br>EGTCLRFSPLMATAVLGTRGEDVDQLVACIESKLPVLCCTLQLR<br>EEFKQVEEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLSYPQ<br>GENTHAGLLKLNLESDLTFFKIGPEYKSMKSLVVGMA SDNVH<br>AELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS<br>EERLLEEGVLRQIPVVGSLNWFSPVQALQGRTEFNLTAGSLES |



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|------------|--|--|--|
|            |  |  | TEPIVYKAGGAGVTLPTTPSGSRTKQRLPGQKPFKRSRLRGSDA<br>LSETSSVSHIEDLEKVERLSSGPEQITLSEASTEGHPGAPSPQH<br>TDQTEAFQKGVPHPEDDHSQVEGPESLR   |
| 5813       | 2936   | 699  | HRDGVSGSLERPLTDRSRTGAFQAQQRGKMATAGGSGADPGSRG<br>LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLNATHQI<br>GCQSSISGDTGVIHVVEKEEDLQWVLTGDPNPFYVVLLESKHFT<br>RDLMEKLGRTSRIAGLAVSLTKPSPASGFSFSVQCPNDGFGVY<br>SNSYGPEFAHCREIQWNSLGNLAYEDFSFPIFLLEDENETKVI<br>KQCYQDHNLSQNGSAPTFFPLCAMQLFSHMAWLSFSTAT\CMRRS<br>SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLLKPDPRVVVA<br>ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL<br>PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL<br>GQVALRTSLELNMHTDPVSQKNESVRNQEVDLLATLEKSGAGVP<br>AVILRRPNQSQPLPPSSLQRLRARNISGVVLADHSGAFHNKYY<br>QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV<br>LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNWSFQS<br>ILQGRDLRSYLG*RGLFQH\YIAV\SSPTNTIYV/VLQYALANL<br>TGTVVNLTREQCQDPSKVPSENKDLYESWVQGPLHSNETDRLP<br>RCVRSSTARLARALSPAFELSQWSSSTEVSTWTESRWKDIRARIFL<br>IASKELELITLVGFGILIFSLIVTYCINAKADVLFIAPREPGA<br>VSY  |
| 5814       | 8500   | 432  | ALKCRPRRVLAILVGFVQPDMAEEGAVAVCVVRPLNSREESL<br>GETAQVYWKTHNNVIYPVDGSKSFNDRVLHGNETPKNVYEA\I<br>AAPIIDSAIQGYNGTIFA\VGQT\ASGKTYTMMGSEDHLGVIPO<br>GQPHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTQKM<br>KPLIREDVNRNVYVADLTEEVVYTTSEMALKWITKGEKSRHYGE<br>TKMNQSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA<br>GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSQGVGGFI<br>NYRDSKLTRLQNSLGGCNPKTRIICTITPVSFDETLTALQFAST<br>AKYMNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLERAQ<br>AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLQOEL<br>KAKRKRRTVWCLGKINKMKNSYADQFNIPNTITTKTKHKLINL<br>LREIDSVCSSESDFVSNLTDLTSEIBWNPATKLLNQENIESELN<br>SLRADYDNLVLDYEQLRTEKEEMELKLEKNDLDEFEALBRKTK<br>KDQEMQLIHEISNLKNLVKHREYVYNQDLENELSSKVLELLREKED<br>QIKKLQEIYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV<br>ALDAKRESAFLRSENLELKEKMKELATTYKQENDIQLYQSQLE<br>AKKMQVDLEKELQSAFNEITKLTLIDGKVPKDLLCNLELEGK<br>ITDLQRELNKEVEEALREBEVILLSELKSLPSEVERLRKEIQD<br>KSEELHIITSEKDLFSEVVHESRVQGLLEEIGTKDDLATTO<br>SNYKSTDQEFQNFKTLHMDFEQKYKMLEENERMNQEIIVNLSKE<br>AQKFDSSSLGALKTELSYKTQELQEKTRVQERLNEMEQLKEQLE<br>NRDSPLOTVEREKLITTEKLQOTLEEVRKLTQEKDDLKQLQESL<br>QIERDQLKSDIHDVTVMNIDTQEQLRNALESLOHQTETINTLKS<br>KISEEVSRLNLMHEENTGETKDFEQKMGVIGDKQDLEAKNTQTL<br>TADVKDNEIEQQRKIFSLIQEKNELOQMLESVIAEKEQLKTDL<br>KENIEMTIENQBELRLGDELKKQEIIVAOEKNHAIKEGELSR<br>TCDRLAEVEEKLKKSQQLQEKQQLLNQVEEMSEMOKKINBIE<br>NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERV<br>KELQKSFETERDHLRGYIREIATGLQTKELKIAHILKEHQE<br>TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP<br>NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF<br>QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE<br>SQSKQEQLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIMLG<br>LSKRLQESHDEMKSVAKEKDDLQRLQEVLSQESDQLKENIKEIV<br>AKHLETEELKVHCCLEKEEETINELRVNLSEKETEISTIQKQ<br>LEAINDKLQNKIQEIEYEKEEQNLKQISEVQEKVNELQKFKEHR<br>KAKDSALQSIKSMLELTNRLQESQSEIQQIMIKEKEEMKRVQEA<br>LQIERDQLKENTKEIVAKMKESQEKQYFPLKMTAVNETQEKMCB<br>IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD<br>DLRSVEETLKVVERDQLKENLREITITRDLKEQEELKIVHMLKEH |

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|------------|--|--|---|
|            |  |  | QETIDKLRGIVSEKTEISNMQKDLHSNDALKAOQLKIQEELR<br>IAHMLHLEQOETIDKLRGIVSEKTDKLSNMQKDLNSNAKLQEK<br>IQELKANEHQILITLKKOVNETQKKVSEMEQLKKQIKDQSLTSLK<br>LEIENLNLAQKLHENLSEMKSVMKERDNLRRVEETLKLRLDQLK<br>ESLQETKARDLEIQEELKTARMLSKHEKETVDKLRKISEKTIQ<br>ISDIQKDLDSKDELQKKIQELQKKELQLLRVKEDVNMSSHKKIN<br>EMEQKKQFEPNYLCKCEMDNFQTKKLHESLEEIRIVAKERDE<br>LRRIKESLKMEDQFIATLREMIARDQNHQVKEPKRLSDGQQ<br>HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDEKEIEFH<br>RIMKKLYVLSYVTKIKEEQHECINKFEMDFIDEVKKQKELLIK<br>IQHLQDQCDVPSRELRLDLNQNMDLHIEEILKDFSESEFPSTIK<br>TEFQOVLNRRKEMTQFLEWLNTRFDIEKLKNGIQKENDRICQV<br>NNFNNRIIAIMNESTEFEEERSATISKWEQDLKSLKEKNEKLF<br>KNYQTLKTSLSAGQVNPPTQDNKNPHVTSRATQLTTEKIRELE<br>NSLHEAKESAMHKEISKIKMQKELEVINDIIAKLOAKVHESNKC<br>LEKTKETIQVLQDKVALGAKPYKEEIEDLKMKGIDLEKMKNA<br>KEFEKEISATKATVEYQKEVIRLLRENLRSSQAQDTSVISEHT<br>DPQPSNKPLTCGGGSGIVQNTKALILKSEHIREKEISKLKQON<br>BQLIKQKNELLNNQHLSEVKTWKERTLKREAHKQVTCENSEPK<br>SPKVTGTASKKXQITPSQCKERNLQDPVPKESPKSCFFDSRSKS<br>LPSPHPVRYFDNSSLGLCEPVQNAESVDSQP\GPWARLFQCK<br>DVP\ECKTQ |
| 5815       | 23   | 1460   | SELVMWTVQNRRESLGLLSFPVMITMVCCAHSSTNEPSNMSYVKT<br>VDRLLKGYDIRLRPDPFGPPVDVGMRIDVASIDMVSEVMNDYTL<br>TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDITYFLNDKK<br>SFVHGVTVKNRMIRLHPDGTLYGLRITTTAACMMDLRRYPLDE<br>CNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY<br>KMVSKKVEFTTGAYPRLSLFRLKRNIGYFILQTYMPSLTITIL<br>SWVSFWINYDASAAARVALGITTTLTMTTISTHLRETLPKIPYVK<br>AIDIYLMGCFVFFLALLEYAFVNYIFFGKGPOKKGASKQDQSA<br>NEKNKLEMNKVOVDAGNILLSTLEIRNETSGSEVLTSVSDPKA<br>TMSYSDASIQYRKPLSSRE\A*GRAPJRHGVPSKGRIRRRAS\<br>QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVWLYYVH   |
| 5816       | 861  | 191  | TSSRSRAAAQEGDAETPGSVERRGRAGAEDEGMSQAQGAQSPSP<br>TVYHERQRLCAVHALNNVLQQLFSQEAADBI CKRLAPDSRL<br>NPHRSLLGTGNYDVNVIMAAQLGLLAAVWDRRRPLSQLALPQ<br>VLGLILNLPSPVSLGLLSLPLRRRLRWPCLRL/VTVSYYNLDS<br>K\LRAPGPGGLRTE\*GFLAALAAQGLCEVLLVVTKEVEEKG<br>SWLRDT   |
| 5817       | 851  | 118  | RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCFPC*PPSPFAAD<br>VMSNTTVPNAPQANSDSMVGYVLGPFLLITLVGVVAVVMYVQK<br>KKRVDRRLRHLLPMYSYDPAEELHEAEQELSDMGDPKV\QAG<br>RVATSTSGCHCWSRRDLTPLHPSEPGVLDCIGPCHLLPLSP<br>GSPCWVLGLHPSLHPPSAASASHALTITSLPPGLLPFVGVELTA<br>HPQALMGRGFFPSGMAAAGRHLCL   |
| 5818       | 3  | 3918   | QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQKQIAAFAFDKGD<br>DRRLGKKPIFSSSQQRKQVSDSGDIKISWRGNNKKECWSYLSL<br>NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI<br>TXELKTGGKQVSGKPKTIVTKSTENGDKARLENMSPRQVVERSA<br>TAAAAATGQKNLLNGKGVNRQEGQISGARPKVLTGNLNVQAKAK<br>PLKKATGKDSPLCSIAGPSSRSTDSSMEFSISTECLDEPKENG<br>TEEEKPSGHKLSFCDSPGQMMKNVDSVKNSTVAIKSRPVSRVT<br>NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPAIILKRGTS<br>NGCTAAQQRKTSTPSNLTKQGSQCESPNSVKSSVSRQSDENV<br>AKLDHNTTTEKQAPKRKMVQVHTALPKVNAKIVAMPKNLNQSK<br>KGETLNNKDSKQKMPGQVISKTPSSQRPLKHETSTVQKSMFH<br>DVRDNNNKDSVSEKPKHKLINLASEISDAEALQSSCRP\DPQK<br>PLNDQEKELALECQNI SKLDSLKHELESKQICLDKSETKFPN<br>HKETDDCAANICCHSVGSDNVNSKFYSTTALKVMVSNPNENSL<br>NSNPVCDLSDTSAGQIHLISDRENQVGRKDTNKQSSIKCV3DVS<br>LCNPRTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH   |

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|------------|--|--|---|
|            |  |  | <p>ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH<br/> WNLSTGVLHQRESPESDTGSATTSDDIKPRSEYDAGGSQDDD<br/> GSDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK<br/> MKXQSSNDLFQVNSTSDDEIPRKRPEIWSRAIVHSRERENIPR<br/> GSVQFAQEIQVSSSADETERSEAEVNAFNSISNPAPQQFQ<br/> GIINLAFEDATENECEFSANKKFKRSVLLSVDECEELGSDGE<br/> VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESDNILE<br/> CKQNKGNVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL<br/> SSRSRQLLREDKKVNNGSNVENDIQQRKFLDSDVKSQERPCHL<br/> DLHQREPNSDIPKNSSTKSLDSFRSQVLPOEGPVKESHSTTEK<br/> ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPYEMDVIEAEFQ<br/> KVESETHVTMDMF*DDQHFAKQDWTLLKQLLSEQDSNLDVTSV<br/> PEDLSLAQYLINQTLILLARDSSKPGQITHIDTLNRWSELTSPLD<br/> SSASITMASFSSDCSPQGEWTILELETOH</p>   |
| 5819       | 1  | 5557   | <p>AAAGLLGALHLVMTLVVAAARAEEAFVQSESIIEVLRFDGGGL<br/> LQTETTLGLSSYQKKSISLYRGNCRIPEPPMLDFHEQPVGMP<br/> KMEKVLHNPSS*ITLVSIPTTSHFASFFONRKILPGGNT<br/> SFDVS/VFLARVGVNVENTLFINTSNHGVFTY\QVFGVGVNPNY<br/> RLRPLFGARVTNVSFPIINIHNPHEPLQVVMYSSGGDLHL<br/> ELPTGQGGTRKLWEIPPYETKGVMRASFPSSREADNHTAFIRIK<br/> TNASDSTEFIIILPVEVEVTTAPGIYSSTEMLDFGLRTQDLPKV<br/> LNLHLNLSGTDKVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK<br/> YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV<br/> LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFALLIHDVL<br/> LPEEAKTMFKVHNFSKPVILPNEGSIYFTLLFMPSTSSMHIDN<br/> NILLITNASKFHLPRVRYTGFLDYFVLPPKIEERFIDFGVLSAT<br/> EASNILFAIINSNPIELAKSWHIIGDG\LSIELVAVDRGNRTT<br/> IISLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH<br/> DGAIQITTDYEILTIIPVK\AVIAGVSLTCSPKHVVLPPSPFGKI<br/> VHQSLNIMNSFSQKVKIQQIRSLSEVRFYKRLRGNKEDLEPG<br/> KSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM<br/> WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI<br/> TABLSWPSILSSPRHLKPLTNTNCSS\EEBITLENP/SQDVPV<br/> YVQFIPALYSNPVSFVDKLVSRFNLKSKVAKIDRLTLEQVFRN<br/> SAHPLQSSSTGFMEG\LSPHLILNLILKPEKKSXKVK\FTPVHN<br/> RTVSSLIIVRNLTVMDAVMVQGGTTENLRVAGLPGPGSSLR<br/> FKITEALLKDCDTSKLRPNFTLKRFTKVENTGQLQIHETIE<br/> ISGYSCGYGFKVNCQEFTLNANASRDIIILFTPDFTASRVIR<br/> ELKFITTSSEFVFIILNASLPYHMLATCAEALPRPNWELALYII<br/> ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPFD<br/> VGRFFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA<br/> GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA<br/> SSQPANKTRPLVLDSENTGAQHSAGRKSKGAKQSQHGSQHHAHS<br/> PLEQHPQPPLPPVPQPEPQPERLSPAPLAHPHSHPERASSARH<br/> SSESDITSLEIAMDKDFDHDHSPALEVFTEQPPSPLPKSKGKG<br/> KPLCRKVKPKPKQBEKEKKGKGPQDELDKDSLADDDSSSTTE<br/> TSNPDTEPLLKEDTEKQKQKQAMPEKHESEMSQVKQKSKLLNI<br/> KKEIPTDVKPSSELEPYTPPLESKQRRNLPSKIPLPTAMTSGSK<br/> SRNAQKTGTSKLVDRNPPALAKFLPNSELGNTSSSEGEKDS<br/> PPEWDSVPVHKPGSSDLSLYKLSLOTLNADIFLKQRTSPTPAS<br/> PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA<br/> SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS<br/> HAPVDSGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE<br/> VFSKGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSWPA<br/> SGSPHTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN<br/> TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPITGR<br/> RSSDPWNSNSHFPHEN</p> |
| 5820       | 310  | 1270   | <p>RVLSGPPVSLGVLCCARSSMTGKRDNRVAYMNPAMARSRGPIQ<br/> SSGPITQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEKMN<br/> ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\<br/> SSSDSSSSSSSDEDEKKQKRRKKKQNRSHKSSSSSMTES</p>  |

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|------------|--|--|---|
|            |  |  | DSKDSLKKKKSKDGTETEKDIKLSKKRMYSEDKPLSSSLS<br>ESEYIEVRAKKKSSSEEREKATEXTKKKKKKKKHKKKKKAA<br>SSSPDSP*H*EKSGFPYKESAMSEEISTVKTITTYLLKCMNFLVF<br>GIIPGLFSSSHSDATV  |
| 5821       | 179  | 915  | KWRNQSWRWPKPGTNWMI.SCSVCWRRVWTGTGSVMNRKLGKHPQT<br>PT/IKDCSIAATGKRPSARFPHQRRKKRREMDGLAEGGPQRSN<br>TYVIKLFDRSVDLAQFSENTPLYPICRAWNRNSPSVRERECSPS<br>SPLPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\<br>SRIPSPLAALRMQGT*P*RWSPFEPSPSTLIYRNMQRWKRIRO<br>RWKEASHRNQLRYSESMKILREMYERO  |
| 5822       | 464  | 4379   | QTLKEMPIMVARDLEETASSEDEKEVISQEDHPCIMWTGGCRRRI<br>PVLVFFHADAJLTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA<br>HGFHEVHPSSDYDNLMTGSHLKPFLRLTLSEAQKVNHFPRSYE<br>LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLPLPAEYAEFCNSYS<br>KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP<br>LLIDDFXFDVRLVVLVTSYDPLVIYLYEEGLARFATVRYDQGA<br>NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLR<br>LKQEGRDITLMAHVEDLIKTIISAELAIATACTFVPHRSSC<br>FELYGFDVLIDSTLKPWLEVNLSPSLACDAPLDLKIKASMISD<br>MFTVVGFCQDPAQRASTRPIYPTFESSRRNPFQKQRCRPLSA<br>SDAEMKNLVGSAREKGPGLGSSVLGLSMEEIKVLRVKEENDR<br>RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG<br>APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRRSSRLRAMRP<br>KYPVITQPAEMNVKTETBSEEEEEVALDNEDEEQAESQESAGF<br>LRENQAKYTPSLTALVENTPKENSMKVREWNKGGHCCKLETOE<br>LEPKFNLMLQLQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG<br>QTFASAWAKEDEQMELVVRFLKRASNNLQHSRLRMVLPSSRLAL<br>LERTRILAHQLGDFIIVYNKETEQAEMKSKKKVEEEEDGVNM<br>ENFQBFIRQASEAELEEVLTFTYQKNKSASVFLGTHSKISKNN<br>NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSKLSRFTTSA<br>EKEAKLVYNSSSSGPTATLQKIPNTHLSVTTSDLSPPGCHHS<br>LSQIPSAIPSPMPHQPTILLNTVSASASPCLHPGAQNIPTGLP<br>RCRSGSHTIGPPSSFQSAAHISYQKLSRPSAKAGSCYLNKHS<br>GIAKTQKEGEDASLYSKRYNSQSMVTAELQRLAEKQAAQYSPSS<br>HINLLTQQVTNLNLATGIINRSSASAPP*TLRPIISPSGPTWSTQ<br>SDPQAPENHSSSSPGSRSLQTGGFAWEGEVNNVYSQATGVVPOH<br>KVHPTAGSYQLQFALQLEQQKLQSRQLLDQSRARHQAIQSGST<br>LPNSNLWTMNGAGCRISSATASGQKPTTLPOKVVPPSSCASL<br>VPKPPPNHEQVLRATSQKASKGSSAEGQLNGLQSSLNPAAFVP<br>ITSSTDPAHTKIMNHKHTKQPVHHSWVHD |
| 5823       | 42   | 2293   | LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLADEKDFD<br>DLSLSSSSANEDDEVFFGPFHGKERCIAASLELNNPVPEQPPLP<br>TSSEPPFAWSPLAGEKFVEVYKEAHLALHIESSSRNQAAQAKP<br>EDPRSQGVVERFIQESKF\KINLFEKEKEMKKSPTS LKRETYYS<br>DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP<br>RESCTAHAASQAATQRKPGTKLLPRAASVRGRGIPGAEEKPKK<br>EIPASPSRTKIPAEKESHDRDVLDPKPAPGAVNVPAAGSHLGQK<br>RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWGSASSA<br>CTPQPVAKAKSSEFASIPAN*LPGLCPNISK\GRMGFAMLRPA<br>L\PAGPVG\ASSWQAKRVDVSELAEEQLTAPP\SASPTQPQTPE<br>GGG\QWLNSSCAWSESSQLNKTIRSIRRRDSCLNSKTKVMPTPTN<br>QFKIPKFSIGDS\PDSSTPKLSRAQRQSCSVGRVTVHSTPVR<br>RSSGPAPQSLLSAWRVSALEPTASRRCSGLPMPPTPKTMPRVGS<br>PL\CVPARRRSSSEPRKNSAMRTEPTRESNRKTDNR\LVDSVDR<br>GSPPSRVPAALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS<br>BALLVDIKLEPLAVTPDAASQPLIDLPLIDFCOTPEAHVAVGSE<br>SRPLIDLMTNTPDMNKNVAKPSPVVGLIDLSSPLIQISPEADK<br>ENVDSPLLKF   |
| 5824       | 42   | 2293   | LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLADEKDFD<br>DLSLSSSSANEDDEVFFGPFHGKERCIAASLELNNPVPEQPPLP<br>TSSEPPFAWSPLAGEKFVEVYKEAHLALHIESSSRNQAAQAKP  |

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|------------|--|--|--|
|            |  |  | EDPRSQGVVERFIQESKF\KINLFEKEKEMKKSPTSLSKRETYLLS<br>DSPLLGPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP<br>RESCTAHAASQAATQKPGTKLLLPRAASVGRGIPGAAEKPKK<br>EIPASPSRTKIPAEKESHDRVLPDKPAPGAVNVPAAGSHLGQK<br>RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA<br>CTPQPVAKAKSSEFASIPAN*LPGLCFNISKS\GRMGFAMLRPA<br>L\PAFVPG\ASSWQAKRVDVSELAEEQLTAPP\SASPTQPQTPE<br>GGG\QWLNSSCAWSESSQLNKTRSIIRRDSCLSNKTVMPTFTN<br>QFKIPKFSIGDS\PDSTPKLSRAQRQSCTSVGRVTVHSTPVR<br>RSSGPAPQSLLSAHRVSALPTPASRRCSGLPPMTPKTMPRAVGS<br>PL\CVFARRRSSEPRKNSAMRTEPTRESNRKTDSDR\LVDVSPDR<br>GSPPSRVQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS<br>EALLVDIKLEPLAVTPDAASQPLIDLFLIDFCDTPEAHVAVGSE<br>SRPLIDLMTNTPDMKNVAKPSPVVGQLIDLSSPLIQLSPDADK<br>ENVDSPLLK  |
| 5825       | 2  | 4210   | FLQIESASPAFFSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL<br>SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAGALERSFVEL<br>SGAERERPRHFREFTVCSIGTANAVAGAVKYESAGGFYVESG<br>KLFSVTRNRFIHWKTSQDTLELMEESLDINLNNAIRLKFQNC<br>VLPGGVYVSETQNRVILMLTNQTVHRLLLPHPSRMYRSELVVD<br>SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD<br>GEALFALPCASGGIFVLKLPYDIPGMVSVVELKQSSVMQRLLT<br>GWMPTAIRGQDQSPDRPLSLAVHCVHEDAFIFALCQDHLRMWS<br>YKEQMLMVMADMLEYVPVKDLRLTAGTGHLRLAYSPTMGLYL<br>GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISLFTSQETLIDF<br>ALTSTDIWALWHDENQTVVKYINFEHNVAGQWNPVFMQPLPEE<br>EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL<br>DLSWSELKKEVTLAVENELQGSVTEYEFSSQEEFRNLQGEFWCKF<br>YACCLQYQEALSHPLALHNPHTNMVCLLKKGYLSFLIPSSLVD<br>HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTQ<br>DMVIMEMSCYNLQSPKAAEQILEDMITIDVENVMEDICSLKQ<br>EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTLQY<br>GSNTAGYIVCRGVHKIASTRFLICRDLILQLQLMRLQDAVING<br>TGQLFQAQDQLHRTAPLLSYLIRKGECLATDVPLDTLESN<br>LQHLVLELTDGALMANRFVSSPQTIVELFFQEVARKHIIISHL<br>FSQPKAPLSQGLNWPMTITATSILLQLLWPSNPGCLFLECLM<br>GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVGTGEGQKAL<br>ECFCQAASEVGKEEFLDRILRSEDGEIVSTPRLQYDKVRLRLD<br>VIGLPELVIQLATSATBASDDW\KSQATL\RTCIFKHHL\DLG<br>\HNSQAYGSL*PQIPDSSRQLDCLRQLVUVLCERSQLQDLVEFS<br>YVNLHNEVVGIIESRARAVDLMTHNYELLYAFHIYRHNRYKAG<br>TVMFEYGMRLGREVRTLRGLEKQGCNYLAALNCLRLIRPEYAWI<br>VQPVSGAVYDRPGASPKRNDGECTAAPTNRQIEILELEDEKE<br>CSLARIRLTLAQHDFSAVAVAGSSSAEEMVTLVVOAGLFDTAIS<br>LCQTFKLPLTPVFEGLAFKCIKLPQGGAAQAEAWANLAANQLS<br>SVITTKESSATDEAWRLSTYLERVKVQNNLYHHCVINKLLSHG<br>VPLPNWLINSYKKVDAEALLRLYLNYDLDDLTPYQVIRICGC |
| 5826       | 3  | 871  | KSQLLRDHSAPPPKPTSVGAMGC*PRO/SPKEQQRQLKKQKNR<br>AAQRSRQKHTDKADALHQHESLEKDNLALRKEIQSLQAEALW<br>WSRTLHVHERLCPMDCASCAPGLGCDQAEGLLGPQPGQHG<br>CREQLELFQTPGSCYPAQPLSPGPQPHDSFSLQCLPLSLSLGP<br>AVVAEPPVQLSPSPLLFASHTGSSSLQSSSKLSALQPSLTAQTA<br>PPQPLELEHPTRGKLGSSPDNPSSALGLARLQSRHHPALSAAT<br>WQGLVVDPSPHPLLAFLPSSAQVHF   |
| 5827       | 194  | 2287   | GMGSENSALKSYTLREPFFTLPSGLAVYPAVLQDQGFASVFVYK<br>RENEDKVNKAAPV**HLKTLRHPCLLRLFLSCTVEADGIHLVTE<br>RVQPLEVALETSSAEVCAGIYDILLALI FLHDRGHLTHNNVCL<br>SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP<br>EEMSPEFTTLPECHGHARDAFSFGLTVESLLTILNEQVSADVLS<br>SFQQLHSTLLNPIPKWRPALCTLLSHDFRNDLFLEVNFKSL<br>TLKSEEEKTEFFKFLLDVRSCLSEELIASRLVPLLNQLVFAEP   |

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|------------|--|--|--|
|            |  |  | VAV\KSFLPYLLGPKKDHQAQGETPCLLSPALFQSRVIPVLLQLF EVHEEHVRMVLISHIEAYVGALSREQLKKV\IL\POVLLG\LR D\TSDSIVAITLHSLAVLVSLGPEVVVGERTKIFKRTAP\SF TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSFNFPSSSK SEENPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV BESSWDDCEPSSLDTKVNPGGITATKPTVTSGEQKIPALLSLT EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQBRPLKVPSEL GLGEEFTIQVKKKPVKDFEMDWFADMIPEIKPSAAFLILPELRT EMVPPKKDDVSPVMQFSSKFAAAEITEGAEGWEEEGELNWEDNN W   |
| 5828       | 2  | 257  | AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFOAVV MAVGGGSRMTDLTSSIPKPLLPVGNKFLIYWP\LNLLERVGFEV IVVTTRDVQKALCAEFKMKMKPDIVCIPDDADMGADSLRYIYP KDKTDVLVLSCLITDVALHEVVDLFRAYDASLMLMRKGQDSI EPVPGQKGGKKAVEQDFIGVDSGKRLLFMANEADLDEELVIK GSIQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS BL\IPYLV/RGKQFSSASSOQGRKEREGGSKGKRLKSFRIYS SFY*KEANYTGTGAPY\D\ACWI   |
| 5829       | 260  | 1259   | PDGRLIVSCSEDKTIKIWDITNKQCVNNFSDSVGFANFVDFNPS GTCIASAGSDQTVKVDVVRNKLQHYQVHSGGVNCSIFHPSGN YLITASSDGTLLKILDLKGRLLIYTLQHTGPVFTVSFKGGELF ASGGADTQVLLWRTNFDLHCKGLTKRNLKRLHFDSPPHLLDIY PRTPHPEEKVETVDFLHLLRLIQSLR*SICRSLPLLLWISF LLILPQQQKPVVGLCQTRVKRPVDIS*TL*CHQNVCCQPRKRK QKT*VTPSVVK/VSIPLAVTDALEHIMEQLNVLQTQVSI LEQR LTLTEDKLKDCLENQKLFSAVQQKS   |
| 5830       | 4496   | 3139   | GGKMAAPEERDLTQEQTEKLLQFODLTGIESMDQCRHTEQHNN NIEAAVQDRLENEQEGVPSVFNPSPSRPLQVNTADHRIYSYVVS R PQRGLLGWGYLLIMLPFRFTYITLIDIFRFAIRFIRDPDRSRV TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELRF L LVYLHGDDHQDSDEFRCNTLCAPEVISLINTRMLFWACSTNKPE GYRVSQALRENTYPFILAMIMLKDRRE*PV\VGRLEGLI\QPD DL INQLTFIMDANQTYLVSERLEREERNQTVLRQQDEAYLASLR ADQEKERKKREERERKRRKKEEVQQKLABERRRONLOEEKER K LECLPPEPSPDDPE3VKIIFKLPNDSRVERRFHFSQSLTVIHDF LFSLKESP\EFQIEA\NFFRR\VLPCIPSEE\WPNPPTLQE\A GLSHTEVLFVQDLTDE   |
| 5831       | 71   | 2897   | FCSKDKCCLYLPDSINRSKSC\AKPGAHSQDRHAVMDSERQVKD TDDIESPKRSIRDSGYIDCWDSESDSLSPRRHGRDSDSFDLSDS FGSRSRQTPSPDVVLRGSSDGRGSDSESLPHRKLDPVKKDDMS ARRTSHGEPKSAVPFNQYLPNKSNTAYVPAPLRKKKABREEYR KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRCSE EAAVQPHSRARQEQQLINNQLREEDDKWQDDLARWKSRRKRSVS QDLIKKEERKKMEKLLAGEGDTSEERRKSIKTYREIVQEKERRE RELHEAYKNARSQEEAEGILQYYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKPTATVETTIARAS VLDTSMSAGSGSPSKTVPKAVPMLTPKPYSPKNSQDVLKTFK VDGKVSVNGETVHREBEKERECTVAPAHSLTKSQMFEGVARVH GSPLELKQDNGSIEINIKKPNVSPQELAATTEKTEPNSQEDKND GGKSRKGNIELASSEPHFTTTVTRCSPTVAPVEFPSSPQLKND VSEKDKKPPENEMSGKVELVLSQKVVKPKSPEEATLTFPFLD KMPEANQLHLPLNLSQVDSPSSEKSPVTPFKFWAWDPBEEERRR QEKWQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEBERRY YEEEP*II\EDPVVPFTVSSSSADQLSTSSMTEGSGTMNKIDL GNCQDEKQDRRWKKSFGDDSDLLKTRSDRLEBKSLTEGAL AHSGNPFVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNNQTSN PTHSSEVVKPTLPDKSINHQIESPSERRKISGKKLCSGCL PLGKGAAMIETLNLVYFHIQCFRCG\ICKGQLGDAVSGTDVIR NGILNCNDCYMRSRSAGOPTL |
| 5832       | 2454   | 829  | PGRFRHGSACAFQOKCYIMLHICQYFLOGECKFGTSCKRSHDFSN SENLEKLEKLGMSDDLVSRLPTTYRNAHDIKNKSSAPSRVPLPF   |

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|------------|--|--|--|
|            |  |  | VPGTSEKDSGSSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH RVHFHLPYRWQFLDRGKNEDLDNMELIEEAYCNPKIERILCSES ASTPHSHCLNFNAMYGATQARRLSTASSVTKPPIITTDWIW YWSDEFGSWQEQYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGVR PGSHLEVPGRKAQLRVRFQSLRSEKPLWHN*XGLPQTQIR/AP QDVTMTQTCNTKFFGPKSIPDYWDSSALPDGPFQKITLSSSSEE YQKWNHFNRTLPPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG GKAVDERQLFHGTSIAIFVDAICQQNFDWRVCGVHGTSYKGGSYF ARDAAYSHHYSKSDTQTHMTFLARVLVGFEFVRGNASFVRPPAKE GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV TPSILLALGSLFSSRQ   |
| 5833       | 170  | 3289   | SILCLLSPCVVQFGKPVVVSILSSRSRHSPTCKKGWEGMRKHLHT RQGHK*VHVEISKALWVYRDDYFIRHSISVS AVIVRAITHKXR GRDWNVWKEENLLHAVAKNYTLTQTI PPFERPFKDHQVCLEWNM GYIWNLRANRIPQCPLNDVVALLGFPYASSGENTGIVKKFPFR RNRELEATRRQMDYPVFTVSLWL YLLHYCKANLCGILYFVDSN EMYGTPSVFLTEGYLHIQMHVKGEDLAVTKFIIPLKEWFRL DISFNGGQIVVTTSIGQDLKSYHNQTI SFREDFHYNDTACYFII GGSRYVAGIEGPFGLKYRLRSLHPAQIFNPLEKQLAEQIKL YYERCAEQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR PSMCRAFPWEKELDKHPSLFQALLEMDLLTVPRNQNESVSEIG GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYLLAV FYETGLNVPRDQLQGM LYSLVGGQGSERLSSMNLGYKHYQGIDN YPLDWELSYAAYSNIATKTPLDQHTLQGDQAYVETIRIKDDEIL KVQTKEDGDVFMWLKHEATRGNAQAQRLAQMLFWGQQGVAKNP EAAIEWYAKGALETEDPALIYDYAIVLFKGGQVKKNNRLALELM KKAASKGLHQA VNGLGWYHKKFNKYA\KAAKYWLKA\BE\MCN PDASYNLGVHLHDGIFPGVPGRNQTLAGEYFHKAQGGHMEGTL WCSLYYITGNLETFFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN AYLEGSWHEALLYVLAETGIEVSQTNLAHICEERPDLARRYL GVNVCVWRYNFSVFQIDAPSFAYLKMGDLYYGHQNGSQDLELS VQMYAQAALDGDSDGFFNLALLIEEGTIIIPHILDFLEIDSTLH SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLWLGAILH SALIYFLGTPLLSILIAWTVOYFQSVASDPPPPRPSQASPDAT STASPAVTPAADASDQDQPTVTNNPEPRG   |
| 5834       | 17   | 4020   | RFRGGGRVFPFGAPFASPSDSLQGGNSQGFPTPKPPRT/QECG SAAPGPPIPGQSSS*VPLRLEQIQKADCP LSLALKPRMAAQV TLBDALSNVDLLEELPLPDOQPCIEPPSSLLYQNFNTNFEDR NAFVTGIARYIEQATVHSSMNELEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVLEVLEPEVTKLMNFYFORNAIERFC GEVRRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMDPQSTQESQNLMSFLANHNKITQSLQ QCLEVISGYEBLLADIVNLCDVYENRMYLTFSEKMLLKVMGF GLYLMGDSVSNIIYKLDKRRINLSKIDKYFKQLQVPLFGDMQI ELARYIKTSAHYEENKSRWCTSSGSSPOYNICEQMIQIREDHM RFISELARYSNSEVVTSGRQEAQKTD AEYRKLFDLALQGLQLL SOWSAHVMEVYSWKL VHPDTKYSNKDCPDAAEYERATRYNYS EEKFPALVEVIAMI KGLQVLMGRMESVFNHAIHRTVYAALQDFSQ VTLMEPLRQAIKKKNV IQSVLQAIKRTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRAVGPSSSTQLYMVRTMLES LIADKSGSK KTLRSSLEOPTILDIEKPHRESFFYTHILINFSETLQCCDLSQL WFRFFLELTMRRIQFPPIEMSPWILTDHILETKEASMMYVL YSLDLYNDSAHYALTRFNKQFLYDEIRAEVNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGAT IHLPPSNRYETLLKQR HVQLLGRSIDLNLITQRVSAAMYKSELAIGRFESEDLTSIVE LDGLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL HVFWELNYDFLPNYCYNGSTNRVVRTVLPFSQEFQORDKQPNAP QYLHGSKALNLAYSSYGSYRNFGVPPHFQVICRLLGYQGIADV MEELKVVKSLLQGTILQYVKTLMVMPKICRLPRHEYGSPGIL EFFHHQLKDIVEYAEKTVCFQNLREVGNAILFCLLIEQSLSE EVCOLLHAAPFQNILPRVHVKEGERILDAMKRLSEKYAPLHLPV |

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|------------|--|--|--|
|            |  |  | LIERIGTPQQIATAREGDLTKERLCCGLSMFEVILTRIRSFLD<br>DPIWRGPLPSNGVMHVDECFEHLWSAMQFVYICIPVGTHEFTV<br>EQCFDGLHWAGCMIIIVLGGQRRFAVLDFCYHLLKVQKHGKD<br>EIIKNVPLKKMVERIRKQFQLNDEIITILDKYLKSGDGEPTVE<br>HVRCPQPIHQSLASS   |
| 5835       | 4209   | 1904   | SGNIRMAQGSQIDFQVLHDLRQKFPPEVPEVVSRCMLQNNNNL<br>DACCALVLSQBSTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLQ<br>SQNIYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSELFQQEPQ<br>TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSQQT<br>PRFNPIMVTLAPNIQTGRNTPSLHHIGVPPVVLNSPQGNISYI<br>RPYITTPGGTTROTQOHSGWVSQFNPMNPQQVYQSPQGPWTTTC<br>PASNPLSHTSSQPNQOQHQTSHVYMPISSTPTTSQPPTIHSSGS<br>SQSSAHSQYNIQNIISTGPRKNQIEIKLEPPORNNSKLRSSGPR<br>TSSTSSSVNSQTLNRNOPTVYIAASPPNTDELSRSQPKVYISA<br>NAATGDEQVMRNQPTLFISTNSGASASRNMSGQVSMGPAPFIHH<br>HPPKSRAGNNSATSPRVVVTQFNT\EYTFKITVSPNKPAPVSP<br>GVVSPTELTNLLNHPDHVYETENIHLTDPTLAHVDRISETR<br>LSMGSDDAAYTQDI*RI NSWLGWVAHACNSSALGGQDGRII*A<br>QEFETSWGNIWRLRLRYRF*NYAGMVAHTCSPSYSD*ALLVHQ<br>KARMERLQRELBIOKKLKLKSEVNEMENLRRRLKRSNSIS<br>QIPSEEMQQLRSCNRQLQIDIDCLTKEIDLQARGPHFNPSAI<br>HNFYDNI GFVGPVPPKPKDQRSIIKTPTQDTEDEGAQWNCTA<br>CTFLNHPALIRCEQCEMPRHF  |
| 5836       | 361  | 2303   | FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKRQGPNSSKQLLK<br>SDVNYQCLFSAHVLHLRGVLTTPQVEDERGNVFLWNGEIFSGIK<br>VZAEENDTQILPNYLSCKNESEILSLFSEVQGPWSFIYYQASS<br>HYLWFGDRDFGRRSLWHFNSNLGKSFCLSSVGTQTSGLANQWQE<br>VPAS\DFSELILSLSFDPALFYNCILGNIFLGRILLKKMLIA*<br>VXFQOTYQHLRYOR*OMKPNCILKNLLEL*I*CCHKLHWRLIAVI<br>FPMCHLQERYFKSFLMYT*KEVIOQFIDVLSVAVKKRVLCPLR<br>DENLTANEVLKTCRKANVAILFSGGIDSMVIATLADRHIPLE<br>PIDLLNVAFIAEBKTMTPTTFNREGNKQKNCIEPSEEFKDVAA<br>AADSPPNKHVSVPDRITGRAGLKEQAVSPSRINWFVEINVSHE<br>ELQKLRRTRICHILRPLDVLDDSIGCAVWFASRGIGWLVAQEG<br>VKSYSQNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM<br>MELGRISRNRLRDDRVIDGHGKEARFPFLDENVVSFLNSLPIW<br>EKANLTLPRGIGELKLLRLAAVELGLTASALLPKRAMQFGSRIA<br>KMEKINEKASDKCGRQLQIMSLENLSIRKETKL  |
| 5837       | 4792   | 903  | NGNAVAQAPVTNCCYLATGSKDQTRIRWSCSRGRGMILKLPFL<br>KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT<br>QSWRRKYTLFSASSEGNHSRIVFNLCPLOTEDDKQLLSTSM<br>RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG<br>MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT<br>DDGKVGLYDTYSNKPQISSTYHKKTVYTLAWGPPVPPMSLGGE<br>GDRPSLALYSCGGGIVLQHNPKLSGEAFDINKLIRDNTSIKY<br>KLPVHTREISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH<br>HKLVTNISWHHE\HGSPAQKLSYL\MPSGSQCSPTFCHNLKNC<br>P*KAAPESPSPDLQSPYRTPPQGHATAQDYFVWAWEPHIH*WEG<br>VFCPPIDGYSFGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL<br>DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGGKSIBLEKKRLSQ<br>PKAKPKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSQDQ<br>EGEQAREPELPCGLAPAVSREPVICTPVSSGFESKSVTINNKV<br>ILLKKEPPKEKPEPETLIKRRKARSLPLSTSLDHSKEELHQDCL<br>VLATAKHSRBLNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG<br>HLENGHPELFHQLMLWKGD LKGVLTAAERGETLNDLVAMAPAA<br>GYHWLWAVEAFKQLCFQDQYVKAASHLLSIHKVYEAVELLKS<br>NHFYREAIAIAKARLPEDPVLDLYLSWGTVLERDGHYAVAAK<br>CYLGATCAYDAKVLAKKGAASLRTAELAIAVGEDELSASLA<br>LRCAQELLANNWVGAQALQLHESLQGQRLVFCLELLSRHLE<br>EKQLSEKSSSSYHTWNTGTEGPFVERVTAWKSIFSLDTPQWY<br>QEAQKLQNIKYPSATNNTPAKQLLLHI CHDLTLAVLSQQMASW |



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|------------|--|--|---|
|            |  |  | DEAVQALLRAVVRSDSGSFTIMQEVYSAFLPDGCDHLRDKLGD<br>HQSPATPAFKSLAEFLYGRLYEFWWSLRPCPNSSVWVRAGHR<br>TSLVEPSQQLDTASTEETDPETSPQEPNRPSELRLTEEGERM<br>LSTFKELFSEKHASLQNSQRTVAEVOSTLAEMIRHQKSQLCS<br>TANGPDKNBPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRTE<br>ANQMAKFPESIKAWFFPDVLECCLVLLLRSHFPGCLAQEMQQ<br>QAQELLQKYGNTKTYRRHCQTFM   |
| 5838       | 110  | 98   | KTMPHLLVTRDVAIDFSQEWECLDPAQRDLRYDVMLENYSNL<br>ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG<br>LGDNMECKGNLEGQVSKSEGLYMCVKITCEKATESHSTSTTFH<br>RII/HYQKGIVKCKECRQGFSLYSLCLIOHBEHNI*KCSEVNKH<br>RNTFSKKPSYI*HQ\KFRLGKPYECMECGKAFGRSDLIQHQK<br>IHTNEKPYQCACGKAFIRGSQLEHQRVHTGEKPYDCKCKGKA<br>FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG<br>EKPYECKECGKAFILGSHLYHQRVHTGEKPYICECKGKAFILCA<br>SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPY<br>KCKECGKAFISNSNLQHQRIHTGEKPYKCKECGKAFICGKQLS<br>EHQRIHTGEKPFCECKECGKAFIRVAYLTQHEKIHGEKHYECKEC<br>GKTFVRATQTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQ<br>RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRHTGEKPYECKEC<br>GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL<br>HN*EYSSHKIKMHSIALASLDFAHLQEKNPEN   |
| 5839       | 1  | 2425   | GRPFPRPRALPRLPLRGRQRQGRWTVDFEECLD\SPRFRAL<br>EEVEGDVAEELKL\DKLVKLCIA\MIDTGKAFVANKQFMNGI<br>RD\LAQNS\NDA\VVETKFAPSFDSLQEMINFHTIL/L*PNS<br>EIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNA<br>PSRPASLEL*KPPNILTATRKCFRHIADYVLQINVLQSKRRSE<br>ILKSMLSFMAYHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGD<br>AKEKREMEQKHSTIQQKDFSRDSDSKLYNVDAANGIVMEGYLFK<br>RASNAFKTNRRWFSIQNNQVYQKKFKDNPTVVVEDLRLCTVK<br>HCEDIERRFCFEVVSPTKSCMLQADSEKLQAWIKAVQTSI<br>ATYRKDDSEKLDKKSSPSTGSLDSGNESKEKLLKGESALQVRQ<br>CIPGNASCCDGLADPRWASINLGITLCIECSGIHRSGLVHFSK<br>VRSLTLDTWEPPELLKIMCELGNQVIRVYEANVEKMGIKKPPQ<br>QROEKEAYIRAKYVERKFDKIPL*SLSP\BQKK\FVSKSSE<br>EKRLSISKFGP\GDQVRASQSSVRSDSGIQSSDDGRSLPS<br>TVSANSLEYEPGERQDSSNFDLSKHLNPGQLYRASYEKNLPKM<br>AEALAHGADVWANSSEENKATPLIQAVLGSLVTCFELLQNGAN<br>VNQRDVQGRGPLHATVLGHTGQVCLFLKRGANQHATDEBGKDP<br>LSIAVEAANADIVTLRLARMNEEMRESEGLYQPGDETYQDIF<br>RDFSQMASNNPEKLNRFQDQSKF   |
| 5840       | 698  | 3610   | KHLHLPRQHLTTLWQISSPRWRSPQAFMSALSKTQTQSAPALQ<br>GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPS<br>AQFFIPKSFNYPNSSTSEVSSTASAKASIGQSPGLPSTAFKLP<br>SNTKGFTATHNTSPAAPPTEVTICQSSSEVSKPKL\SESTSPSL<br>\EMKIHNFLKGNPGFSVA*NLKHPNPGSLGSSAPSEHPSDFQ<br>RGPTSTSIDNIDGTPVRDRSGTPTQDEMMDKPTSSSVDTMSLL<br>SKIISPGSSTPSSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE<br>SPYKQPSDGMERPSSSLDSSQEKFPDTSFQEDEDYRDFEYSGP<br>PPSAMNMLQKKPAKSLKSSKSLDTEYQPILESSYSHRAQEFV<br>KSAFPSPVRALLDSSENCRLSSSPGLFGAFSVRGNEPGSDRSP<br>SPSKNDSFFTSDSNHNSLSQSTTGHLSLPQKQYVPSPHVPHRS<br>LFSPQNTLAAPTGHPTPSGVEKVLASTISTTSTIEPKNMLKNAS<br>RKPSDDKHFGQAPS KGTSPDGVLSNLTPSLTATDQOQOBEHY<br>RIETRVSSCLDLPDSTEEKGAPIETLGYHSASNRMSGEPIQT<br>VESIRVPGKNGRNGHREASRVGFDLSTSGSSFDNGPSSASELA<br>SLGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH<br>LPPSPLEHGTTPQREPVGPPSAPPVPPKDHGGIFSRDAPTHLPS<br>VDLSNPFTKEAALAHAAAPPPGEGSGIFPFTPPPPPPGEGHSS<br>SGGSGVPFSTPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP<br>KHSSLLQGTLAEHFGVLPGRDHGPGTQRDLNGPGLSRVRESL |

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|------------|--|--|---|
|            |  |  | TLPSHSLEHLGPPHGGGGGGSSSGPPLGPPSHRDTISRSGIILRSRPFDFRPREPFLSRDPFHSLSKRPRPPFARGPPFFAPKRPPFP  |
| 5841       | 1908   | 762  | GLRLPLVLTVWPMMPKPSWL3RTEFSKRLLCRTLWCOSGWSSRSYTRSMKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTWRHCWMTARSCSGEKGHWAPROQGVYLLPGRVGCVSRSVSPSFGDGLDSGLARRGSVAVALASGLVEEPMGLGPPPHPTPRFKAVSAKSKEDLVSQGFTEFTIEDFHNFTMDLIEQVEKQTSVADLLASFNDQSTSDYLVVYLRLLTSGYLQRESKFHEFIEGGRTVKEFCQ\QEVPEPMCKESDHIHIALAQGLQRVHPGWEYMGPRPRAATTNPHIFP*GLPSKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPCLLARA LGHCYRGFSVVVWWSYFTPFLLSHD?PPMFY   |
| 5842       | 307  | 1918   | QBPADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPVRKLVSSRRPRTRRNLLGTACATYLGFLVSQVGRASLQHQAAEKSGHRSRDTAEPSPFPEIPLDGTLPAPESQGGNGSTLQPNVYITLRSKRSPANIRGTVPKRRKKHVASAAPGQEAALVGPQLQPEA\EGKML*HLGTLREQTWLRLESPPGGWCVRE/WRAGGPDFLQPSRESNIRIYSESAPSWLSKDDIRRMRLADSAGVLRPVSSRSGARLLVLEGGAPGAVLRCPGSPCGLLKQPLDMSEVFAFHLDRILGLNRTLPSVSRKAEBFIQDGRPCPIILWDASLSSASNDTHSSVKLTWGTYYQLLKQKCNQNGRVPKPESGCTEIHHEWSKMLPDLFLQIYNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAAALHI IQRKHDPRHLVFI DNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSOHLRQKLQSLFLDKGYWESQGGRGIEKLIDVIEHRAKILITYINAHGVKVLPMNE   |
| 5843       | 500  | 1453   | GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPGKWGLGAGMRGSRMSQPPQLRRAQSSCCHFMVKLLDDGTMPMPGKVAHTSLDALVTFHQQKPIEPRELLTQPCRQKDPANVDYEDLFI.XSNAVAEEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQSGSHFLPPKIPSWRDP PETLEEQNAPRERPEGPAAAKKPPRHCHLVVTLGCPEIHGDLRPWDRKQPRSLRGSHLGGQRLHGSCLGHI SQKPLTAPGTQRQKGPHEGREVQQLH*GDPRGQELAPNGSESPIPLGVQARAPGLGRA  |
| 5844       | 202  | 2471   | FDSAVLSSINVMVAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGIKPLPQIPPPMPPIQYQPLGQVPHMPLAKDGLAMGKEMPHLYQYKEYPHLPQYMKELQAPAPRMGKEAVPKKGEIPLASLRGEQGPREGPPRGPPGPPGLPGHGIPIGKGPQGVPGVKGPMGMPGPKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPFGHGLPGIGKPGGPGLPQGPQKDRGPKGLPGPQGLRGPQKDGFGMPGAPGVKGPPGMHGPFGPVGLPGVKGPGVTGFPOP\QGPLGK\PGAPGEPGQGPPIGVPGVQGPPIPGIGKPGQDG\IPGQPGFPGGKGEQGLPGLPGPPGLPGIGKPGFPKGDRGMGGVPGALGPRGEKGPIGA PGIGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPPQPPGPKGEPGLQGFPGKPGFLGEVGPFGMRGFPGPPIGPKGEHQKGVPLPGVPGLLGPKEGPGIPGDQGLQGPPIPGIGGPGSGPIGPPGIPGPKGEPGLPGPPGFGIGKPGVAGLHGPFGKPGALGPQGPGLPGPPGPPGPPGPAVMPPTPPQGEYLPDMGLGIDGVKPPHAYGAKKGKNGGPAYEMPAFTAELTAPFPVVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYFYAYHVHCKGGNVWVLFKNNEPVMYTYDEYKKGFLDQASGSVALLRPGDRVFLQMPSEQAAGLYAGQYVHS SFSGYLLYPM |
| 5845       | 215  | 2061   | HASNKASLQDKMANPKEKTAMCLVNETARFNRVQPYKLLNERGPAHSMFVSQVLSLGEQTWESESSIKKAQQAVGNKALTESTLFPKI*KKPSNVNNNPGCITPTVELNGLAMKRG/KPAIHRPLDPKFPNNRANYNFQVMYNQRYHCPFKIFYVQLTVGNNEFFGEGKTRQAARHNAAMKALQALQNEPIPERSPQNGESGKMDDDKDANKS EISLVFEIALKRNMFPVSFEVIKESGPPHMKSFVTRVSVEGFSAE GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKTIVKAGPEYQGGMNPI SRLAQIQAKKEKEPDYVLLSERGMPRRREFFVMOVKVGNEVATGTGPNKKIAKNAAEAMLLQLGYKASTNLQDLEKTGENKGWSGPKPGFPEPTNTNTPKGIHLHSPDVYQEMEAS  |

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|------------|--|--|--|
|            |  |  | RHKVISCTTLGYLSPKDMNPSSSFFSISPTSNSSATIARELLM<br>NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC<br>DRQSGKECVTCLTLAPVQMTFPAIGSSIEASHDQV*YATAILLC<br>YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSAARLEKSKLFALG<br>N.   |
| 5846       | 1126   | 456  | FSKLIMKTFIIGISGVNNSGKTTLAKNLQKHLNPNCSVISODFF<br>KPESEIETDKNGLQYDVLALNMEKMSAISCMESARHSVVS<br>TDQESAEIPIILIEGFLFNYPKPLDTIWNRSYFLTIPYEECKR<br>RRSTRVYQPPDSPGYFDGHVWPMYLYKRYQEMQDITNEVVYLDGT<br>KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTNPS/CK*IRK<br>LQGV  |
| 5847       | 2769   | 505  | APEMEDLSSPDSTLLQGGHNLSSASFQESVTFKDVIVDFTQEE<br>WKOLDPGQDRLFRDVTLENYTHLVSIGLQVSKPDVISQLEOGTE<br>PWIMEPSIPVGTCAWETRELSVSAPEPDISEEELSPVIVEK<br>HKRDDSSWSSNLLSWYEGSLERQANQQTLPKEIKVTEKTIPS<br>WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSTKQNSNPVK<br>KEKCKCNECGKAFSYCSALIRHQRTHTGKPKYKCN*/CWEKAF<br>SRSENLIHQRIHTGDKPYKCDQCGKGFIEGPSLTQHQRHTGE<br>KPYKDECGKAFSQRTHLVQHQRHTGKPYTCNECGKAFSQRG<br>HFMEHQKIHTGKPKCDECDKTFTRSTHLLTQHQRHTGKPYK<br>CNECGKAFNGPSTFIRHHMIHTGKPYECNECGKAFSQHSNLTO<br>HQKTHTGKPYDCAECGKSFYSWSSLAQHLKIHTGKPYKCN<br>GKAFSYCSSLTQHRRHTREKPFECSECGKAFSYLSNLNQHQKT<br>HTQEKAYECKECGKAFIRSSSLAKHERIHTGKPYQCHECGKTF<br>SYGSSLIQHRKIHTGERPYKCNCGRAFNONIHLTQHKRIHTGA<br>KPYECAECGKAFRHCSSLAQHQRHTGKPYKCNCKEKTFSQSS<br>HLTQHQRHTGKPYKCNCGKAFSRSTHLLTQHQRHTGKPYK<br>CNECGK\TFSQSTYLIHQHRIHSGEKPPGCNDCGKSFYRSALN<br>KHQLHPGI   |
| 5848       | 22   | 2961   | AAPRLLRGGGDRTPRFLPALLRGPPAAEAPERRKMPAVSK<br>GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFGDKAL<br>DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG<br>YLFISVLVNSNELIRLNNAIKNOLASRNPTFMGLALHCIASV<br>GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLRLRYRTSPDL<br>VPMGDWTSRVVHLLNDQHLGVVTAATSLITLQAKNPEEFKTSV<br>SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY<br>PPDPNAVGRGLTECLETLNKAQEPKSKKVQHSNAKNVLFEA<br>ISLIHHDSEPNLLVRACNLQGLQHQHRETNLRYLAESMCTLA<br>SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN<br>APQIVAEMLSYLETADYSIREEIVLKVAILEKYAVDYTW\YVD<br>TILNLIIRIAGDYVSEEVYRVIQIVINRDDVQGYAAKTVFEALQ<br>APACHENLVKVGYYILGEFGNLIAGDPRSSPLIQPHLLHSHFHL<br>CSVPTRALLLSTYIKFVNLFPPEVKPTIQOVLRSDSQLRNADVEL<br>QRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKK<br>GPSTVTDLEDTKRDRSDVNGGPEPAPASTSAVSTPSPSADLLG<br>LGAAPPAPAGPPSPSGGSLVDVFSDSASVVAPLAPGSEDNFA<br>RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIYGNKTSQFL<br>NFTPTLICDDLOPNLNIQTKPVDPTVEGGAQVQVUNIECVSD<br>FTEAPVLNIQFRYGCTFQNVSVQLPITLKNFFQPTEMASQDFPQ<br>RWKQLSNPQEQVQNIIFKAKHPMDTEVTAKIIGFGSALLEZVDP<br>NPANFVGAGI IHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV<br>SQRCELLSAQF |
| 5849       | 3545   | 1895   | KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ<br>P*DPMSLSPPCFTEEDRFSLEALQTIHKQMDDDKGGIEVEES<br>DEFIREDMKYKDATNKSHLHREDKHITIEDLWKRWKTSEVHNW<br>TLEDTLQWLEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI<br>SQLKISDRSHRQKLQKALDVVLFGLPLTRPPHNMKDPILTISI<br>VIGVGGCWFAYTQNKTSKEHVAKMMKDLESQTAEQSLMDLQER<br>LEKAQENRNVAVEKQNL*RKMMDEINYAKEACRLRELREGAE<br>CELSRRQYAEQLEQVRMALKKAEKEFELRSSWVDPDALQKNLQ<br>LTHEVEVQYINIKRONAEMQLAIKAEASKIKKRSTVFGTLHV  |

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|------------|--|--|--|
|            |  |  | AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWOQIEKICGFQIAHNSGLPSTLSSLYSDHSWVMPRVSIIPPY7IAGGVDDLDSDT.PPIVSQFPPTMAKPPGSLARSSSLCRSSRSIVPSSPQPQRAQLAPHAPHPSHPRHPHPQHTPHSLPSPDDILDVSSCPALYRNBBEEBAIYFSAEKQWEVDPDTASECDLNSISGRKQSP/ SKPRDIPN IIS/DERYQEMRCP*RIIPSGGIL   |
| 5850       | 3  | 1895   | XAVLNFSASGVSISLTGNSPMHDSMWHLKKNGIIVYLDVPLLN LI CRCLKMKTDRIVQNSGTSMDLLKFRQQYKKWYDARVFCESGASPEEVADKVLNAIKRYQDVSDFPISTRHVWPEDCQKVSAEFFIEAVIEGLASDGGFLVPAKEFPKLSCGEWKSIVGATYVERA QILLERCIHPADIPAAARLGEMIEATAYGENFACSKIAFVRHLSGN QFILELFHCGPTGSFKDLSLQMPHIFAQCIPPSCNMILVATSG DTGSAVLNGFSRLNKNQKQRIAVVAFPPENGVSDFQKQAIIGSQ RENGWAVGVESDFDFCQTAIKRIFNDSDFGTFLTVEYGTILSSA NSINWGRLLPQVYHASAYLDLVSQGFISFGSPVDVCPTGNFG NILAAVYAKMMGIPIRKFICASNQNHVMTDFIKTG\HYDLRGKE N*AQTFFTVO*IFLPNLSNLERHLHLMANKDQGLMTELFNRLES QHHFQIEKALVEKLOQDFVADWCSEGECLAINSTYNTSGYILD PHTAVAKVVDVRVQDKTCPIVISTAHYSKFAPAIMQALKIKEI NETSSQLYLLGSYNALPPLHEALLERTKQQEKMEYQVCAADMN VLKSHVEQLVQNQFI |
| 5851       | 3120   | 1802   | RCYLQFLALLLTSTSAARAAATAAAEPAAGSPVMTAGDHNRO RGCCGSLADYLTSAKFLLYLGHSLSTWGDNRMHFAVSFVLVELY GNSLLLTAVYGLVVGASVVLGAIIGDWDKNARLKVQTSLVV QNVSVILCGIILMMVFLKHHELLTMYHGWLTSCYILITIANI ANLASTATAITIQRDWIVVAGEDRSKLANMNATIRRIDQLTNI LAPMAVGQIMTFGSPVIGCGFISGWNLSMVCBYVLLWKVYQKT PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH ELEHEQEPTCASQMAEPFRTFRDGVSYYNQPVF/LGWHGSCFP LYDCPGL*LHHHRVRLHSGTENFHPQYFDGSI SYNWNNGNCSFY LATSKMWFSGSDRDLRIGTAFLLFDLVCDLCHAWKPPGLVRFSE   |
| 5852       | 1  | 422  | KTFPSSSLCPLRQLPEVRGYSGOPLTDPLISLCRSHKCRGKGG SSSYPSLPA LRARSAPGHCTHRSCGPEWRIDSISRLMEQARR SGWAQAQPTILLVPRRLKSLPSIWG/SLMGFFITSFGPG/WFRQ YYFFISGRH*VLFTESDFYVAMDFGGHGLSSHYSPOVPYLYQT FVSBIRRVVAGKKQSVYPRRCGGCSRAPPLITGGGVGSRKQRWP ESGAWALAPGLPAIHGRSWES  |
| 5853       | 223  | 1346   | RLGLSRVKGLHGPASAWISDPETRGDPGGPWGMWRGSDLRPR PVSILTGLTVCK*AAQGPQV\HSVKLCFLGGLPCLL\FPIFRP LLLHPRRPRLHPGTRGVAVEPHALRVVHVHAGEEAGIRAAGPGH GGVEIPQG/VGSLGARRGLRPSRPSRRHRNRVPAPPPGRPLATP HRRRFPDPALTCPLGQDQGPREQQKQSGRHDITLGDWGESE SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGLSVLSIQEEGPD T GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP LSSLCITESPSQNWTPCLLLLTCPRGFL   |
| 5854       | 86   | 938  | KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHITQE LXHLCAMIKRVLLERLENTKRLRELTEGRTLDPQNRITEVSAK RQIVTEYREKGRN*EEKRDLEGRSRRYNLCIIGIPETEDRAS GAETIKDLE/ENFPELKNELDLQMEKAHRIPLKFNEKKAASRH IRVTFL/KFQRRNIIQASSQKQVTKYGAKVRLTSDFPSAILNA RRQW/N/PISRVLRNNFEPRIIYSAKLSFLYKGNWKTFLDIQG LGKYINQELSLKILLKDLLQLTENLN   |
| 5855       | 536  | 2391   | LRSYGCKAPSRISHLHK\FLPFLLPSSLMGYSESPPITDSWAP FLSLTHHVLSSQSPLSSNCWICLSHTQ*FTALPADLLTWTQS NVSLHISYLAIPPLADSFLLKPV/L*PGNSAKHLSFKLSLSMVS GRAVALLHLIASGLTSIQNTASSKPIWGY\LSOTSTFISPPP LCLSRTPYN*AHATMVGQVPSLGLIFTL/RTPCRPSILHPNY KIISTSAWQKVLCSGSPTIHTSLHLLTGSSFLSFHPIPGFPAA NSALYVSSLKGPFGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN   |

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|------------|--|--|---|
|            |  |  | FFLSPKPNSLHQLPSQ\TFYQALTGAALAGSYPIWENENTLSWL<br>PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN<br>ILPPNQITILISVEASISSSPIRNKWLHLITLLTGLGITAALGT<br>GIAGITTSITSYQTLFTLSTNTVEDMHTSITSLQRQLDFLVGVI<br>LQNRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD<br>RAAEL*HQVADSWWQGSLLRWIPWVAPFLGPLIFLLLMIGP<br>CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH<br>SEAPEPRP  |
| 5856       | 173  | 1137   | PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAIGILYK<br>FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNIL<br>IRYTGDNSPYSPITIIYFHGNAGNIGHRLPNALLMLVNLKVNLL<br>VDYRGYKGESEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG<br>RSLG\GAAAIHLASDNHRISAIMVENTFSLIPHMASTLFSFPP<br>MRYLPLWCYKKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ<br>LYELSPSRTRKLAIFPDGTHNDTWQCCQCYFTALEQFIKEVVKSH<br>SPEEMAKTSSNVITII  |
| 5857       | 1597   | 563  | KLIGKVLVLSVADAMAAFAVEPQGPALGSEPMMLGSPSPKPG<br>VNAQFLPGFLMGDLPAVPTPQPRISIGPSVGMEMRSPLLAGGS<br>PPQPVVPAHKDKSGAPPVRSIYDDISSPGLSTPLTSRRQPNIS<br>VMQSPVLGVSTPPTGTCQSMFSPASIGQPRKTLSPAQLDPFYTQ<br>GDSLTSEDH\LDSDWGDICWGLKASA\SYILL\QFAQYGGIS*<br>NMWMSNTGNMWHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI<br>DKSVMESSDRCALSSPSLAFTPIKTLGTPTQPGSTPRISTMRP<br>LATAYKASTSDYQVISDRQTPPKKDESLVSKANEVFMGW   |
| 5858       | 355  | 1419   | PPHQPAASTSXHQQQQPPPPPPQDSSKPVVAQGGPAPGVGSAP<br>PASSSAPPATPPTSGAPPGSGPGPTTPTPPAVTSAPPGAPPTP<br>PSSGVPTTPPQAGGPPPPPAAVPGPGPGPKQGGPGGPKGGMKMP<br>GGPKPGGGPGLSTPGHKKPPHRRGGEPGRGRQHPPYHQHHQ<br>GPPPGGPGGRSEEEKISGPRRGFKANLSLLRRPGKTYTQRCRFC<br>LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKADSEFIKLESR<br>ALA*NCPKFLG*YTP*GGRQLPSSLPPTHACLPLSCSVIFSPF<br>MFPQ*NCWGRKPFPRNLGPHLKGAVCNRRWDDPWEGPTGKGHCLN<br>FAS   |
| 5859       | 307  | 1503   | GGSSARPRASSRRMLSRKKTKEVSKPAEVQGGYVKKETSPLLR<br>NLMPSPFIRHGPTIPRTDICLPDSSPNAFSTSGDGVVSRNQSF<br>RTPIQRTPEINRRSRLSAPSYLARSADVPREYSSSQSFVT<br>EVSFAVENGDGSGRYYSNFDGQRKPLGDRAHEDYRYEYN<br>HDLFORMPQNGRHSAGIGRVAATSLGNLTNHGSEDLPLPPGWS<br>VDWTRGRKYIIDHNTNTTHWSHPLERGLPPGWERVESSEFGT<br>YVVDHTNKKAY\RHPCAPTCTSV*STTSCHI/AS/RQOTERNQ<br>SLLVPANPYHTAEIPDLQVYARAPVKYDHILKWELFQADLDT<br>YQGMKLLFMKBLEQIVKMYEAYRQALLTELENRKORQWYAAQ<br>HGKNF  |
| 5860       | 2956   | 1270   | TIRVEEFLPCPGGGKAQLSSASLLGAGLLLPPTPPPLLLLP<br>LLLFSLRCLGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI<br>SWEKIHGKSSQTAVVHHPPQYGFVSQGEYQGRVLFKNYSLNDATI<br>TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTVLVEPTVSLIKG<br>PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSFP<br>NETATIIISQYKLEPTRFARGRRITCVVKHPALEKDIRYSFILD<br>QYAVEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG<br>QWPDGLLASDNLHFVHPLTFNYSYGVYICKVT\NSPGSKEVTQK<br>VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LAEP*KIA<br>PSPLSTL\ATIKGTQLPTIIA*CSGVGALFIV\LVKCFGLGIF<br>CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDDELDPYPSV<br>KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYIEDL<br>KMGMKFVSDEHYDENEDDLVSHVDGVSISRRENVV<br>EVCACVQAFNLVASSGDDSGGDKCGCEVGSWVGSMRVVMARLL<br>SEGEQGIPTACAAFAQQPAG/BPRRLAGVGEQPGQCSWVNYRC<br>TLEFLVSLGTDLARGRNSASGPTAPADSKQL/ML*DVHRRVI<br>LE*RMNSGSPARDNAPSQRFCNTLSEGLRFGISPSWREALYGC |
| 5861       | 2051   | 1305   |   |

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|------------|--|--|--|
| 5862       | 1556   | 483  | A<br>PPFQLIMGEIKVSPDYNWFRGTVPLKKTIIVDDDDSKIWSLYDAG<br>PRSIKCPILIFLPPVSGTADVFRRQILALTGWGYRVIALQYPVYW<br>DHLEPCDGRKLLDHLQLDKVLHFGASLGGFLAQKFAEYTHKSP<br>RVHSLILCNSFSDTSIFNQWTWANSFWLMPAFMLKKIVLGNFSS<br>GPVDPMMADAIIDFMVDRLESLGQSELASRLTLNCQNSYVEPHKI<br>RDIPVTIMDVFDQSALSTEAKEMYKLYPNARRAHLKTGGNFPY<br>LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWVPSRLRCRKA<br>ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRFPSPGSSGS<br>PVLTVSGK  |
| 5863       | 2714   | 249  | PPFSRGSFLAAPREDTMGPLMVLFCLEFLYPGLADAPSCPN<br>VNISGGTFTLSHGWA PGSLLTYSCPGLYPSASRLCKSSGQWQ<br>TPGATRSLSKAVCKPVRCPAPVSFENGITYTPRLGSPVGGNVSF<br>ECEDGFI\LRGSPVRQCRPNMGWDETAVCDNGAGHCNPGISL<br>GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECQNGVWSGLE<br>PICRQPYSDFPEDVAPALGTSFSHMLGATNPTQKTESLGRKI<br>QIQRSGHLNLYLLDLCQSQVSENFDFLIFKESASLMVDRIFSFEI<br>NVSVAIITFASEPVLMSVLDNSRDMTEVISSLENANYKDHE<br>GTGTNTYAALNSVYLMNMNQMRLGMETMAW\QEI RHAI ILL\T<br>DGK\SHMGSGPKTAVDHIREILNINQKRDYLDIYAIGVGKLDV<br>DWRELNLGSKKDGERRHAFILQDTKALHQVFEHMLDVSKLTDIT<br>CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT<br>AAHCFRDGNDHSLWRVNVGDPKSPQWKEFLIEKAVISPQFDFVA<br>KCNQGIL\EFYGD\DIALL\KLAQVKVM\STHCQGPSCLP\CTM<br>\EANLGFLRETFKGSTCR\DHENEL\WNKQSV\PAHF\VAL\N<br>GSKLEHLTLRMGVEWTSRCLGSPKKKTMT\FENLT\DVRE\VVT<br>D\QFL\CS\GPOEDESP\CK*E\SGGA\VFLEHRFRLSAGGVWC<br>SWGL\YNP\CIGSA\DKNSPKKGPSVAKVPPPTR\DFHIN\LFP<br>Q*SPWL RQHPPGMS*IFLPLL ANGLHSPFACPARICRPLHFLPS<br>EWATLRTL |
| 5864       | 173  | 1013   | PLISVPQSLISLPQPLLCTPGGQEPSAPSCLYSFLWACSFTMG<br>KLPPSIPSSPLACVLKKNLKPQLTDLKPKCLIFFCNTAWPOY<br>KLDNDSK*PENGTFEFSILQVLNDNSCHKMGKWEVDPVQAFF\S<br>HWSLPSLCSQC/GLIPNLSSFSPPFCSEFG/PPPQVPS/TESFFS<br>MDSSDLPPSPQAAPRAEPGNHSLASAPPYPNPFITSPHTWS<br>SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL<br>GSFSSNIKIQPSWLIWQQP   |
| 5865       | 568  | 1684   | CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC<br>LSVCVCVQVGSWICV/CVSMCAVSLCTC\ICRCISMYTREHAC<br>ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCMVCLIGYA*AC<br>TCV*MCVCMHEHVC MC/VCAACSVLL/CRGHIC/MCMSAYICI<br>/CVYVCVLCVWACMRMSTCVWL VYG*ACTCVWMM/CSCTCR/C<br>VHVCCMSMHACBCLCVYLHICGAGTRRWAGSARGSRSCSRLP<br>CHAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW<br>GSPAACSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEEGCG<br>GGRGWVCAPLLNGPQCCCFSIKPELKAKKKK  |
| 5866       | 98   | 3197   | ARPEVPAPPAWLSRRGAAGMDKDDKDSPPKKNKGKERRDLDDL<br>KKEVAMTEHKMSVEEVC RKYNTDCVQGLTHSKAQEILARDGPNA<br>LTPPPTTPEWVKPCRQLFGGFSILLWIGAILCFLAYGIQAGTED<br>DPSGDNLYLGIVLA AVVIITGCFSYQEA KSKIMESFKNMVPO<br>QALVIREGEKMQVNAEEVVVDLVEIKGGDRVPADLRIISAHGC<br>KVDNSSLTGESEPTQTRSPDCTHE\NPLKTRNITFFSNFVEGTA<br>RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFILQITGV<br>AVFLGVSFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV<br>CETLTAKRMAKNCLVKNLEAVETLGSTSTICS DKTGTLTQNR<br>TVAHMWFNDQIHEADTTEDQSGTSFDSKSHTWALF*H/LLGFC<br>NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE<br>RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD<br>RCSTILLQKKEQPLDEEMKEAFQNAYLELGLGGERVLGFCHVYL<br>PEEQFPKGFAFDCCDDVNFITDNLCFVGLMSMIGPPRAAVPDVAG<br>KCRSAGIKVIMVTGDHPITAKAIAGVGIFEGNETVEDIAARL  |

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|------------|--|--|---|
|            |  |  | NIPVSQVNPDAKACVHGTDLKDPTEQIDELQNHTEIVFAR<br>TSPOQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI<br>AGSDVSKQAADMILLDDNFASIVTGVVEGRILFDNLKKSIAITL<br>TSNIPEITPFLLFIMANIPPLPGTITILCIDLGTDMVPAISLAY<br>EAAESDIMKRQPRNPRTDKLVNERLISMAYGGIIGMIQALGGFFS<br>YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGOQWTFEOR<br>VVEFTCHTAFFVSIVVQWADLIICKTRNSVFQGMKNKILIF<br>GLFEETALAAFLSYCPGMDVALRMYPPLKPSWFWCAFFYSFLIFV<br>YDEIRKLILRRNPGGWKEKETY  |
| 5867       | 3  | 1485   | LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP<br>GPVKTLTRKKNKKKRFNKSAREVSKKPSGPGAVVRP7KAPE<br>DPSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQONKK<br>BTSPOVKGEEMPAGKQDEASRGSPSGSKMDRRAPVPRTKASGT<br>EHNKKGTKERTNGDIVPERGDIHKKRKAK\GQPPHPPR/IDI<br>WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLVKEQAFG<br>GLTRALALDCEMVGVGPKGEESMAARVSVNQGKCVYDKYVVP<br>TEPVTDYRTAVSGIRPENLKQGEELVVQKEVAEMLKGRILVGH<br>ALHNDLKVFLDHPKKKIRDTQYKPFKSQVKSGRPSLRLLSEK<br>ILGLQVQQAHECSIQDAQAAMRLVVMVKKEWESMARDRRPLTA<br>PDHCSDDA*QSCPPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS<br>ESWQRGVAWCY  |
| 5868       | 2122   | 833  | LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR<br>AVTVYDKPASFFKETPLDLQHRLFMKGSMHSPFRARSEPDPV<br>TERSAFTERDAGSGLVTRLRERPALVSSSTWTEDEDFSIILAA<br>LESRV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKHQFH<br>IQVCTPWLEAEDYPLLGSADLGVLHTSSSGLDLPKVVDMFG<br>CCLPVCVAVNFKCLHELKHEENGLVFEDSBEAQAQQLMFSNFP<br>DPAGKLNQFRKNLRESQQLRWDESQVQTVLPLVMDT   |
| 5869       | 2122   | 833  | LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR<br>AVTVYDKPASFFKETPLDLQHRLFMKGSMHSPFRARSEPDPV<br>TERSAFTERDAGSGLVTRLRERPALVSSSTWTEDEDFSIILAA<br>LESRV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKHQFH<br>IQVCTPWLEAEDYPLLGSADLGVLHTSSSGLDLPKVVDMFG<br>CCLPVCVAVNFKCLHELKHEENGLVFEDSBEAQAQQLMFSNFP<br>DPAGKLNQFRKNLRESQQLRWDESQVQTVLPLVMDT   |
| 5870       | 2122   | 833  | LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR<br>AVTVYDKPASFFKETPLDLQHRLFMKGSMHSPFRARSEPDPV<br>TERSAFTERDAGSGLVTRLRERPALVSSSTWTEDEDFSIILAA<br>LESRV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKHQFH<br>IQVCTPWLEAEDYPLLGSADLGVLHTSSSGLDLPKVVDMFG<br>CCLPVCVAVNFKCLHELKHEENGLVFEDSBEAQAQQLMFSNFP<br>DPAGKLNQFRKNLRESQQLRWDESQVQTVLPLVMDT   |
| 5871       | 3  | 3465   | FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS<br>VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP<br>LKSINLPRPDNETLWDKLDHYIRIVKSTLLLYQSPTTGLFPTKT<br>CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI<br>KCMRGILYCYMRQADKVQQQKQDPRPTTCLHSVFNVTGDELLS<br>YEEYGHQLINAVSLYLLYLVEMISSGLQIIYNIDEVSFIQNLVF<br>CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ<br>L*KQFNGFNLFNGQGSWSVIFVDLDAHNRRNROTLCSSLPRESR<br>SHNTDAALLPCISYPAFALDDEVLSQTLDDKVVRLKGYGFKR<br>FLRDGYRTSLEDPNRCYYPKAEIKLFDGIECEFFIFFLYMMIDG<br>VFRGNPKQVQEQDQLLTPVLHHTTEGYVVPVKKYVVPADFVEYE<br>KNNPGSQKRFPSCNRDGLFLWGOALYIAKLLADELISPDI<br>DPVQRYVPLKDQNVSMRFSNQGPLENDLVVHVALIAESQRIQV<br>FLNTYGIQTTPQOQVEPIQIWPQQLVYKAYLQGLINEKLGLSGR<br>PDRPIGCLGTSKIYRILGKTIVVCPYIIFDLSDFYMSQDVFLIID<br>DIKNALQFIKQYKMHGRPLFLVLIREDNIRGSRFNPIIDMLAA<br>LKKGIIGGVKVHVDRLQTLISGAVVEQLDPLRISDTEELPEFKS<br>PEELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHEIL<br>QKLNDCSCLASQAILLGILLKREGPNFITKEGTVDHIERVYRR |

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|------------|--|--|---|
|            |  |  | AGSQKLWSVVRRAASLLSKVVDLSAPSIITNVLVQKQVTLGAFG<br>HEEEVISNPLSPRVIQNI IYKCNTHDEREAVIQQELVIHIGWI<br>ISNNPELFSGLTKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP<br>SEVKQLLLDILQPQNGRCNLNRRQIDGSLNRTPTGPDYDRVWQI<br>LERTPNGIIVAGKHLPPQPTLSDMTMYEMNPSLLVEDTLGNIDQ<br>PQYRQIVVELLMVSVIVLERNPELEFQDKVDLRLVKEAFNEFQ<br>KDQSRLEKEIKQDDMTSFYNTPLGKRGTCSTLTKAVMNLLEG<br>EVKPNNDPCLIS   |
| 5872       | 68   | 665  | VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPPWPTPTVFF<br>NIAIDSESLGCI\SFKLFPADKV/PKRWKNFVLLNTEKVLGDK<br>CPCFYRIIPG\LCQGGDFTHHNGTGKSLYSKEFDENFI/LKH<br>TAPGVLTANAGPTTNGSQPFICTAKTEDG*QHVVFQKVKDGM<br>IVEALERSGSRNGKTSKKITANCGQL  |
| 5873       | 2240   | 506  | RRPEGGSGGGRTRARMPLPWSLALPILLSWVAGGFGNAASAR<br>HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF<br>GECVGPKNKRCRCPGYTGKTCSDVNECGMKRPPCQHRVCNTHGS<br>YKCFCLSGHMLMPDATCVNSRTCAMINCOYSCEDTEEGPQCLCP<br>SSGLRLAPNGRDCLDIDECASGKVICPNRRVCNTEFGSYCKCH<br>IGPELQYISGRYDCIDINECTMDSHTCSHANCNTQGSFKCKC<br>KQYKGNGLRCSAIPENSVEVLRAPGTIKDRIKKLLAHKNSMK<br>KAKIKNVTPPEPTRPTPKVNLQPFNYEEIVSRGNSHGG/KKG<br>NEEKMKEGLEDEKREEKALD*HRRERPPRG\DVFFPKVNEAGE<br>FGLIL\VQRKALTSKLEHKADLNI SVDCSFNHG\ICDW\KQDR\<br>EDDPDW\NPADR\DNAI\GFY\MAVPGWLQGHK\KDIGRLKLL<br>PDLQPSNFCLLFYRLAGDKVGLRVFVKNSNNALAWKTTSE<br>DEKWKTKGIQLYQGTDATKSIIFEAERGKGTGEIADVGVLLVS<br>GLCPDSLSSVDD   |
| 5874       | 2  | 3397   | ACPRLARRRRRVRSLRRRGWLRARWSRGQNNMAARRITOETFD<br>AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAMYYDD<br>VHSDGRYSLSGSVAHSRDAGRESLSDVFGSPFRSSNPSISDD<br>SYFRKECGRDLEFHSNSRDQVIGHRKLGHERSQDWKFALRGSW<br>EQDFGHVPVSQESSWSQEYSFGPSAVLGDGSSRLIEKECLEKE\<br>SRDYDVHDSG\BA\DSVLRGS\SOVQA\RGRALNIVDQEGSLG<br>KGETQGLLTAKGGVGLVTLRNVSTKKIPTVNRITPKTQGTNQI<br>QKNTPSPDVLTGTNPGTEDIQFPPIQKIPLGLDLKNLRLPRRKMS<br>FDIIDKSDVFSRFGIEIKWAGFHTIKDDIKFSQLFQTLFELET<br>ETCAKMLASFCKSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL<br>NMLLDKGAVKTKNCFEIKPFDKYMRLQDRLLKSVTPPLMAC<br>NAYELSVKMKTLNPLDLALALETTNSLCRKSALLGQTFSLAS<br>SPRQEKIL*AVGLQDIAPSPAAPNFEDSTLFGREYIDHLKAWL<br>VSSGCPLOVKKAEPEPMREBEKMIPTTKPEIQAKAPSSLSDAVP<br>QRADHRVVGTTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN<br>SLEYKYKLLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV<br>RNLKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTOTLLFLR<br>APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP<br>QDPSEASGSPSPKAGVDISEAPQTSSPCPSADIDMKDNGRTAE<br>KLARFVAQVG\PEIEQF\SI\ENSTDNPLDWFL\HDQNSS\AFK<br>FY\RKKVFEELCPSICTSSPHNL\HTGGGDTT\GSQESPVDLME<br>GEAEFEDEPPPREAELESPEVMPEEDEDDEDEGGEAPA\PGRG<br>GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPPG<br>RQFSSKSLKVGMIAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS<br>KKKPKDLDFQAQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK<br>GIR\SRSACTQQAAGGSGWGLSPSTCSLPLGSFTAKMAYSQWL<br>IFVF |
| 5875       | 296  | 1848   | LAALGGLPLWRLSRRGFREYLLGLSAPSALGAMRSVSVVQVRA<br>LEFSGSLFPHAI CLGDVDNDTLNELVVGDTSGKVSVYKNDSSRP<br>WLTCSCQGMILTGVGDVNCNKGKLLVAVSAEGWFHLDLTPAK<br>VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL<br>VVGYYTDRVVRARFWEELGEGPEHLTGQLVSLKMWLEGGVUSLS<br>VTGLPLGLPELMVSPQGCAYAILLCTWKKDTGSPASEGPTDGS<br>/SGDPSCPRRGAAPDIWPYPQOECLHSPNWQHQTT\SHGTESSGS  |



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|------------|--|--|---|
|            |  |  | GLFALCTLDGTLKLMEMEERADKLLWSVQVDHQLFALEKLDVTG<br>NGHEEVVACANDGQTYIIDHNRTVVRFOVDENIRAFCAAGLYACK<br>EGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETXP\ST<br>TACCRSWAWILTSL*LVPCFTKRSTIQTSHHSVLPQASRIPPS<br>WTCLIIAGEGFF*TPTLPPKGVFGSHCAAAGSITKQ  |
| 5876       | 1122   | 224  | HLPLGVPSKVAGAAAMEPQEEERETQVAWLKKIFGDHPIQYEV<br>NPRTEILHHLSENRNRDRDYLVIEDLKQKASEYESEAKYLQ<br>DLLMESVNFSPANLSSTGSRYLNALVDSVALETKDTSLASFIP<br>AVNDLTSDFRTKSKSEIKIELEKLEKNLTATLVLEKCLQEDV<br>KKAELHLSTER\AKVDNRQNM\DFLKAKSEEFRTGIAAGEQL<br>SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD<br>LMP\NPSHCSK*RIEBAK\RELA\SIEBELTRRVS\MMEI   |
| 5877       | 2030   | 1907   | GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLE<br>LSRELIEMLAISRNQKLQAGEENQVLELLIHRDGEFQELMKLA<br>LNQGGIHHMQVLEKEVEKRDSDIQQLQKLEAEQILATAVYQ<br>AKEKLKSIKARKGAISSSEIKYAHRISSANAVCAPLTWVPGD<br>PRRPYPTDLEMRSGLLQGMNPNSTNGVNGHLPGDALA\RRKIAR<br>CPCSTVS\NGSQMTCR*INIILILQKSVCEL  |
| 5878       | 950  | 2113   | GLWKCMQLQGPHTRVQF*PTPRQGGPQ\VPVAVIAGNRPNLY<br>RMLRSLLSAQGVSPQMITVFIDGYEEPMDDVVALFGLRGIQHTP<br>ISIKNARVSQHYKASLTATFNLFPFAKFAVLEEDLDIAVDFFS<br>FLSQSIHLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG<br>LQWVLRRLSLYKEELEPKWPTPEKLWDWDMWMMRPEQRRGECI<br>PDVRSYHFGIVGLNMNGYFHEAYFKKHKFNTPVQVQLRNVDSL<br>KKEAYEVEVHRLSEAEVLHDSKNPCEDSFLPDTEGHTYVAFIR<br>MEKDDDDFTWTQLAKCLHWDLDVRGNHRLGLFRKKNHFLVV<br>GVPASPSYVKKPPSVTPIFLEPPPEKEGAPGAPEQT  |
| 5879       | 3  | 981  | RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCATMASSDED<br>GTNGGASEAGEDREAPGKRRRLGLFATAWLTFFDIAMTAGWLVL<br>AIAMVRFYMEKGTTHRGLYKSIQKTLKFFQTFALLEIVHCLIGIV<br>PTSVIVTGQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT<br>EITRYSFYTFSLDLHLPYFIKWARYNFFIILYVQVAGELLTIY<br>AALPHVKKTGMFSIRLPKNYNVSFDYYYFLITMASYIPLFPOL<br>YFHMRLQRRKVLHG*G*L*KRMK*SLQTRCFFQNNQDYLSPSF<br>NNKNKQLCEISWIVWFLKI   |
| 5880       | 1138   | 1324   | SLWCLVAGGLGLPSSQNPLQAGILARPREARGTFSSALTACSA<br>SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD<br>*KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL<br>CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERS<br>DQSEHTDGHSTVSQSVIEKLQENRLLKQKVTHVEDLNKQWRYN<br>ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC<br>AEVQKQELAASTARDAALERVQMLEQQILAYKDDFMSEADRE<br>AQSRIOELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA<br>ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAQRGGDLQCPH<br>CLOCFSEDEGEELLRHVAECCQ   |
| 5881       | 26   | 441  | GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLQSG<br>SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAFGKGLE*MGPF<br>LQDVETIYQKQFQGRVSMTEETSTETTQ/AYLESSLRSED<br>TAV<br>HHCATDTV   |
| 5882       | 2407   | 2216   | SGCVEMLYSHSLEYNPEWISVQSAVAPQALNDSGDL*LHSGE<br>RTRRD*QLPEAGGPGLQEPQLQGLDITSDEFILDEVG\VDLR<br>HYSKQVELELQIEQKSIQDYIQESENIALHNQITACDAVLER<br>MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNQAARVGRKL<br>ELVDGLVPSALVTAILEAPVTEPRFLEQLQELDAKAAVREQE<br>ARGTAACADVGRVLDRLRVKAVTKIREFILQKIYSFRKPMYNYQ<br>IPQTALLKYRFFYQFLGNERATAKEIRDEVETLSKIYLSYR<br>SYLGRIMKVQVEEVAEKDDLMGVEDTAKKGFSSKPSLRSRNTIF<br>TLGTRGSVISPTLEAPILVPHTAQRGEQRYPFPEALFRSQHYAL<br>LDNSCREYLFICEFFVVGPAHDLPHAVMGRTLSMTLKHLSY<br>LADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLAALLW |

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|------------|--|--|--|
| 5883       | 2  | 1374   | <p>PRFELILEMNVQSVRSTDPQRLGGDTRPHYITRRYAEFPSSALV<br/>SINQTI PNERTMQLLGQLQVEVENFVLRVAAFPSSRKEQLVFLI<br/>NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS<br/>PPFGGLVAFVKEAEALIRGQAEERLRGEARVTQLIRGFGSSWK<br/>SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L<br/>SQPQLRALPARAELINIHLMVELKKHKPNF</p> <p>EFPGRRFRVMEAGAGAGAGAAGWSCPGPGTPTVTLGSYEASEG<br/>CERKKGQRWGLERRGMQAMEGEVLLPALYSEEEEEEEEEVE<br/>EEEEQVQKGGSVGSLSVNKHRLSLTETEELELRAQVLQVLAEL<br/>EETRELGAQHEDDSLELQGLLEDERLASAQAEVFTKQIQQLQG<br/>ELRSLREEISLLEHEKESLKEIEQELHLAQAEIQSLRQAEDS<br/>ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME<br/>MKSESPSGSLGLSDYSGLQEELEQLRERYHFLNEEYRALQESNS<br/>SLTGQADLESERTQRATERWLQSQTLMSSTAESQTSSEMDPLEP<br/>DPEMQLLRQQLRDAEEQMHGMKNKQELCCELEELQHHRQVSEE<br/>EORRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL*A<br/>LVVISALLWCWMAETSS</p> |
| 5884       | 4261   | 2522   | <p>GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR<br/>SRLRDCGDYTPSERLPGKAMLWFQGAIPAAIATAKRSGAVFVV<br/>FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLOF<br/>SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTIRHKVRQM<br/>HLLKSETSVANGSQSESSVSTPSASFENNTCENSQSRNAELCE<br/>IPSTSDTKSDTATGGESAGHATSSQEPSCGSDQRPADLNIRVE<br/>RLTKKI.EERREEKREKEEQREIKKEIERRTKTKEMLDYKRRQEE<br/>BLTKRMLEERNREKAEDRAARERIKQQIALDRAERAARFAKTKE<br/>EVEAKAAALLAKQAEVMEVKRESYARERSTVARIQFRLPDGSSF<br/>TNQFPSDAPLEEARQFAAQTVGNITYGNFSLATMFPREFTKEDY<br/>KKLLDLELAPSASVLLP/ALFINF*AGRPTASIVHSSSGDIW<br/>TLGTVLYPFLAIWRLISNLFSPNPPPTOTSVRVTSSSEPPNPAS<br/>SSKSEKREPVRKRVLEKRGDDPFKEGKIYRLRTQDDGEDENNTW<br/>NGNSTQQM</p>   |
| 5885       | 900  | 467  | <p>AAGGRRSRLSRWPTGPKSPSGVRCCG\RR\AWEDKDEFLDV<br/>IYWFROI IAVVLGVINGVLPRLGFLGIAGFLINAGVLYLYFSN<br/>YLQIDEEYGGTWELTKEGFMTPA/IVHGHLDHLLHCHPL*LM<br/>VYSSQVLP IQSKGPS</p>  |
| 5886       | 86   | 1341   | <p>PFGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAASQSPSPSGS<br/>GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSPLPLKNG<br/>EVLLLEALFLTVDPYMRVAAKRLKRGDTMMGQVAKVVESKNVAL<br/>PKGTIVLASPGWTHSISDGKDLKLLTEWPDITPLSLALGTVG<br/>MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC<br/>KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY<br/>DCYFDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGFLPPGP<br/>PPEIGIYQELRMEAFVYRWQGDARQKALKDLKLVLELPYFVI<br/>D*LOANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE<br/>NMPAAMFMMLKGDNLGKTIVKA</p>   |
| 5887       | 1937   | 104  | <p>APGCRGCRATRCPCRGPRWDSLGDEAARSPPAAGGAPGLLGLRE<br/>RPDRCHPGGDDRGVQLHRGSPG/SFSELSRRPGPPGLPGLQGGP<br/>PAPGLPQSRTL/PVLCVCDLSPAQCDINCCDPCSSVDFSVFS<br/>ACSVFVVTGDSQFCSQKAVIYSLNFTANPPQRFVFLVDQINPSI<br/>FCIHITN\*NLHYPLLIQKYL/ENNNDFTLMKTSDFGLTNAESY<br/>VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP<br/>AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPPSRK<br/>KVPITVQSVIQLNKTLTRREDDTVLQPTLVNAGHFSLCVNVV<br/>LEVKYSLTYTDAEVTKADLSFVLGTVSSVVVPLQKFEIHLQ<br/>ENTQPVPLSGNPGYVVGPLAAGFQPHKSGI IOTNRYGQITI<br/>LHSTTEQDCLALEGVRTPVLFYTMQSGCKLRLTGALPCQLVAQ<br/>KVXSLWGGQPPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK<br/>DSCQLPGALVIEVKTKYGSLLNPQAKIVNVNANLISSEFPEAN<br/>SGNERTILISTAVTFVDVSAPAEAGFRAPPAINARLPNFFFPF<br/>V</p>  |

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|------------|--|--|--|
| 5888       | 375  | 2302   | LLCRTPGVAMQRADSEQPSKPRCDSPRTPSPNTPSAEDWSPG<br>LELHPDYKTWGPEQVCSFLRRGGFEPEVLLKNIRENEITGALLP<br>CLDES RFENLGVSSLGERRKLLSYIQRVLQIHVDTMKVINDPIH<br>GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYVFPGASHNRFH<br>SLGVGYLAGCLVHALGEKQPELQISERDVLQVQIAGLCHDLGHG<br>PFSHMF DGRFIPLARPEVKWTHEQGSVMFEHLINSNGIKPVM<br>QYGLIPEEDICFIKEQIVGPLESPEVDSLWPYKGRPENKSFLEY<br>IVSNKRNIGIDVDKWDYFARDCHHLGIQNNFQYKRFKIFARVCEV<br>DNELRICARDKEVGNLYDMFHTNSLHRRAYQHKVGNIDTMIT<br>DAFLKADDYIEITGAGGKKYRISTAIIDMEAYTKLDNIPILEIL<br>YSTDPKLDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES<br>LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQENPIDHVS<br>FYCTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDKRS<br>LYA\ARQYFVQW\CADR\NFT\KPDGRCY*PPTP*HPQKKGW\<br>NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM |
| 5889       | 1831   | 731  | LPAACGRPV TARPRQAEGRSGRPRDLDPYPPQVFPFRPRDVAI<br>VTGTDGIGYSTAKHLARLGMHVIAGNNDKAKQVVSKEIKET<br>LNDKET*VLLCCPGWLCWNSSDPPTSASRGAGTTGVHHHFLK<br>FGIFIL\DLASMTSIRQFVQKFKMKKI?LHVLINNAGVMVMPQR<br>KTRDGFEEHFGNLNYLGHFLLTNLLDLTKESGSPGHSARVVTS<br>SATHYVAELNMDLQSSACYS PHAAYAQSKLALVLFYHLQRL<br>AABGSHVTANVVDPGVVNTDLYKHVFWATRLAKLLGWLFLFKTP<br>DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLOQQ<br>LWSKSCMTGVLDTL   |
| 5890       | 1322   | 200  | FRGWSAAGRAVPVAFCSRISSSPRRPRGAVRLQSGTEAACRS<br>GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTGVAIITCP<br>LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVSPGPLHCLKV<br>ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCCKELNDVFD<br>PDSTQVHMI SAAMAGFTAITATNPIWLIKTRQL*/SQGTAGKR<br>RMGAPEFCVRKVYQTDGLKGFYRGMSASYAGISETVIFHVIYESI<br>KQKLEKYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI<br>AYPHEVVRTRLREEGTKYRSFFQTL SLLVQEEGYGSLYRGLTTH<br>LVRQIP\NTAIMMATYELVVYLLNG   |
| 5891       | 1322   | 200  | FRGWSAAGRAVPVAFCSRISSSPRRPRGAVRLQSGTEAACRS<br>GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTGVAIITCP<br>LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVSPGPLHCLKV<br>ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCCKELNDVFD<br>PDSTQVHMI SAAMAGFTAITATNPIWLIKTRQL*/SQGTAGKR<br>RMGAPEFCVRKVYQTDGLKGFYRGMSASYAGISETVIFHVIYESI<br>KQKLEKYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI<br>AYPHEVVRTRLREEGTKYRSFFQTL SLLVQEEGYGSLYRGLTTH<br>LVRQIP\NTAIMMATYELVVYLLNG   |
| 5892       | 1764   | 379  | VVLRCGRLSVNSAVSSRTGGWSAGLT CAMQRLQVVLGHLRGP<br>DSGMPQAAAPCLSGAPHASAADVVVHGRRTAICRAGRGGFKDT<br>TPDELLSAVMTAVLKDVNL RPEQLGDICVGNVLQPGAGAIMARI<br>AQFLSDIPETVPLSTVNRQCSSGLQAVAS IAGGIRNGSYDIGMA<br>CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITS ENVAER<br>FGISREKQDTFALASQQAARAQSKGCFQAEIVPVTTTVHDDKG<br>TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS<br>DGAAILLARRSKAEELGLPI LGVLSYAVVGVPPDIMGIGPAY<br>AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCEKRLRLP*EG<br>*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC<br>PCAIGSWNGSPLPVFEYPWGT  |
| 5893       | 3  | 1653   | ILSKRRRCQAKTKELMAKKVAVIGAGVSGLISLKKCVDEGLEPT<br>CFERTEDIGGVWRPFKENVEDGRASIYQSVVNTSKEMSCSFDFP<br>MPEDFPNLFHNSKLLYFRIFAKKFDLLKYIQFQTVLSVRKCP<br>DFSSSGQWKVVTQSNKEQSAVFDAMVCSGHHILPHIPLKSF<br>GMERFKQGYFHSRQYKHPDGFEGKRILVIGMGNLGS DIAVELSK<br>NAAQVFISTRHGTWMSRIS EGYPDWSVFHTRFRSMLRNVLPR<br>TAVKWMIEBQQMNRWFNHNENYGLBPQNKYIMKEPVLNDVPSRL<br>CGAIKVKSTVKELTETSAIFEDGTVEENIDVIFATGYSFDFP  |

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|------------|--|--|--|
|            |  |  | LEDSLKVENNMVSLYKIFPAHLDKSTLACIGLIQPLGSIFPT<br>AELQARWVTRVFKGLCSLPSEPTMMMDIIKRNEKRIDLFGESQS<br>QTLQTNVVDYLDLALAEIGAKPDFCSLLFKDPKPLAVRLYFGPCN<br>SY*YRLVGPQGWEGARNAIPTQKQRIKPLKTRALKDSSNFSVS<br>FLKILGLLAVVVAFF\COLQWS   |
| 5894       | 174  | 1673   | RYSPPKVLQNKESLKLGMATALVSAHSLAPLNLKKEGLRVVRE<br>DHYSTWEOGFKLQGNKSLGQEPCKQFRLRYEBTTGPREALS<br>RLRELCOQWLQPEHTHKEHILELLVLEQFLIILPKHLQARVQEH<br>HPESREDVVVLEDLQDLGETGQOVDPDQPKQKILVEEMAPL<br>KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIIVTDSGCRVES<br>SGKISEPMEAHNEGSLNRHQAKPKKIEYKCSEREQRFIOHLD<br>LIEHASTHTGKKLCSQSSSLTGHHKVL*ERKVIQC\HGV<br>LGKAFQRRSSHLVRHQIHLGKPYQCNECGVFSQAGLLEHLR<br>IHTGEKPYLCIHCGKNFRSSHLNRHQRIHSQEEPCECKECCGT<br>FSQALLLTHHQRIHSHSKSHQNECGKAFSLTSLIRHHRIHTG<br>EKPFKCNICQKAFRLNSHLAQHVRIHNEKPYQCSECEAFQR<br>SGLFQHQRYHHKDKLA  |
| 5895       | 2967   | 86   | HPSSLGAIPFYPPSSPPPPPLYLFWNSHRKSRHFINQRGHGE<br>MRLFVSDGVPGCLFVLAAAGRARGRAEVLISTVGPEDCVVPFLT<br>RPKVPVLQDLSGNLYFSTSAICRYFF\LLSGWEQDDLNTQWLEW<br>EATELQPTLSAALYYL\VVQGGKG\EDVLGSRVRLTHIDHSL<br>RQ\NCPFLAGETESLADIVLWALYPLLQDPAYLPEELSALHSW<br>FQTLSTQ\EPQCR\AARLVLKQ\QGVLAALR\PYLQKQPQPSA<br>EGKGLSPIEPSEELATLSEEEIAMA VTAWEKGLSLPPLRPQQ<br>NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADVFAVYS<br>RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEI CDKYHIIHA<br>DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD<br>TVEQLRCEHCARF\LA DRFVEGVCPFCGYEEARGDQCDKCGKLI<br>NAVELKKPQCKVCRSCPVSQSHFLDLPLKLEKRLLEWLGRTL<br>PGSDWTPNAQFITPFFGFREWPSPKPRWQ*TRDLK\WGNPGTP*E<br>GFEDK\VFYVWFATIGYLSITANYTDQWERWW\KNPEQVDLYQ<br>FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLYNEDG<br>K\FSKSRGVGVFRDM\AHDGTGIPDISRFYL\LYIRPEGK\DSA<br>FSWTDLLKNN\ELNLLGNFINRA\GMFVSKFFGG\YVPEMV<br>LTPDDQRLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH<br>GNQYI\QVNEPW\KRIKGEADRQAGTVTGLAVNIAALLSVML<br>QPYMPTVSATIQALQLPPFACSILLTNFLCTLPAGHQIGTVSP<br>LFQKLENDQIESLRQRFGGQAKTSPKPAVVETVTAKPQIQIA<br>LMDEVTKQGNIVRELKQKADKNEVAASVAKLLDLKQLAVAEG<br>KPPEAPKGGKKK |
| 5896       | 2967   | 86   | HPSSLGAIPFYPPSSPPPPPLYLFWNSHRKSRHFINQRGHGE<br>MRLFVSDGVPGCLFVLAAAGRARGRAEVLISTVGPEDCVVPFLT<br>RPKVPVLQDLSGNLYFSTSAICRYFF\LLSGWEQDDLNTQWLEW<br>EATELQPTLSAALYYL\VVQGGKG\EDVLGSRVRLTHIDHSL<br>RQ\NCPFLAGETESLADIVLWALYPLLQDPAYLPEELSALHSW<br>FQTLSTQ\EPQCR\AARLVLKQ\QGVLAALR\PYLQKQPQPSA<br>EGKGLSPIEPSEELATLSEEEIAMA VTAWEKGLSLPPLRPQQ<br>NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADVFAVYS<br>RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEI CDKYHIIHA<br>DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD<br>TVEQLRCEHCARF\LA DRFVEGVCPFCGYEEARGDQCDKCGKLI<br>NAVELKKPQCKVCRSCPVSQSHFLDLPLKLEKRLLEWLGRTL<br>PGSDWTPNAQFITPFFGFREWPSPKPRWQ*TRDLK\WGNPGTP*E<br>GFEDK\VFYVWFATIGYLSITANYTDQWERWW\KNPEQVDLYQ<br>FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLYNEDG<br>K\FSKSRGVGVFRDM\AHDGTGIPDISRFYL\LYIRPEGK\DSA<br>FSWTDLLKNN\ELNLLGNFINRA\GMFVSKFFGG\YVPEMV<br>LTPDDQRLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH<br>GNQYI\QVNEPW\KRIKGEADRQAGTVTGLAVNIAALLSVML<br>QPYMPTVSATIQALQLPPFACSILLTNFLCTLPAGHQIGTVSP<br>LFQKLENDQIESLRQRFGGQAKTSPKPAVVETVTAKPQIQIA<br>LMDEVTKQGNIVRELKQKADKNEVAASVAKLLDLKQLAVAEG<br>KPPEAPKGGKKK |

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|------------|--|--|---|
| 5897       | 2967   | 86   | <p>LMDEVTKQGNIVRELKAQKADKNEVAEVAKLDDLKQLAVAEG KPPEAPKGGKKK</p> <p>HPSLLGAIPFYPPSSPPWPPPLYLFWNSHRKSRHFINQRGTHGE<br/> NRLFVSDGVPGCLPVLAAGRARGRAEVLISVGPEDCVVPFLT<br/> RPKVPVLQLDSGNLYFSTSAICRYFF\LLSGWEQDDLNTQWLEW<br/> EATELQPTLSAALYYL\VVQGGK\EDVLGSRVRLTHIDHSLS<br/> RQ\NCPFLAGETESLADIVLWALYPLLQDPAYLPEELSALHSW<br/> FQTLSTQ\EPQCR\AARRLVLKQ\QGVLAALR\PYLQKQPQPSPA<br/> EGKGLSPIEPSEELATLSEEEIAMAVTAWEXGLESPLPLRPQQ<br/> NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVARYS<br/> RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA<br/> DIY\RWFNISFDIFGRITTPQQ\TKIT\QDIFQQLLKRGFVLQD<br/> TVEQLRCEHCARF\LA DRFVEGVCPFCGYEEARGDQCDKCGKLI<br/> NAVELKKPQCKVCRSCPVVQSSQHLFLDLPLKLEKRLBEWLGRTL<br/> PGSDWTPNAQFITPFFGFREWPSPKPRWQ*TRDLK\WGNPGTP*E<br/> GFEDK\VFYVWFDAITIGYLSITANYTDOWERWW\KNPEQVDLYQ<br/> FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLYNYEDG<br/> K\FKSRGVGVFRDM\AHDGTIPDISRFYL\LYIRPEGK\DSA<br/> FSWTDLLKNN\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV<br/> LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH<br/> GNQYI\QVNEPW\KRIKGEADRQAGTGTGLAVNIAALLSVML<br/> QPYMPTVSATIQALQLPPPACSI LLTNFLCTLPAGEQIGTVSP<br/> LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQIQIA<br/> LMDEVTKQGNIVRELKAQKADKNEVAEVAKILDLKQLAVAEG<br/> KPPEAPKGGKKK</p> |
| 5898       | 2967   | 86   | <p>HPSLLGAIPFYPPSSPPWPPPLYLFWNSHRKSRHFINQRGTHGE<br/> NRLFVSDGVPGCLPVLAAGRARGRAEVLISVGPEDCVVPFLT<br/> RPKVPVLQLDSGNLYFSTSAICRYFF\LLSGWEQDDLNTQWLEW<br/> EATELQPTLSAALYYL\VVQGGK\EDVLGSRVRLTHIDHSLS<br/> RQ\NCPFLAGETESLADIVLWALYPLLQDPAYLPEELSALHSW<br/> FQTLSTQ\EPQCR\AARRLVLKQ\QGVLAALR\PYLQKQPQPSPA<br/> EGKGLSPIEPSEELATLSEEEIAMAVTAWEXGLESPLPLRPQQ<br/> NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVARYS<br/> RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA<br/> DIY\RWFNISFDIFGRITTPQQ\TKIT\QDIFQQLLKRGFVLQD<br/> TVEQLRCEHCARF\LA DRFVEGVCPFCGYEEARGDQCDKCGKLI<br/> NAVELKKPQCKVCRSCPVVQSSQHLFLDLPLKLEKRLBEWLGRTL<br/> PGSDWTPNAQFITPFFGFREWPSPKPRWQ*TRDLK\WGNPGTP*E<br/> GFEDK\VFYVWFDAITIGYLSITANYTDOWERWW\KNPEQVDLYQ<br/> FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLYNYEDG<br/> K\FKSRGVGVFRDM\AHDGTIPDISRFYL\LYIRPEGK\DSA<br/> FSWTDLLKNN\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV<br/> LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH<br/> GNQYI\QVNEPW\KRIKGEADRQAGTGTGLAVNIAALLSVML<br/> QPYMPTVSATIQALQLPPPACSI LLTNFLCTLPAGEQIGTVSP<br/> LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQIQIA<br/> LMDEVTKQGNIVRELKAQKADKNEVAEVAKILDLKQLAVAEG<br/> KPPEAPKGGKKK</p>  |
| 5899       | 326  | 1078   | <p>NCPKSEFNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ<br/> EANEKAEIDAKAEENIEKGRVLVQTRLKIMEYIEKKEKQIE<br/> QQKILMSTMRNARLKVLRARNDLISDLSEAKLRLSRIVEDP<br/> EVYQGLLDKLVQLGLRLLEPVMIVRCRP\ODLLLVEAAVQKAI<br/> PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVS<br/> NLESRLDLSAQKMPFIRMALEFANTNRKFFI</p>   |
| 5900       | 64   | 1409   | <p>KASRDSPCLEFPCLCGVSSHDLQHRMWHRLSHLSRLQDLLK<br/> GGVIYPALPQPNFKSLPLAVHWHHTASKSLTCAWQOQEDHFEL<br/> KYANTVMRFDYVWLRDHCRSASCYNKTHQRSLODASVLDLCKP<br/> KTIRLDETTLFFTWPDGHVTKYDLNWLKNSYEGQKQKVIQPRI<br/> LWNAEYQQAQVPSVDCQSFLNETNEGLKKFLQNFLLYGI AFVEN<br/> VPPTQEHTEKLAERISLIRETIYGRMWFYTSDFS RGDATYTKLA<br/> LDRHTDTTYFQEPGCIQVFHCLKHEGTGGRITLLVDGFIYAAEQVL</p>   |

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|------------|--|--|---|
|            |  |  | OKAPEEFELLKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE NEFWVKLPGRVLFIDNWRVLHGREGCTGYRQLCGCYLTRDDVL NTARLLGLQA  |
| 5901       | 1  | 2121   | VAIEQTSLKMMQAVGGAPARPTGEYICNQCQAKYTSLDSFQTHL KTHLDTVLPLKLTCPQCCKEFPNQESLLKHVTIHFMITSTYYICE SCDKQFTSVDDLQKHLDMHTFVFFRCTLCQEVFDSKVSIOQLHL \AVKHSNEKKVYRCTSCNWDNRNETDLQHVKNHLENQKGVHK CIPCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL REKHCVFETKTPNCGTNGASEQVQKEBELQTLTNSQESHNSH DGSEEDVDTSEPMYGCDCGAAAYTMETLLQN:IQLRDHNIIRPGES AIVKKKAELIKGNYKCNVCRTFFSENGLRHEMQTHLGPVK:YM CPIICGERFPSLLTLTEHKVTHSKSLDTGNCIRCKMPLQSEEEFL EHCQMHFDLRNSLTGFCVVCMTVTSTLELKHGTFFHMQKTGN GSAVQTTGRGQHVQKLYKCASCLEFRSKQDLVKLDINGLPYGL CAGCVNLSKSASPGINVPPTNRPGLQGNENLSAIEGKGKVGGL KTRCS*LATFKF*VLKVELPEHPKPFHRGVSRRPDSNSTQLKTP QVSPMPRISPSQSEKKTQYQCIKQCMVFYNEDIQVHVANHMD EGLNHECKLCSQTFDSPAQLQCHLIEHSFEGMGGTFFKCPVCFTV FVOANKLQQHIFSAHQEDKIYDCTQCPQKFFQTELOHNTMTQ HSS |
| 5902       | 712  | 209  | LKNRRRSRPSIROSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF IPLXPRQ*ED*MFQSWLHAWGDTLEEAPEQCAMAMFGYMTDTGT VEPLQTQVTVETQGDQLSLFLHFLDENLYKFSADFFIP\GWGE EFSLSKHPOGTEVKAITYSAMQVYNEENPEVFIIDI  |
| 5903       | 2106   | 735  | DTFGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQLQGRGLEPT PALFALSAPVPGGAASPMPPSGLRLLPLLLPLLWLVLTGPRPAA GLSTCKTIDMELVKKRIEAIHQILSKRLASPPSQGEVPPGP LPEAVLALYNSTRDRVAGESAEPEPEADYAKEVTRVLMVET HNEIYDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLRL KLKVEQHVELYQKYSNNSWRYLSNRLAPSDSPEWLSFDVTGVV RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL ATIHGMNRPFLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSP HGGNCLRC/VHC*HLIFRKDL\GW\KWI\HE\PKGYHANFC\L GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGRKPKVEQLSNMIVRSCKCS  |
| 5904       | 3  | 1126   | MMEIENAINTFKEQRLLYEELIKEEKTNNELSAISRKIDTW ALGNSETKAFRAISSKVPVDKVTPTSLPBEVLDFEKLQQTGG RQGAWDYDQHFQVKNRKHGKPTFMEEVLEHLPGKTQDEVOQ HEKWKQFLALEERKKESIQIWKTKKQKREEIFKLKEADNTP VLFHNKQEDNQKKEBQRKKQKLAVEAWKKQKSIEMSMKASQL KEEEEEKHKHQRQRQFKLLLESYTOQKKEQEEFLRLEKEI REKAKEAEKRKNAADEISRQERDLHKLKILDRQAKEDKESQ KORRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQDRTNRLW ATSTYPT*GYSNLETRNTEKSMR  |
| 5905       | 287  | 2912   | MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPSWQCLQNFLHGTKNVTNSSSLRLPR QNSDGGQKNPREHIIDCGDIVWSLAFGSSVPEKQSRVCNIEWH RFRFGQDQLLATGLNSGRIKIWDVYTGLLLNLVDHTGVVRDL TEAPDGLSILVSASRDRTLRVWDLRDDGN\MMKVLRGHQNVVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SPFLFFFPKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIVSQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMKVF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFLAVNILFACSICFSS*A QVGDPSSL*TSYDLKGRQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTFLISVYFS*LVFGINGFYQSVVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLMTLSIFFKLLIYNA* YNLN*I*QF*YKMHFVLCMSE*SYNICLFIAGF\LWNMDKYTM        |

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|------------|--|--|---|
|            |  |  | IRKLEGGHHHDVVACDFSPDGLLATASYDTRVYIWDPHNGDILM<br>EFGHLFPPTPIFAGGANDRWVRSVSFSDGLHVASLADDKMVR<br>FWRIDEDYPVQVAPLSNGLCCAFSTUGSVLAAGTHDGSVYFWAT<br>PRQVPSLQHLCRMSIRRVMPQTQEQVQLPSPKLEFLSYRI  |
| 5906       | 146  | 2038   | REGAGSGRMASGA\NYPYIEIEQPRQRGMFRYKCEGRSAGSI<br>PGEHSTDNRTYPSIQIMNYGKGV\RITLVTK\NDPYKPHPH<br>DLVGKDCRD\GYEAEFGQE\RRP\LFPQN\LGIRCVKKKEVKE<br>A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVRLWFRVFLPDG<br>HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCVRVKNKCGSVRG<br>DEIFLLCDKVQKDDIEVRVFLNDWEAKGIFSQADVHRQVAIVPK<br>TPPYCKAITEPVTVMQLRRPSDQEVSESMDFRYLPDEKDTYGN<br>KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLLELLTSGDPPTLAS<br>QSAGITVNFPERPRPGLLSIGEGRYFKKEPNLFSHDVAVREMP<br>TGVSSQAESYYPSDGPISGLSHASMAPLSSSSWSSVAHPTPR<br>SGNTNPLSSFSTRTLPSNSQGI PPFLRIPVGNDLNASNACIYNN<br>ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET<br>DNPRLLSMNLENPSCNSVLDPDRDLRLHQMSSSSMSAGANSNTT<br>VFVSQSDAFEGSDFSACADNSMINESGSPNSNTNPNSHVVFQUSQY<br>SGIGSMQNEQLSDSFYEFFQV  |
| 5907       | 99   | 1873   | TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK<br>KATSKVPSAPHFVHPNDHANREAELEKKKWEEMREKQQAAREQE<br>RQKRRTIESYCQDVLRRQEEFEHKEEVLQELNMFQQLDDEATR<br>AYYKEFRKVVEYSVDVILEVLDAEDPLGCRFCQMEAVLRAQGNK<br>KLVVLNKKIDLVPEVVEKWLVDYLRNELPTVAFKASTQHVKNL<br>NRCSVPVDQASESLLSKACFGAENLMRVLGNVCRLGEVTRTHIR<br>VGVVGLPNVKGSSLSLNLKRSRACSVGAVPGITKFMQEVYLDKF<br>IRLLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPTVETILQRC<br>NLEEISNYGVSGFQTEHFLTAVAHRLGKKKGLYSQEQAAK<br>AVLADWVSGKISFYIPPPATHTLPTLSAEIVKEMTEVFDIEDT<br>EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI<br>ENKTTVYKIGDLTGCTNPNRHQMGWAKRNVDRPKSNSMVDVC<br>SDRRSVLQRI METDPLQQQALASALKNKKKMQKRAKIASKL<br>SDSMNSALDLSGNADGVDG   |
| 5908       | 247  | 975  | HCGIKKRGEKSGSPSPASGGFQLGCIPEPSLPSEETHPHTRA<br>HTRTLRATLRRPPKSHSTRLRFPMLDGDGGLASWK/PMRER*<br>GWRPAPAKAAGASLGAATGKRCRMSKRYLQKATKGKLLIIIFI<br>VTLWGVVSSANHHKAHVKTGTCEVVALHRCCKNKNKIEERSQT<br>VKCSFPFGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGECK<br>VLPDRKGWSSCSGNKVKTRVTH   |
| 5909       | 1  | 5002   | PAIPGSTIIWAPGSHSAARADGRHGSLSQSQAPGALCGARAPP<br>SSNLRADRSIMCAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR<br>CKEPIRYSYNPDQFHNMDLRGGPHDGVITIPRSTSDTLVTSDSR<br>STLMGRSSYYISIGSQDLVIHNDIKEEVDAGDWIGMYLIDEVLS<br>ENFLDYKNRGVNGSHRQI IWKIDASSYFVEPETKICFKYYHGV<br>SGALRATTPSVTVKNSAAPIFKSIGADEVQGGSSRLISFSL<br>DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHQERRSK<br>IIGNTVNPIWQAEQFSVSLPTDVLEIEVKDKFAKSRPIIKRFL<br>GKLSMPVQRLLEHHAIGDRVSYTLGRRLPTDHSVGGQLQFRFEI<br>TSSIHDPDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE<br>SSESWKPEQLGEGSVDPDRPGNQSIELSRPAEEAAVITEAGDOGM<br>VSVGPEGAGELLAQVQKDIQAPASAEELAEQLDLGEEASALLLE<br>DGEAPASTKEEPLLEEATTSRAGREEBEKEEEDGVSTLEQG<br>EGRQLRLASVKKRSRPSLPSLELTVIASACDGPETPRTHYIR<br>IHTLLHSMPSAQGGSAAEEDGAEESTLKDSSEKDGLESDVT<br>AADPSALEEDREEPEGATPGTAHPHSGGHFPLANGAAQDQDT<br>HPSTGESDSSPRQGGDHSCGCDASCCSPSCYSSSCYSTSCYS<br>SSCYASACYSPPSCYNGNRFASTRFSSVDSAKISESTVFSSQDD<br>EEEENSASFESVPDSMQSPELDPESTNGAGPWQDELAAPSCHVER<br>SPEGLESPVAGPSNRRREGCEPILHNSQPVSQLPSLRPEHHHYPT<br>IDEPLPPNWEARIDSHGRVYVVDHVNRTTWRPTAAATPDGMR<br>RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCQAPAGG |

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|------------|--|--|---|
|            |  |  | GGGGSDSEAESSQSSLDLRREGSLSPVNSQKITLLQSPAVKFI<br>TNPEFTVLHANYSAIRVFTSSTCLKHMILKVRDARNFERYQH<br>NRDLVNFIMFADTRLELPRGWEIKTDQOGKSFVDHNSRATTF<br>IDPRIPLQNGRLPNHLTHROHLQRLRSYAGEASEVSRNRGASL<br>LARPGHSLVAAIRSQHGHESLPLAYNDKIVAFRLQPNIFEMLQE<br>RQPSLARNHTLREKIHVIRTEGNHGLEKLSCDADLVILLSLFEE<br>EIMSYVPLQAAPHGYSFSPRCSPPSSPQNSPGLQASARAPSP<br>YRRDFEAKLRNFYRKLEAKGFGQPGKIKLIIRRDHLEGTNPQ<br>VMAYSRKELQRNKLYVTFVGEGLDYSGPSRBEFFLLSQELFNP<br>YYGLFEYSANDTYTVQISPMASAFVENHLEWFRFSGRILG\LALI<br>HQYLLDAFFT\RPFYKALL\RLPC\D\LSDEYLDDEEFHQSLOW<br>MKDNNITDILDLTFTVNEZVFGQVTERELKSGGANTQVTEKNKK<br>EYIERMVKWRVERGVVQTEALVRGFYEVVDSRLVSVDARELE<br>LVIAGTAEIDLNDWRNNTYRGYHDCGLVIRFWAAVERFNNE<br>QRLRLQFVTGTSSVPYEGFAAPPWEPMLGRPLP*KKWGKITS<br>LPPRG\HTCLQPDWDLPTVSPRTPMLEYK\LLTA\VEETSTFGT |
| 5910       | 1526   | 446  | VAEFAAMEFGRTQIKLDPRTADLLEVLKNTYGPSACFSQPF<br>AAQLLRALGPVELALTSILTLLALGSAIFLEDAVLYKNTLCP<br>IKRRTLLWKSSAPTIVSVLCCFGLWIPRSLVLVEMTITSFYAVC<br>FYLLMLVMVEGFGGKEAVLRLTDRTPMMVHTGPCCCPCCPRL<br>LLTRKKLQ\R*CWALSNTPS*R*R*PWWACFSSPTASMTQQTFL<br>RGAQLVSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKE<br>ALFQVLLILTALQPSIFSVLANGGQIACSPYSSKTRSQVMNCH<br>LLILETFIMTVLTRYRRKDIHKVGYETFSPPDLNLKALRWM<br>AWTMKGCCTH  |
| 5911       | 109  | 595  | QSLAPCIQKGLEMRSPKQSFIIRSSHSGAGLLVKNPSTVPF<br>CGHRRGGAAPKYKPTPVVGPEQRPTGQKHMRRGVSLSPRLECS<br>GTISAHCNLRPLSSNSPAPAS*LAGITGVCHHAQLIFVFLVET<br>GPHVVGAGLELL/NVVIHLPRPPKVLGLQA   |
| 5912       | 924  | 277  | MILNKALMLGALALTVMSPCGGEDIADHVASGVNLYQSYGP<br>SCQYSHFEDGDEEFPYVDLERKETVWQLPLFRFRFDPQFALTN<br>IAVLKHNINIVIKRSNSTAATNEVEPTVFSKSPVTLGQPNLTI<br>CLVDNIFPPVNVITWLSNGHSVTEGVSETRPSSPKSDHFI.LQDQ<br>VTSPPSFPFE*DL*TAKVEQLGAWFEPLLKHGAEIPTTL   |
| 5913       | 46   | 1198   | QLRMAGAEGAAGRQSELEPVVSLVDVLEDELENEACAVLGG<br>DSEKCSYSQGSVKRQALYACSTCTPEGEPAICLACSYECHOS<br>HKLFEYLYTKRFRCDGNSKFKNLECKLLPDKAKVNSGNKYNDN<br>PFGLYCICKRPYPDPDEIPDEMIQCVVCEWDFHGRHLGAIPPE<br>SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM<br>E*/DDQEVIKPENGBHQDSTLKEDVPEQKDDVREVKEQNSP<br>CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT<br>YVPLNWRSKLCTCQDCMKMYGDLVDLFLTDEYDTVLAYENKGI<br>AQATDRSDPLMDTLSSMNRVQVELIC/GIQ*FED   |
| 5914       | 960  | 124  | NLGGSELPPHEALFIQVASMNRQRRVDFYLASIEDMLVAI/GGRN<br>ENGALSSVETYSPTKDSWSYVAGLPRFTYGHAGTIYKDFVYISG<br>GHDYQIGPYRKNLLCYDHRTDVWEERRPMTARGWHSNCS\GDS<br>IYSIGGSDDNIESMERFDVLGVEAYSPPCQNWTRVAPLLHANSE<br>SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP<br>KAIAGGSACFIAP*SLGQRTKRKAKARGTRTGASDPSCASWDH<br>PHRHLPLGCRPAATS  |
| 5915       | 1604   | 703  | FPGRPTRPLKLGRRRKRARI IQAPHCHSPRPRCPPGALQAPEA<br>PASRAEGPVAVVNGHTEGPAPARSAPKEPPGLPRPLGSPFCPT<br>PQEDFPALGGPCPPMPSPGFSVAVLLKGTPPPPPPGLVPPIS<br>KPPPGFSGLLPSHP\PVSPAPPPPPQK/RPRLLPAP/PGLPS<br>PRELPGREPSAHPVHQGLPAERRRGLQVQEPRLRGVQTGPDLS<br>PVLQELPGPAGGEFPEGL**AAGPAAH   |
| 5916       | 256  | 633  | SPRMWEIWPWHRNESFSEGEWPSRIPEPSPDSTKGTSGKGR<br>TVTGAVRHLNHHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH<br>PTRLIQ*NQATADKN*TTALLQPHQRL\VSPRMAEA   |
| 5917       | 1343   | 827  | AHQILTYLEP/ICLVVYNKILTVELTKSVLEI*KPIHTPQTYR   |



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|------------|--|--|--|
|            |  |  | *NDFFGIKVYVSRRLRKTSE/RLAVTFLEQAVVSKECVPDQ<br>FMEHLLPSLLSLASDPVPVNVRLAKALRQMLLBKAYFRNAGNP<br>HLEVIETILALQSDRDQDVSPFAALEPKRRNIIDTAVLEKON   |
| 5918       | 13   | 1247   | EGAQVARRRRRRQRWAGRCGRGRGRRAERTGGRRPGRPRPLP<br>PGPARRRRRRMETPFYGDALSGLCGASGGTFASPGRLFP<br>APPTAAAGSMKKDALTLSEVAAALKPAPAPASYPPA\ADG<br>A7SAAPPDGLLASPDGLLKLASPELERLI IQSNGLVTTPTSS<br>QFLYPKVAASEEQFAEGFVKALEDLHKQNLGAGRAAAAAA<br>AGGPGSGTATGAPPGELAPAAAAPEAPVYA\NLSSY\AGGCRGL<br>RGAAT\VAFAAEPVPPPPPPPGALGPRRP/RLAQGRRPQTV<br>PDVP\SGGES\PLSPIET\DTPRRI\KAKRKRL\RNQIRAPK<br>PASRKLGAQSRALERESDEPS*SPEHGSLASTASLLREQVAQLK<br>QKVLSHVNSGCQLLPQHQPAPAY   |
| 5919       | 1  | 4254   | TSVQGDSSQGTPTSSQGSINMEHWISQAIHGSTTTSTSSSTQSG<br>GSGAAHRLADVMAQTHIENHSAPPDVTYTTSEHSIQVERPQGST<br>GSRTAPKYGNABLMETGDGVPVSSRSVAKIQQLVNTLKRPKRP<br>LREFFVDDFEELLEVOQPDNPQPKPEGAQMLMRGEQLGVVNTW<br>PPSLEAALQRWGTISPAPCLTTMDTNGKPLYILTYGKLWTRSM<br>KVAYSILHLKGTQKQPMVRPGDRVALVFPNNDPAAAFMAAFYGC<br>LAEVVPVPIEVPLTRKDAGSQQIGFLIGSCGVTVALTSDACHKG<br>LPKSPTEGIPQFKGWPKLLWFVTESKHLSKPPRDWF\PHIKDAN<br>NDTAYIEYKTC\DGSVLGVTVTRTALLTHCQALTOACGYTEAE<br>TIVNVLDFFKDVGLWHGILTSVMNMHVISIPYSLMKVNPISWI<br>QKVCQYKAKVACVKSMDHVALVAHRDQDINLSSLRMLIIVD<br>ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRP<br>DDSNQPPGRGVLSMHGLTYGVIRVDSEKLSVLTQDVGVLMPG<br>AIMCSVKPDGVPQLCRTDEIGELCVAVATGTSYYGLSGMTKNT<br>PEVFAMTSSGAPISEYPPFIRTGLLGFVGPGLVVFVVGKMDGLMV<br>VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIVI<br>VAEQRPDSTEEDSFQWMSRVLQADSIHQVGVYCLALVPANTLP<br>KTPLGGIHLSETKQLEGLSLHPCNVLMCPHTCVTNLPKPRQKQ<br>PEIGPASVMVGNLVSGKRIAQASGRDLQIEDNDQARKFLFLSE<br>VLQWRAQTTPDHILYTLNCRGAIANSLTCVQLHKRAEKIAYML<br>MERGHLQDGDHVALYPPGIDLIAAFYGCYAGCVPIITVRPPH<br>QNIATTLPTVKMIVEVSRSACLMTTQICKLLRSREAAAADVDR<br>TWPLILDIDD*PKKRPACICKPCNPDTLAYLDFSVSTTGMLAGV<br>KMSHAATSAPCRSILKQCELYPSREVAICLDPYCGLGFVLWCLC<br>SVYSGHQSILIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL<br>CTKGLGSQTESLKARGLDLSRVRTCVVVAERPRIALTQSFSKL<br>FKDLGLHPRAVSTSFQCRVNLAIQLQGTSGDPPTTVYVDMRALR<br>HDRVRLVERGSPHSLPLMESGKILPGVRIIANPETKGLGDSH<br>LGEIIVHSAHNASGYFTIYGDESQSDHFNLSRSLFGDTQTIWAR<br>TGYLGLFRLRTELTDANGERHDALYVVGALDEAMELRGMRYHPID<br>IETSVIRAHKSVTECAVFTWNLVLLVVVVELDQSEQALDLVPLV<br>TNVVLEEHYLVGVVVVDIGVIPINSRGEKQRMHLRDGFLADQ<br>LDPIYVAYNM |
| 5920       | 1381   | 1499   | QLGAVAHAGVSRIPP*LFPPPLHPTFLSLWCLHHKLP/HPPGASM<br>VRPPVVRPPPAHISSVRQASTQVPRTVPHTORVANIGTQTTPG<br>SGVGCCTPGRPLLPCCKSSAAHSTYRVQEPVHIPGQEPPLTASM<br>LAAAPLHEOKQMIGERLYPLIHDVHTQLAGKITGMLEIDNSEL<br>LLMLESPESLHAKIDEAVAVLQAHAQAMEQPKAYMH  |
| 5921       | 727  | 157  | VCPGTGGE*GLWGQLGLPKETPLKPMDAFTGSGLKRKFDVVDV<br>GSSVNSDDEISSSDSADSCSLNPPTTASFTPTSLKRQKQLR<br>RKNVRFQDVTVYYPARRQGFSTSVPSQGGSSLGMAQRHNSVRSY<br>LCEFAQEVEVNHREILREHLKEELHAKMKLTKNGTVESVEAD<br>GLTLDVSDDEDIDVENVEVDYFFLOPLTKRRRALLRASGVHR<br>IDAEKQELRAIRLSREECGDCRLYCDPEACACSQAGIKCQVD<br>RMSFPCGCSRDCGNMAGRIEFNPIRVTRTHYLHTIMKLELESKR<br>Q\GAQQPQ\*GALPDCQLQPDRTGL*DPWSIGSKLSFTGKG<br>AAATHLIIILRVENRGAEGRRK  |
| 5922       | 2475   | 495  | SYSNWGLFPSVFIQVPRSRRTGNLKPFIIFYSYE\CMETLKG\T   |

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|------------|--|--|--|
|            |  |  | CLYNATQYKVCSPNDRPDACYNPSEPAATTVFEIRTGILLGDT SKIIRTEEKEIPKQITLRFDAACAINSKKLEIGCGSLN*ERS* RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNSVYLQKGEAN PSKAAGHCNPLELIIITNPLDPHWKGERVTLGINRTGLKQPQVVI LKGEVHKCSPKPVFQTFYEELNLPAPPELLKTKNLFQQAENV IFLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIIPI*KAE ASNF*VLKTSIIROYCIAREGKDFIIPVGKPNICIGQLYNSTTK TIT*DLNHTKPNPFSKFSKLKTA*AAHESH*DWTPVSGLY*IC RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGFSVYASR EKKGIVIGNWKDNEWPRERIIQYGPATWAQDGSWGYR/TP/VY MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIVQNRLAL DYLLVAEGGVCRKFNLNCCQLINDQGVVKNIVRDMTKLAHVP IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL PLLQMIKIGIVATLVHQKTSAHVNYMNHYSISQRDSKSEDESE NSH    |
| 5923       | 137  | 638  | OLCGRRGQRFRITSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL QQENRELWISLEEHQDALELIMSKYRKQMLQMLVAKKAVDAEPV LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDQFCIKIEKLA QLELENKELRELLSISSESLOARKENSMDTASQAIAK   |
| 5924       | 274  | 2146   | EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLNSLTPTTSVRRM PLITTVTLKMMVARHMKLLCSKAPSTQLQOKIFLHSCQMGIIHQ SVCCKLKPNTSHIISILMGQPMALVQLETAPLTIIOKQFQTD HMKFWKNLPLHSHHLTPSVPTVPIPKTGSPEIKLKITKTIONG RELFESSLCGDLNFWQASE\Q*NQSIERSRKEKRKSNKH:DSR SEERKSHKIPKLEPEQNRPNRVDTVSEKPREEPVLKEGSPSS ANTI FCSNNGSVHW\FKFQVGDVWVKVGTYPWPCMVSSDPQL EVHTKINTRGAREYHVQFSSNQPERAWVHEKRVREYKGHKQYEE LLAEATKQASNHSEKQKIRKPRPQREARQWDIGIAHAELKMT REERIEQYTFIYIDKQPEEALSQAKKSVAKTEVKKTRRPRSVL NTQPEQTNAGEVASSLSSTEIRHRSQRRHTSAEEEEPPPVKIAW KTAARKSLPASITMHKGSLLDQKCNMSPVVKIEQVFALQNTG DGKFIDQFVYSTKGIGNKTEISVRGQDRLIISTPNQRNEKPTQS VSSPEATSGTSGSVEKKQRRSIRTRSESEKSTEVVPKKKIKKE QVGFLHVES |
| 5925       | 216  | 1911   | MHTAESREATGLSPQAAQEKDGIIVKVEEEDHMMWGDSTL QDTPPPDPPEIFRQFRFRFCYQNTFGPREALSRLKELCHOWLRPE INTKEQILELLVLRLQFLSILPKELQVWLQEQYRPSGEEAVTLE DLELDLSGQVPGQVHGPEMLARGMVPLDPVQESSFSDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALT ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAP PQGGENRNENEESTSKAETSSEDASRGETTGRSQKEFGKRDQE CKTGERQQKNPEEKTRKEKRDSPGPAIGDKKKTITGERGPREGK GLGRSFSLSNFTTPEEVPTGTGSHRDECCKCFTRSSSLIRHK IHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHCECNE CGKAFSHSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSLTLLHHRHARERASEYSPASLDAGFAFLKSCV   |
| 5926       | 2  | 233  | DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAIEP SDSPHHTPVHPPPEHSAACPAPATCCPPRSSMS   |
| 5927       | 4146   | 1248   | KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAKYGIPLA YKKGDKKLHEKKPLQKHQAHTPEKRVNTGEERRKISEBAAR KRRLEFIEKEKKQKDQIIISLMKAEQMKRQSKERLERINRAREQG WRNVLSAGSGSEVKAPFLGSGGTIAPSSFSRRGQYEHYHAFDO MQQRAEDNEAKWKREIYGRGLPERQKQGLAVERAKQVEEFLQR KREAMQNKARABGHMGILONLAAMYGGRPPSSRGKPRNKEEV YLARLRQIRLQNFNERQIKAKLRGEKKKEANHSEGGQGSSEADM RRRK\IESLKAHANARAVALKEQLERKRKEAYEREKKVWEHLV AKGVKSSDVSPPLGQHETGGSPSKQMRSVISVTSALKEVGVD SLDTDRETSEEMQKTNNAISSKREILRLNENLKAQBUKQKQNS LSDTFEINVHEDAKEHEKSVSSDRKKWEAGQLVPLDELTL DTSFSTTERHTVGEVILKGPNGSPRRAWGKSPTDSVLKILGEAE   |

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|------------|--|--|---|
|            |  |  | LQLQTELENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS<br>AIVDSPVETKSPFSEASPMQSLKLEGNLEEDDLETEILQEPS<br>GTNKDE\SLPCTITDVWISSEKETKETQSADRITIQENEVSE<br>VSSTVDQLSDIHIEPGTNDQSQSKCDVDSVQPEPFHKVHSE<br>HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG<br>LFDANNPKMLRRTCSLPDLSKLFRTLMVPTVGDVRQDNLEIDEI<br>EDENIKEGPSDESIVFEETDTDLQELQASMEQLLREQPGEYS<br>EEESVVKNSDVEPTANGTDVAEDDNPSSSALNEEWHSDNSD<br>GEIASECECDVSFNHLEELRLHLEQEMGFEEKFVYVYKIKAIHE<br>DSDENIEICISKIVCNILGNEHQHLYAKILHLVMDAGAYQEDNDE  |
| 5928       | 4146   | 1248   | KHFSKFGSQALYQLKRPASQNSISVMPAQKITKPAKYGIPLA<br>YKYGDKKLHEKKPLQKHQAHTPEKRVNTGEERRKISEEAAAR<br>KRRLEFIEKKKQKQDIISLMKAQMKRQEKERLERINRAREQG<br>WRNVLSAGSGSEVKAFLGSGGTIAPSSFSRGGQYEHYHAFDQ<br>MQOQRAEDNEAKNKREIYGRGLPERQKGLAVERAKQVEEFLQR<br>KREAMQNKARAEGHMGILQNLAAHYGGPSSRGGKPRNKEEBV<br>YLARLRQIRLQNFNERQKIKALRGEKKEANHSEGGQESSEADM<br>RRKK\IESLKAHANARAALKEQLERKRKAYEREKKVWEEHLV<br>AKGVKSSDVSPPLGQHETGGSPSKQMRSVISVTSALKBVGVDS<br>SLDTRTSEEMQKTNNAISSKREILRLNENLKAQEDKKGON<br>LSDTFEINVHEDAKEHEKESVSSDRKKWEAGQLVPLDELTL<br>DTSFSTTERHTVGEVIKLGPNGSPRAWGKSPTDSVLKILGEAE<br>LQLQTELENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS<br>AIVDSPVETKSPFSEASPMQSLKLEGNLEEDDLETEILQEPS<br>GTNKDE\SLPCTITDVWISSEKETKETQSADRITIQENEVSE<br>VSSTVDQLSDIHIEPGTNDQSQSKCDVDSVQPEPFHKVHSE<br>HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG<br>LFDANNPKMLRRTCSLPDLSKLFRTLMVPTVGDVRQDNLEIDEI<br>EDENIKEGPSDESIVFEETDTDLQELQASMEQLLREQPGEYS<br>EEESVVKNSDVEPTANGTDVAEDDNPSSSALNEEWHSDNSD<br>GEIASECECDVSFNHLEELRLHLEQEMGFEEKFVYVYKIKAIHE<br>DSDENIEICISKIVCNILGNEHQHLYAKILHLVMDAGAYQEDNDE |
| 5929       | 3  | 1558   | LDFSMTQLPAYVAILLFYVSRASCQDTFTAAYVEHAAILPNAT<br>LTPVSRREALALMNRNLDILEGAITSADQGAHIIVTPEDAIYG<br>WNFNRLSLYPYLEDIPDEPNWIPCNRRNRFQTPVQERLSC\A<br>AKNNSIYVAVANIGDKKPCDTSPPQCPDGRYQYNTDVV\DSQ<br>KLVARVHKQNLFMGENQFNVKPEIIVTNTTFFGSFGIFTCDI<br>LFHDPAVTLVKDFHVDITVFPTAMNVLPHLSAVEFHSAWAMGM<br>RVNFLASNIHYPSSKMTGSGIYAPNSSRAHYDMKTEEGKLLS<br>QLDSHPHSAVNVNTSYASSIEALSSGNKEFKGTVFDEFTFVK<br>LTGVAGNYTVCCQKDLCHLSYKMSNIPIVEYALGAFDGLHTE<br>GRYYLQICTLLKCKTNTNLTCGDSASTASTREMFSLSGTFTGTQ<br>YVFEVLLSENQLAPGEFQVSTDGRFLSLKPTSGPVLTVTLFGR<br>LYEKDWNASSGLTAQARIIMLIVIAPIVCSLSW   |
| 5930       | 113  | 6082   | RGNCFWIVPFTMAORTGLEDFERYLFVDRAVIYNPATQADWTAK<br>KLWVWIPSERHGFEEAASIKEERGDEVMVELAENGKAMVNKDDIQ<br>KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYYSGLF<br>CVVINPYKNLPIYSENIEMYRGKKRHEMPPHIYAISESAYRCM<br>LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHRGRKDH<br>IPGE\LERQLLANPILESFGNARTVQNDNSSRFGKFIIRINFDV<br>TGYIVGANIETYLLEKSAVRQAKDERTFHFYQLLSG\AGEHL<br>KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG<br>FSHEEILSMLKVSSVLQFGNISFKKERNTDQASMPENTVAQKL<br>CHLLGMNVMEFTRAILTPRIKVGDRYVQKAQTKEQADFAVEALA<br>KATYERLFRWLVRINKALDRTRKQASFIGILDIAFGFIEFELN<br>SFEQLCINYTNEKLQQLFNHTMFIQEYEQREGIEWNFIDFGL<br>DLQPCIDLIERPANPPGVALLDEECWFPKATDKTFVEKLVQEQ<br>GSHSKFKQPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND<br>NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT<br>KKGMFRTVGQLYKESLTKMATLRNTNPNFVRCIIPNHEKRAKT<br>LDPHLVLDQLRCNGVLEGIRICRQGFPPNRFVQEFQRQRYEILTP   |

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|------------|--|--|--|
|            |  |  | <p>NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH<br/> LEERDLKITDIIIFQAVCRGYLARKAFKKQQQLSALKVLQR<br/> NCAAYLKLRLHWQWRVFTKVKPLLQVTRQEEELQAKDEELLKVK<br/> BKQTKVEGELEEMERKHQQLLEEKNILAEQLQAE TELFAEAEEM<br/> RARLAACKQELEEILHDLESRVBEEERNOILONEKKKMQAHIQ<br/> DLEEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF<br/> IKEKKLMEDRIAECSSQLAE EEEKAKNLAKIRNKQEVMSDLEE<br/> RLKKEEKTRQLEKAKRKL DGETTDLQDQIAELQAIQIDELKLQ<br/> AKKEEELQGALARGDDETLHKNNALKVVRQLQAIQAE LQEDFES<br/> EKASRNKAEKQKRDLS EEELEALKTELEDTLDTTAAQQLRTKRE<br/> QEVAE LKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR<br/> FKANLEKNKQGLETDNKLACEVKVLQVKAES EHKRKLDAQV<br/> QELHAKVSEGDRRLRVELAEKASKLQNELDNVSTLLEEAEKKGK<br/> FAKDAASLESQLDQTELLQEEETRQKLNLSRIQLEEEKNSLQ<br/> EQEEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA<br/> KKLLKDAEALSQRLEEKALAYDKLEXTKNRLQQLDLDLTVDDL<br/> HQKQVANSLEKKQ\KKFDQLLAEKSI SARYAERDRAEAEARE<br/> KETKALSARALEEALAEKEEFERQNKQLRADMEDLMSSKDDVG<br/> KNVHELEKSKRALEQQV\ EEMRTQLEEELEDELOATEDAKLRLEV<br/> NMQAMKAQFERDLQTRDEQNEEKKRLLI KQVREAELEDERKO<br/> RALAVASKKKMEIDLKDLAEQIEAANKARDEVI KQLRKLAQAMK<br/> DYQRELEEARASRDEIFAQSKSEKKLSLEAEILQLEBELASS<br/> ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE<br/> ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR<br/> QQLERQNKELKAKLQLEGA VKSKFKATISALEAKIGQLEEQLE<br/> QEAKEAAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA<br/> NARMKQLKRQLEEEAEATRANASRRKLQRELDDEANEGLSR<br/> EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK<br/> TSDVNETQPPQSE</p>   |
| 5931       | 113  | 6082   | <p>RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK<br/> KLWVWIPSERHGFEEASIKEERGDEVVELAENGKKAMVNKDDIQ<br/> KMNPPKFSKVDEMAELTCLNEASVLEHLKDRYYSGLIYVTSGLF<br/> CVVINPYKNLPYSENIIEMRYRKKRHEMPPHIYAISESAYRCM<br/> LQREDQSILCTGESGAGKTENTKKVIQYLAHVASSHGRKDH<br/> IPGE\LERQLLOANPILESFGNARTVQNDSSRFKGFIRINFV<br/> TGYIVGANIETYLEK9RAVRQAQDERTFHFYQLLSG\AGEHL<br/> KSDLLLEGFNRYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHMG<br/> FSHEELSLMLKVSSVLQFGNISFKKERNTDQASMPENTVAQKL<br/> CHLLGMNVMEFTRAILTPRIKVGDRDYVQKAQTEQADFAVEALA<br/> KATYERLFRWLVRINKALDRTKRQASFIGILDIA GFEIFELN<br/> SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL<br/> DLQPCIDLIERPANPPGVALLDEECWFPKATDKTFVEKLVQEQ<br/> GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND<br/> NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT<br/> KKGMFRTVGQLYKESLTKMATLRNTNPNFVRCIIPNHEKRAGK<br/> LDPHLVLDQLRCNGVLEGIRICRQGFPPNRIVFQEFQRQYIEILTP<br/> NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH<br/> LEERDLKITDIIIFQAVCRGYLARKAFKKQQQLSALKVLQR<br/> NCAAYLKLRLHWQWRVFTKVKPLLQVTRQEEELQAKDEELLKVK<br/> EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAE TELFAEAEEM<br/> RARLAACKQELEEILHDLESRVBEEERNOILONEKKKMQAHIQ<br/> DLEEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF<br/> IKEKKLMEDRIAECSSQLAE EEEKAKNLAKIRNKQEVMSDLEE<br/> RLKKEEKTRQLEKAKRKL DGETTDLQDQIAELQAIQIDELKLQ<br/> AKKEEELQGALARGDDETLHKNNALKVVRQLQAIQAE LQEDFES<br/> EKASRNKAEKQKRDLS EEELEALKTELEDTLDTTAAQQLRTKRE<br/> QEVAE LKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR<br/> FKANLEKNKQGLETDNKLACEVKVLQVKAES EHKRKLDAQV<br/> QELHAKVSEGDRRLRVELAEKASKLQNELDNVSTLLEEAEKKGK<br/> FAKDAASLESQLDQTELLQEEETRQKLNLSRIQLEEEKNSLQ<br/> EQEEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA</p> |

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|------------|--|--|---|
|            |  |  | KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQLDDLTVDLD<br>HQRQVASNLEKKQ\KKFDQLLAEKKSISARYAEERDRAEAEARE<br>KETKALSARALEBALEAKEEFERONKQLRADMEDLMSSKDDVG<br>KNVHELEKSKRALEQQV\SEMRTQLESELEDELQATEDAKLRLEV<br>NMQAMKAQFERDLQTRDEQNEBKRLLIKQVRELEAELEDERKQ<br>RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK<br>DYQRELEBARASRDEIFAQSEKSEKLLKSLEAEILQLQEELASS<br>ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLBE<br>BLEEEQSNMELLNDRFRKTTILQVDTLNAELAAERSAAQKSDNAR<br>QQLERONKELKAKLQLEGA VKSKFKATISALEAKIGQLEEQLE<br>QEAKEAAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA<br>NARMKQLKQLEEAEEAATRANASRRKQLQRELDDEANEGLSR<br>EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK<br>TSDVNETQPPQSE  |
| 5932       | 33   | 572  | RHLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEMNG<br>FGATLAVGLTIFVLSVVTIIICFTCSCCCLYKTCRRPRPV\APP<br>PHPP/PVVHAPYPQPPSPVPPSPYQGYHTMPQPGMPAAPPY<br>PMQYPPPYPAQPMGPPAYHETLAGGAAAPYPASQPPYNPAYMDA<br>PKAAL   |
| 5933       | 1  | 3190   | GTRKLKMAADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD<br>SDMPSTRTPKSPRKHNYRNESARES L CDS PHQNLSRPLENKLK<br>AFSIGKMSTAKRTLSKKEQEELKKKBEKAAAEIYEEFLAAFEQ<br>SDGNKVKT FVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP<br>PNQSSNERPPSLLVIETKKPPLKKGEEKKKSNLELFKEELKQI<br>QEERDERHKTGRLSRFEPQSDSDGQRRSMDAPSRNRSSGVL<br>DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKCCCQEFGRFGP<br>LASVKIMWPRTDEERARERNCGFVAFMNRDRAERALKNLNGKMI<br>MSFEMKLGWGA VPIPPHPYIYPPSMMEHTLPPPPSGLPFNAQP<br>RERLKNPNAPMLPPPKNKEDFEKTLQAIVKVVIPTERNLLALI<br>HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW<br>KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPLNPNYLHGMSEEQ<br>ETEAFVVEPSKKGALKKEEQDKLEELRGLTPRKNDIGDAMVFC<br>LNNAEAAEEIVDCITESLSILKTPPKKIARLYLVSDVLYNSSA<br>KVANASYRKFFETKLCQIFSDLNATYRTIQGHQSENFQKQVM<br>TCFRAWEDWAIYPEPFLIKLQNIIFLGLVNIIEKETEDVPPDDL<br>GAPIEEELDGAPELDVDGIPIDATPIDDLGVPKSLDDDLGVP<br>PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVITTSKWEFLD<br>QHEESEEENQNEESEEDEEDTQSSKSEEHLYSNPIKEEMTE<br>SKFSKYSEMSEEKRAKLEIELKVMKFQDELESGKRPKKPGQSF<br>QEQVBHYRDKLLQREKEKELERERERDKKDKELERSKDKKEK<br>DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSESR<br>SHKSSRSRSSHKDSPRDVS KKA KRS PS GSRTPKRSRRSRSRSP<br>KKSGKRSRSQSRSPHRSHKSKGKTNTGRKFFKAVTYWKCDLF<br>LCPERSVF |
| 5934       | 1  | 3190   | GTRKLKMAADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD<br>SDMPSTRTPKSPRKHNYRNESARES L CDS PHQNLSRPLENKLK<br>AFSIGKMSTAKRTLSKKEQEELKKKBEKAAAEIYEEFLAAFEQ<br>SDGNKVKT FVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP<br>PNQSSNERPPSLLVIETKKPPLKKGEEKKKSNLELFKEELKQI<br>QEERDERHKTGRLSRFEPQSDSDGQRRSMDAPSRNRSSGVL<br>DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKCCCQEFGRFGP<br>LASVKIMWPRTDEERARERNCGFVAFMNRDRAERALKNLNGKMI<br>MSFEMKLGWGA VPIPPHPYIYPPSMMEHTLPPPPSGLPFNAQP<br>RERLKNPNAPMLPPPKNKEDFEKTLQAIVKVVIPTERNLLALI<br>HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW<br>KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPLNPNYLHGMSEEQ<br>ETEAFVVEPSKKGALKKEEQDKLEELRGLTPRKNDIGDAMVFC<br>LNNAEAAEEIVDCITESLSILKTPPKKIARLYLVSDVLYNSSA<br>KVANASYRKFFETKLCQIFSDLNATYRTIQGHQSENFQKQVM<br>TCFRAWEDWAIYPEPFLIKLQNIIFLGLVNIIEKETEDVPPDDL<br>GAPIEEELDGAPELDVDGIPIDATPIDDLGVPKSLDDDLGVP   |

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|------------|--|--|--|
|            |  |  | PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD<br>QHEESEEENQNEESEEDEEDTQSSKSEHHLYSNPIKEEMTE<br>SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF<br>QEVEHYRDKLLQREKEKELERERERDKDKKELESRSKDKKEK<br>DECTPTRKERRRHSTSPSPSRSSSGRRVKSPSPKSERSESR<br>SHKESSRSRSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSP<br>KSGKKRSRSQSRSPHRSHKSKGKTNTGRKFFKAVTYWKDLF<br>LCPERSVF   |
| 5935       | 3  | 4493   | SYWLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCEIGASAL<br>SDSGSFVSSRARREKSKKGRQAEALERLKKAKAGERYKYEVDF<br>TGVEVEVDEEQYSLVQARQDDDWIVDDDGIGYVEDGREIFDD<br>LEDDALDADEKGDGKARNKDKRNKVLAVTKPNNIKSMFIACA<br>GKKTADKAVDLSDKGLLDILQDLNTEPTTPTPPVMILKKRS<br>IGASPNPFSVHTATAVPBGKIASPVSRKEPPLTPVPLKRAEFAG<br>DDVQVESTEEQESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD<br>KESEPAEEVKQZADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS<br>VQEVQVDSHLLPLVKGADDEQVHFYWLDAYEDQYNQPGVVFLF<br>GKVVIESAETHVSCCMVKNIERTLYFLPREMKIDLNTGKETGT<br>FISMKDVYEEFDEKIATKYKIMFKSKPVEKNYAFEIPDVPEKS<br>EYLEVVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMNRKIK<br>GPCWLEVKKSTALNQPVSWCKVEAMALKPDLVNVIKDUSPPPLV<br>VMAFSMKTQNAKHNQNEI IAMAALVHSPALDKAAPKPPFQSH<br>FCVVSXPKDCIFPYAFKEVIEKKNVKEVAATERTLLGFFLLAKV<br>HKIDPDIIVGHNIYGFELVLLQRIINVCKAPHWSKICRLKRSNM<br>PKLGGRRSGFGERNATCGRMICDVEISAKELIRCKSYHLSLVQQ<br>ILKTERVVIPIENIQNMYSSESSQLLYLLEHTWKDA\KFILQIMC<br>ELNVLPLALQITNIAGNISRTLMGGRSERNEFLLLHAFYENNY<br>IVPDQKIFRKPQQLGDEDEEIDGDTNKKYKGRKKGAYAGGLVL<br>DPKVGFYDKFILLDFNSLYPSIIQEFNICFTTVQVASEAQKV<br>TEDGEQEQIPELPDPSPLEMGILPREIRKLVERRKQVKQLMKQD<br>LNPDILQYDIRQALKLTANSMYGCLGFSYSRYAKPLAALVT<br>YKGREILMHTKEMVQKMNLEVIYGDTSIMINTNSTNLEBVFKL<br>GNKVKSEVNKLYKLEIDIDGVFKSLLLLKKKYAALVVEPTSD<br>GNYVTQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDITV<br>BNIQKRLIEIGENVLNGSVFVPSQFEINKALTDPQDYDPDKSLP<br>HVHVALWINSQGRKVKAGDTVSYVICQDGSNLTAQRAYAPEQ<br>LQKQDNLTIDTQYLAQQIHPPVARI CEPIDGIDAVLIATGWEL<br>\DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP<br>TCGTENIYDNVFDGSGTDMPSLYRCSNIDCKASPLTFTVQLSN<br>KLIMDIRRFIKKYDGLWICEPTCRNRTRHLPQFSRTGFLCP<br>ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTHHEKDK<br>LKKQFPTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV<br>KS |
| 5936       | 1124   | 139  | RGEEQFDAEFRRFACLGGERLQEFSSRLRAVHRSRANTCYLAI<br>RMLMATCCPSPTTACTGFWQAPPLRLVQKREADSSGLAFAS<br>NSLQRRKKGLLLRPVAPLRTRPPLLSLPQDFRQVSSVIDVDLL<br>PETHRRVRLHKGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI<br>SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN<br>SHN\LIVTVKPAQNRRNVVRGASGRLTGPPSAGPGPAEPDSDDD<br>SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLSPLDD<br>QEQAASSGWSRIRGDGSGFSL  |
| 5937       | 31   | 1600   | PTSLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL<br>YGLTSSYSLWMLRSSLKQYSFEALREKSNYSIDIPVKNDFAPI<br>LHLADQYDPLYSKRFSIFLSEVSENKLGKQINLNNEWTEKLKSK<br>LVKNAQDKIEHLFMLNGLPDNVFELTMEVLSLELIPEVKLPS<br>AVSQLVNLKELRVYHSSLVVDHPALAFLEENKILRLKFTMECK<br>IPRWVFLKONLKELYLSCVLPQLSTMQLEGFODLKNLRTLYL<br>KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLLNNLKKMVNLKS<br>LELISCDLERIPHSIFSLNNLHEDLRENNLKTVEEIIISFQHLQ<br>NLSCLKLWHNNIAYIPAIGALSNEQLSLDHNNIENLPQLFL<br>CTKLHYLDLSYNHLTFIPBEIQYL\SNLQYFAVTNNNIEMLPDG  |

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|------------|--|--|--|
|            |  |  | LPQCKKLQCLLIGKNSLMNLS PHVGELS NLTHREPIG \NYLETL PPELEGCSLKRNC LIVEENLLNTLPLP VTERLQTCLDKC  |
| 5938       | 395  | 1865   | YKGEFFFCNQEARGERKKKKAMSSPNIWSTGSSVYSTPVFSQK MTVWILLLLSLYPGFTSQKSDDDYEDYASNKTWLTPKVPEGDV TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME YTIDIFFAQTWYDRRLKFNSTIKVLRNLNSNMVGKIWI PDTFFRN SKKADAHWITTPNRMRLRIWNGRVLYSRLRTIDAECQIQLHNF MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDRSWRLYQFSF VGLRNTTEVVKTSGDYVMSVYFDLSRRMGYFTIQTYPCTLI VVLSWVSFWINKDAVPARTSLGITTTLTMTLSTIARKSLPKVS YVTAMDLFVSVCFFVFSALVEYG\TLHYFVSNRKPSKDKDKK KNPAPTIDIRPSATIOMNATHLQERDEEYGECLDGKDCASF FCCFEDCRTGAWRHGRIHRIAKMDSYARIFPTAFCLFNLVYW VSYLYL   |
| 5939       | 66   | 1404   | IRPGYLKEVOENSPGHRAGLEPFDFIVSINGSRLNKDNTLKD LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLGVSR FCSFDGANENVVHVLVESNSPAALAGLRPHSDYIIGADTMNE SEDLFSLIETHEAKPLKLYVYNTDTDNCREVITPNSAWGEGGS LGCGIGYGYLHRIPTRPFEQKKISLPGQAGTPIITPLKDGFE VQLSSVNPPLSPPGTGTIEQSLTGLSISSTP\PAVSSVLSTGV PTVP\LLPPQVNQSLTSVPPMESSYLHLPLGMPFTRQGLPNLFO PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNA PSDPAT TTA KADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSA VDA NASESP  |
| 5940       | 145  | 717  | RRSASRSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS LEKLPVHMLVITEVEQEFSFSDIASLVVCMVAGISYISVYDH QGIFKRNSRLMDEILKQQQELGLDCKSKYSPFANSNDKDDQV LNCHLAVKVLSPEDGKADIVRAAQDFCOLVAOKQKRPDLDVDT LA\VYLVQMVLILI  |
| 5941       | 13   | 6147   | MCLGRMGASSPRSPVPVGPAPGLPFCCGGSLLAVVULLALPVA WGQCNAPW\LPFARPTNLTDDEFEP IGTLYLNYECRPGYSGRPF SIICLKNSVWTGAKDRCKRKS CRNPPDPVNGMVHVIKGIQFGSQ IKYSC TKGYRLIGSSSATCIIISGDTVIWNETPICDRIPCGLPP TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRS LFSL NEVVEFRCPQPGFVMKGPRRVKCOALNKWEPELPSCSRVCQPPD VLAERTORDKDNFSPGQEVFYSCBPGYDLRGAASMRCTPQGDW SPAAPTCEVKS CDDFMGQLLNGRVLPVNLQLGAKVDFVCEG FQLKGSSASVCVLGME SLWNSVVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNG VHS SPAPRCGILGHCA PDHFLFAKLKTQTNASDFPIGTS LKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPDPVNGMVH VITDIQVGSRIYSCITGHR LIGHSSAECLSGNAHWS TKPPI CQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRS LFSLNEVVEFRCPQPGFVMKGPRRVKCOALNKWEPELPS CSRVCQPPDVLHAERTORDKDNFSPGQEVFYSCBPGYDLRGAAS MRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRVLPVNLQLGAKVDFVCEG FQLKGSSASVCVLGME SLWNSVVPVCEQIFCPS PVPINGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQNGVWSSPAPRCGILGHCA PDHFLFAKLKTQTNASD FPIGTS LKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCK T PDPVNGMVH VITDIQVGSRIYSCITGHR LIGHSSAECLSGN TAHWSTKPIICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGKVFELVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCT PPNVENGILVSDNRS LFSLNEVVEFRCPQPGFVMKGPRRVKCOA LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPAAPCAVKS CDDFLGQLPHGRV LFPLNLQLGAKVSFVCEG FRLKGSSVSHCVLVGMRLWNSVP VCEHIFCPNPAILNGRHTGTPSGDIPYKGEISYTCDPHPDRGM |

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|------------|--|--|--|
|            |  |  | <p>TFNLIGESTIRCTSDPHGNGVWSSPAPRCBLSVRAGHCKTPEQF<br/> PFASPTIPINDFEFVPGTSLNYECRPGYFGKMFSSISCLNVLWS<br/> SVEDNCRRKSCGPPPEPFGMVHINTDTQFGSTVNYSCNEGFRL<br/> IGSPSTTCLVSGNNVTWOKKAPICEIISCEPPPTISNGDFYSNN<br/> RTSFHNGTVVTVYQCHTGPGEQLFELVGERSIYCTSKDDQVGVW<br/> SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQPG<br/> FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEHTLSHQ<br/> DNFSPGOEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPRCTVKS<br/> CDDFLGQLPHGRVLLPLNLQLGAKVSFVCEGFRLLKGRSASHCV<br/> LAGMKALWNSSVPVCEQIFCPNPAPILNGRHTGTPLGDIPIYGKE<br/> VSYTCDPHDRGMTFNLIGESTIRRTSEPHGNGVWSSPAPRCBLS<br/> PVGAAACPHPKIQNGHYIGGHVSLYLPGMTISYTCDFGYLLVGK<br/> GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKLEMKKVYHY<br/> GDYVTLKCEDGYTLEGSPTSQCQADDRNDPPLAKCTSRTHDALI<br/> VGTLSGTIFFILLIIFLSWILKHKRGNNAHENPKVEAIIHLHSQ<br/> GGSSVHPRTLQTNENSRVLP</p>   |
| 5942       | 4509   | 688  | <p>YLYVRMRANPLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRL<br/> DK\AQMIRFEERTGYFSSDGLGRRTASHYYIKYNTIETFNELFDA<br/> HKTEGDI\FAIVSKAEFDQIKVREEEIEELDTLLSNFCELSTPG<br/> GVENSYGKINILLQTYINRGEMDSFSLISDSAYVAQNAARIVRA<br/> LFEIALRKRWPMTYRLNLNSKAIDKRLWGWASPLROFSILPPH<br/> MLTRLEEKLTVDKLDKMRKDEIGHILHHVNIGLKVKQCVHQIP<br/> SVMMEAFIQPIRTVLRVLTLSIYADFTWDDQVHGTVGEPPWWIWW<br/> EDPTNDHIYHSEYFLALKKQVISKEAQLLVFTIPIFEPLPSQYY<br/> IRAVSDRWLGABAVCIINFQHLILPERHPHTELLDLQPLPITA<br/> LGCKAYEALYNFHFNPVQTQIFHTLYHTDCNVLGAPTGSQGT<br/> VAELAI\FRVFNKYPTSKAVYIAPLKALVRERMDWVKVRIEKL<br/> GKKVIELTGDVTPDMKSIKADLIVTTPKWCQVSRWQNRNYV<br/> QQVTILI\IDEIHLGEEGRGPVLEIVSRNTFISSTHEKPVIRIVG<br/> LSTALANARDLADWLNKQMGFLNFRPSVRPVPLEVHIGGFPGQ<br/> HYCPRMASMNKPAFAIRSHSPAKPVLI\FVSSRRQRLTALELI<br/> AFATEEDPKQWLNMDEREMENI\IATVRDSNLKLTAFGIGMHH<br/> AGLHERDRKTVEELFVNCKVQVLIATSTLAWGVNFAHLVLIK<br/> TEYYDGKTRRYVDFPI\TDVLMQMGGRAGRPOFDDQGVILVHDI<br/> KKDFYKKFLYEPFVPSLLGLVSDHLNAE\IAGGTITSKQDALD<br/> YITWTYFFRRLIMNPSYYNLGDVSHDSVNKFLSHLIEKSLIELE<br/> LSYCIBIGEDNRSIEPLTYGRIASYYYLKHQTVKMF\KORLKPEC<br/> STEEELLSILSDAEYTDLPVRHNEHDMNSELAKCLPIESNPHSF<br/> DSPHTKAHLLQAHLSRAMLPCPDYDTDTKTVLQALRVQAML<br/> DVAANGWLVTNLITNLQNVIQGRWLKSSLLTLPNIENHHL<br/> HLFKKWKPI\MKGPHARGRTSIECLPELIHACGGKDHVFSSMVES<br/> ELHAAKTQAWNFLSHLPEINVGISVKGSDDLVEGHNELSVST<br/> LTADKRDDNKWIKLHADQEVVLQVSLQRVHFGFHGKPKESCAVT<br/> PRFPKSKDEGWFLILGEVDKRELIALKRVGYIRNHVASLSFYT<br/> PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ<br/> GL</p> |
| 5943       | 1  | 2274   | <p>DKPTRHKTYLSSSWAKMAAEGPVGDGELWQTLNPHVFLRLR<br/> RGLKNQSPTEAEKPASSSLPSSPPQLLTRNVVFGGLGELFLWD<br/> GEDSSFLVRLRGPSSGGG\EEPALSQYQRLLCINPPLFEIYQVL<br/> LSPQOHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP<br/> VAERFFTSSTSLTKHAAWYPSIILDPHVLLTSDNVIRIYSLR<br/> EPQTFPTNVII\SEAEESLVNLKGRAYTASLGETAFAVDFGPLA<br/> AVPKTLFGQNGKDEVVAYPLYLYENGETFLTYISLLHSPGN/I<br/> WKAVGSLAHAS\AAEDNYGYDCAVLCPLCPVNI\VIATESGML<br/> YHCVVLEGEEDDHTSEKSWDSRIDLPSLYVFECEVLELAKL<br/> ASGEDDPFSDFCPVKLHRDPKCP\SRHYCTHEAGVHVSGLTWI<br/> HKLHKLFGSDDEEDKDSLQELSTEQKCFVEHILCTKPLPCRPAP<br/> IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR<br/> EDVEVAESPLRVLAETPDSFEKHRSILQRSVANPAFLKASEKO<br/> IAPPPECLQLLSRATQVFREQYILKQDLAKEIQRVVKLLCDO<br/> KKKQLEDLSYCREERKSLREMAERLADKYEEAKEKQEDIMNRMK</p>  |



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|------------|--|--|---|
|            |  |  | KLLHSFHSLEPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK<br>KDYQQQKMEKVLSPKPTIILSAYQRKCIQSILKEEGEHIREMV<br>KQINDIRNHVNF   |
| 5944       | 167  | 3428   | PSIATFTDEPEVLTEPPSATTITTTIGISATWTTLAGSHGKRNT<br>ITTTSSKRKNRKNKITPENVIIFDDPLPISYSQPEKVNAGESKS<br>SSTSESGDSNDMRISSCDESSNSNSRKSNDHSPAVVTTTVSS<br>KKQPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS<br>GPSPLSSPNGLTVASPKRGQKRECGWKEVVRSSKKVSVPTVI<br>SRVIGRGGCNINAIREFTGAIHIDIKQKDKTGDRITIRGGTES<br>TRQATQLINALIKDPDKBIDELIPKNRLKSSSANSKIGSSAPT<br>TAANTSILMGIKMTTVALSSTSQTATALTVPASSASTHKTIKNP<br>VN\NVRPGFPVSFP\LAYPPQFAHALLAAQTFQOIRPPRLPMT<br>HFGGTFPPAQSTWGFPPVRPLSPARATNSPKPHMVPRHSNQNS<br>GSQVNSAGSLTSSPTTTTSSASTVPGTSTNGSPSSPSVRRQLF<br>VTVVKTSNATTTTVTTTASNNNTAPT NATYPMPTAKEHYPVSSP<br>SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEQAEAGSPPVET<br>TNRTPNNSSSSSGSSSAHSNQPPGSGVSEPRPPLQQSQVPP<br>EVRMTVPPLATSSAPVAVPSTAPVTYPMQTPMGCPQPTPKMET<br>PAIRPPPHGTTAPHKNSASVQNSVAVLSVNHKRPHSVPSSVQ<br>LPSTLSTQSAQNSVHPANKPIAPNFSAPLPFGPFFSTLFENSPT<br>SAHAFWGGSVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG<br>FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM<br>YGFAPLGGAPAAANFNRRQHFSPLSLLLTPCSSASNDSSAQSVSS<br>GVRAPSPAPSSVPLGSEKPSNVSDRQVVPVIGTERSARIRQT<br>TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM<br>IHRPMSDPGVFSQHQAMERDSTGIVTSPGT FHQHVPAGYMDFPK<br>VGGMPFSVYGNAMI PPVAPIPDGAGGPIFNGPHAADPSWNSLIK<br>MVSSSTENNGPQTVWTPWAPHMNSVHMNQLG |
| 5945       | 1461   | 197  | GVTHLFLFGKRRLRNGIAEDLKGQADFFLLVSEAVVATGSPRA<br>WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGOQ<br>QPQPEKPESTLQGAARAFYEALIGDESSAPDSQRSQTEPARER<br>KRKKRRIMKAPAAEVAEGASGRHGQGRSLEAEDKMTIRILRAA<br>QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG<br>AAVSYLLGRGAAWVGVELSGRDAQAEEAGFPEARMVRESH<br>GETRSPENRSPTPSLQYCENCDFHQSNDHRTSTAHLLSLSQGP<br>QPPNLPLGVPISSPGFKLLRGGWEPGMLGPRGEGRANPIPTV<br>LKRQDEGLGYRSAPQPRVTHFPAPWDTRAVAGRE\TPPRVATLSW<br>REERRREE\KDRAWERDLRTYMNLEF   |
| 5946       | 541  | 1666   | ILGSYSSIQPEEYS\SVVC\EVVLQDLA\YVSPK\HSYLRDLP<br>SEGSPPQRVNSIDFV\EL\EHLQPDVLVHVLRVVDF/TILTEAV<br>YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG<br>YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDCIRAITFKA<br>KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAPPITASQ<br>KIALNAHSSLSKISFSSLPNIYVTGCAKCGLELTDENRIYKQCF<br>SCLPFTMKKIYRPAALMTAIDGRHDVCIRVESKILIEKILLNISA<br>DCLNRVIVPSSEITYGMVADLFHSLLAASAEPCVLKIQSLFVL<br>DENSYPQQDFSLDFYPIVKGANARL  |
| 5947       | 3  | 1317   | RGIPDRRRRGPIGRVNMDELNVKMKMLGHEQGFAPCLKCKEK<br>CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT<br>KYTTLIAKLKSDGIPMYKRNVMILTNPVAACKNVSINTVYEW<br>PPVQNLALAQYMQMLPKEKQPVAGSEGAQYRKQKQAKQLPAHD<br>QDPSKCHELSPREVKEMEQFVKYKSEALGVGDVKLPCEMDAQG<br>PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCKLSMKEG<br>DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIFYWKNBKLYCG<br>RHYCDSEKPRCAGCDELIFSNEYTQAEQNWLKHFFCCFDCDSI<br>LAGEIYVMVNDKPVCKPCYVKNHAVVCGCHNAIDPEVQRVTYN<br>NFSWHASTEFCCLSCCSKCLIGQKFMPEGMVFCSECKKMS   |
| 5948       | 39   | 3370   | YREYIPVSGGSVLSALEVCWDFLSGLTEGSLLEGGFFSGPIDQ<br>GNHYQMRKGRCHRGSAAHPSSPCSVKHSPTRETLTYAQARM<br>VEIEIEGRHLRISIFDPLEIILEDLTAQEMSECNSENKENSER<br>PVCLRTKRHKNNRVKKQNEALPSAHGTPASASALPEPKRIVEY  |

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|------------|--|--|--|
|            |  |  | <p>SPPSAPRRPPVYKFIKSAEELDNEVEYDMDEEDYAWLEIVNE<br/> KRKGDGCVPAVSQSMFEFLMDRFEKESHENQKQGEQQSLIDEDA<br/> VCCICMDGECQNSNVILFCMDCNLAVHQECYGVPIPEGQWLC/<br/> RAHCLQSRARPADCVLCNPKGGAFKKTDDDRWGHV\VCALW\IP<br/> E\VGFAANTVFIEPIDGVRNIPPARWKLTCNLCKEKGR/VGACI<br/> QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA<br/> YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESVKTVRSTSKVR<br/> KKAkakKALAEPcAVLPTVCAPYIPQRLNRIANQVAIQKKQ<br/> FVERAHSYWLKRLSRNGAPLLRLQSSSQSSSQRENDEEM<br/> KAAKEKLYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA<br/> MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYL DHI<br/> KHMPDFATMRKRLKLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV<br/> FYRAAVRLRDQGGVVLQARREVDSSIGLEEASGMHLPERPAAAP<br/> RRPFSWEDVDRLLDPANRAHLGLEEQRLLELDMLDLCAMKSSG<br/> SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL<br/> GPEAGEEVLPRLETLQPRKRSRSTCGDSEVEEESPGKRLDAGL<br/> TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSNSPLCDSS<br/> FNAPKCGRGKPALVRRHTLEDRSELISCIENGYAKAARIAEV<br/> QSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV<br/> PGHNGVTIPAPPLDVLKIGEHMQTKSDEKFLVLVFFDNKRSWQ<br/> WLPKSKMVLGIDETIDKLMMEGRNSSIRKAVRIAFDRAMNHL<br/> SRVHGEPSTDLSDID</p>  |
| 5949       | 39   | 3370   | <p>YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLEPGFFSGPIDQ<br/> GNHYQMRKGRCHRGSAARHPSSPCSVGHSPTRETLTYAQAQM<br/> VEIIEIGRLHRIISIFDPLEIILEDLTAQEMSECSNKENSERP<br/> PVCRLRTKRHKNNRVKKNEALPSAHGTPASASALPEPKVRIVEY<br/> SPPSAPRRPPVYKFIKSAEELDNEVEYDMDEEDYAWLEIVNE<br/> KRKGDGCVPAVSQSMFEFLMDRFEKESHENQKQGEQQSLIDEDA<br/> VCCICMDGECQNSNVILFCMDCNLAVHQECYGVPIPEGQWLC/<br/> RAHCLQSRARPADCVLCNPKGGAFKKTDDDRWGHV\VCALW\IP<br/> E\VGFAANTVFIEPIDGVRNIPPARWKLTCNLCKEKGR/VGACI<br/> QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA<br/> YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESVKTVRSTSKVR<br/> KKAkakKALAEPcAVLPTVCAPYIPQRLNRIANQVAIQKKQ<br/> FVERAHSYWLKRLSRNGAPLLRLQSSSQSSSQRENDEEM<br/> KAAKEKLYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA<br/> MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYL DHI<br/> KHMPDFATMRKRLKLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV<br/> FYRAAVRLRDQGGVVLQARREVDSSIGLEEASGMHLPERPAAAP<br/> RRPFSWEDVDRLLDPANRAHLGLEEQRLLELDMLDLCAMKSSG<br/> SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL<br/> GPEAGEEVLPRLETLQPRKRSRSTCGDSEVEEESPGKRLDAGL<br/> TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSNSPLCDSS<br/> FNAPKCGRGKPALVRRHTLEDRSELISCIENGYAKAARIAEV<br/> QSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV<br/> PGHNGVTIPAPPLDVLKIGEHMQTKSDEKFLVLVFFDNKRSWQ<br/> WLPKSKMVLGIDETIDKLMMEGRNSSIRKAVRIAFDRAMNHL<br/> SRVHGEPSTDLSDID</p> |
| 5950       | 1166   | 373  | <p>ESRSITMSTSQGACPCQGAASRPAILYALLSSSLKAVPRPRSR<br/> CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSEFWQLPPQ<br/> DQRRLLQGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEP<br/> SSSGGSQGLPDRPQPSLAQVWLQCCLESFWSLELSPKE\YACL<br/> KGPILFNDVPGLQAASHIGHLQQAHHVLCVLEBPWCPAAQGR<br/> LTRVLLTASTLKS IPTSLGDLFFRPIIGDVIDIAGLLGDMLLLR</p>   |
| 5951       | 143  | 5449   | <p>WNVPKSLVVQLFKFSDEKEHEQNDSTSGKTGETGVEEMIAIRK<br/> VEQDSKETVKLSHEDDHILEDAGSSDISDAACTNPNTKENSILV<br/> GLPSCVDEVTECNLEKDTMGIAKTKENTLERNKIEPIGYCEDA<br/> ESNRQLESTBFNKSNLEVVDSTFGPESNILENAICDVPDQNSK<br/> QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVSKHTKP<br/> VIHSKQNMTTDAPKKIVAAKYEVHSKTKVNVKSVKRNTPVPS<br/> QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKQAHSVLKKTLQ</p>   |

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|------------|--|--|--|
|            |  |  | <p>DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQGTGHVSHSSQK<br/> QCHKPQQQAPAMKTNHSHVKELEHDPGEVHFKEEDKLKLPKPEKN<br/> LQPRQRSSSKSFLDEPPLFIPDNIATIRREGSDHSSSFESKYM<br/> WTPSKQCGFCKKPHGNRFMVGCGRCDWPHGDCVGLSLSQAOQM<br/> GEEDKEYVCVKCAEEDKKTEILDPTLENQATVEPHSGDKTME<br/> CEKLGSLSKHTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD<br/> NEIKKWQLAPLRKMGQPVLPSSRSSEKSEKIPKESTTVCTGK<br/> ASKPGTHEKQEMKKKKV\EKGVLVNHPAASASKPSADQIRQSVR<br/> HSLKDIIMKRLTDSNLKVPBEKAATKIEKELFSFFRDTDAK<br/> YKNKYRSLMFLNLDKPKNNILFKKVLKGEVTPDHLIRMSPEELAS<br/> KELAAWRRRENRTIEMIEKEQREVERRPITKITHKEIEIESD<br/> APMKQEAAEMIEQPAANKSLEKPEGSEK\RXEEVDSMSKDTTS<br/> QHRQHLFDLNCIKIGRMAPPVDDLSPPKKVKKVVGVARKHSDNE<br/> AESIADALSSTSNILASEFFBEEKQESPKSTSPAPRPEMPGT<br/> EVSTFLARLNFIVKGFINMPSVAKFVTKAYPVSGSPEYLTEDL<br/> PDSIQVGGGRISPTQVWDYVEKIKASGTKEICVVRFTPTVEEDQI<br/> SYTLFFAYFSSSRKRYGVAANNKQVKDMYLIPLGATDKIPHLV<br/> PFDGPGLELHRPNLLGLIIRQKLKRQHSACASTSHIAETPESA<br/> PPIALPPDKSKIEVSTEEAFEEENDFFNSFTVLHKQRNKPQ<br/> NLQEDLPTAVEPLMEVTKQEPKPLRFLPGVLIGWENQPTTLEL<br/> ANKPLPVDDILQSLLTGGVYDQ\AQSVMEQNTVKBIPLFLNEQ<br/> TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSAEIESVVG<br/> SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSQEETVESKE<br/> KTLKRQLQEDQENNLQDNQTSNNSPCRSNVGKGNIDGNVSCSEN<br/> LVANTARSPQFINLKRDPQQAAGRSQPVTTSESKDGDSCRNGEK<br/> HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQSDNLKVAQNS<br/> PSVENIQTSQAQAKPLQEDILMQNIETVHPFRFGSAVATSHFB<br/> VGNTCPSEFPKSIITTSRSTSPRTSTNPSMPRQPPNQLHLKS<br/> SPPGFP<br/> VWPPVV\HLP\GQPMRMGGLSQAARYIGQNFYQVKDIRPE<br/> RRHSDPWGRDQDQQLDRPFNRGKGRQRFYSDSHHLKRERHEKE<br/> WEQESERHRRDRSDQDKDRDRKREEGHKDKERARLSHGDRGTD<br/> GKASRDSRNVDKPKPKSEDEYKDKEREKSKHREGEKDRDRYH<br/> KDRDHTDRTKSKR</p> |
| 5952       | 3226   | 639  | <p>PPARRSARDLPRALSMEARPSGSGWNGALCRLL\LVTL\AFILF<br/> ASDACKNVTLHVPKSLDAEKLVGVRNLKECFATANLIHSSDPDF<br/> QILEDGSVYTTNTILLSEKRSFTILLSENTENQKKKIFVPLEH<br/> QTKVLKRRHTKEKVLRRARRWAPIPCSMLENSLGPFFLQOV<br/> QSDTAQNTIYYISIRGPGVDQEPNLFYVERDGTNLYCTRPVDR<br/> EQYESFEILAFATTPDGYTPELPLPLIKIEDENDNYPIFTEET<br/> YFTTIFENCRVGTTVGQVCATDKDEPDTMHLTKYSIIGQVPPS<br/> PTLFSMHPTTGVITTTSSQLDRELIDKYQLKIKVQDMGQYFGL<br/> QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTV<br/> DKDLVNTANWRANYTILKGNENGFKIVTDAKTNEGVLGVVKPL<br/> NYEEKQMILOIGVVNEAPFSREASPRSAMSTATVTNVNBDQDE<br/> GPECNPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL<br/> TDPTGWVTIDENTGSIKVFRLDREAETIKNGIYNITVLASDQG<br/> GRTCTGTGLIILQDVNDNSPFI PKKTVIICKPTMSSAEIVAVDP<br/> DEPIHGPPFDLSLESSTSEVQRMWRLKAINDTAARLSYQNDPPF<br/> GSYVVPITVRDLGMSSVTSLDVTLCDCTENDCTHRVDPRIGG<br/> GGVQLGKWAAILLGLIALFFCILFTLVCGASGTSKQPKVIPDD<br/> LAQQNLIVSNTEAPGDDKVYSANGFTTQTVGASAGVCGTVGSG<br/> IKNGGQETIEMVKGGHQTSSECRGAGHHHTLDSRCGGHTEVDNC<br/> RYTYSEWHSFTQPRLGEESIRGHTLIKN</p>  |
| 5953       | 330  | 811  | <p>PLLCNPDPGWYWWVKQSEISKESEQEMDARPKLDLQFKEGQTIK<br/> LCIGNITNKKGGASKPRRTARGGGLSLLPPPPGGKVTIPPPSS/V<br/> KLPSTNHVTPPSIPKSNHGGSDADILLDLDSFAPVTPPTPTVVS<br/> VSNLDWGFSTASSVPNQAPQPSNWWQF</p>  |
| 5954       | 32   | 2130   | <p>PPPPPPKLANMADLEAVLADVSLMAMEKSKATPAARASKRIVL<br/> PEPSIRSVMQKYLAEARNEITFDKIFNQKIGFLFKDFCLNEINE<br/> AVPQVKFYBBIKEYEKLNEEDRLCRSRQIYDAYIMKELLSCSH</p>  |

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|------------|--|--|--|
|            |  |  | <p>PFSKQAVEHVQSHLSKKQVSTLTFQPYIEICESLRGDIYFQKFM<br/> ESDKFTRPCQWKNVELNIHLTMNEFSVHRIIGRGGFGEVYGCRR<br/> ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPPFI<br/> VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVSFSEKEMRFYA<br/> TEIILGLEHMHNRFFVYRDLKPANILLDEHGHARIS\DLGLACD<br/> FSKKKPHASVGTGMYMAPEVLQKGTAYDSSADWFSLGCMLEFKLL<br/> RGHSPFRQHKTKDKHEIDRMTLTNVLELDTFSPELKSLEGLL<br/> QRDVSKRLGCHGGGSEQVEKHSFFKGVDWQHVVYLQKYPPLIPP<br/> RGEVNAADAFDIFSDEEDTKGIKLLDCDOELYKNFPLVTSERW<br/> QQEVTETVVEAVNADTDKIEARKRAKNQGLGHEEDYALGKDCIM<br/> HGYMLKLGNPFLTQWQRRYFYLFPPNRLEWRGEGESRQNLITMEQ<br/> ILSVEETQIKDKKCILFRICKGGKQFVLQCESDPEFVQWKKELNE<br/> TFKEAQRLLRRAPKFLNKPRTSGTVLPKPSLCHRNNGNL</p>   |
| 5955       | 1726   | 444  | <p>KRERFRLAVCLPRLYSAYESSPGTELRCEGLCRSGQEPADCR<br/> PANRQDVLGWINLPVLQTKDPLKTPGRLDHGTRTAFIHHREQ<br/> VHKRCINIRWDVGLFGLVNEIANSEEEVFEWKTASGVALALCR<br/> WASSLHGLSPLPPLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPH<br/> NKFAVALLDDSVRVYNASTIVPSLKHRLQRNVASLAWKPLSAS<br/> VLAVACQSCILWTLDPSTLSTPSSGCAQVLSHPGHTPVTSLA<br/> WAPSGGRLSASPVDAAIRVWDVSTETCVPLPWFRRGGVTNLLW<br/> SPDGSKILATTPSAVFRVWEAQMTWCERWPLTSGRCQTCGWSPD<br/> GSRLFTVLGEPLIYSLSPFERCCEGKG\ALEVQSQQRLWQICL<br/> RQQRHQMVRRLGERLTPWSGTPVGNVWLCL</p>  |
| 5956       | 1705   | 139  | <p>GVGVGARAMATVQEKAAALNLSALHSPFAHRPPGFSVAQKPFGA<br/> TYVNSSIINTLQTVQEVKKRRHRLKRHNDCFVGSEAVDVIFSHL<br/> IQNKYFGDVIDIPRAKVVVRCQALMDYKVFPAVPTKVFGDKKKPT<br/> FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR<br/> SASLEDLWENLSLKPANSPHVNISATLSPOQVINEVWQEEITGRLL<br/> LQVLVDLPLDLSLLKQAEVAPKIPQPKRQSTMVNNSNYLDRGILK<br/> AYSDSQDEDEWLSAIDCEYLDPQMVVEISRSFPEQPORTDLVK<br/> ELLFDAIGRYSSREPLNHLSDVHNGIAELLVNGKTEIALEAT<br/> QLLLKLLDFQNRREFFRLLYFMAVAANPEFKLQKESDNRMVVK<br/> RIFSKAIVDNKNSLKGKTDLLVFLMDHQKDVFKIPGTL\HKI<br/> VS\VK\LMAIQNGRDPNRDAGYIYQRIQORDYSNTEKTKDE<br/> LNLKLTLEDSDKLSAKEKKK\LLGQFYKCHPDIIEHFGD</p>  |
| 5957       | 1479   | 451  | <p>ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKNENIKNAMLIK<br/> GGNANATVTKVLKDVYALKPKPYGVLYKKKNITRPFEDOTSLEFF<br/> SKKSDCSLFFMGSHNKKRPNNLVIGRMIDYHVLDMIELGIENFV<br/> SLKDINKSKCEPGTKPMLIFAGDDFDVTEYRRLKSLIDFFRG<br/> PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLKKGSCRTPRIE<br/> LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD<br/> TFGTYYGRIHMOKQDLKSLQTRKM\KGLKKRPAERITDHEKKS<br/> KRIKKKLMELSQPLLHFCVLLKRIIKHQSIQSFL</p>  |
| 5958       | 1  | 3138   | <p>AAALGMLLNFPAQAFNLDVEKLTVYSGPKGSYFGYAVDFHYPD<br/> ARTASVLVGAPKANTSQPDIVEGGAVYCPWPAEGSAQCRQIPF<br/> DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP<br/> LLFTWRNFKPTPEKGPVGTCTYVAIQNFSAYAEFSPCGNSNADP<br/> EGQGYCOAGFSLDFYKNGDLIVGGPGSFYWGQVITASVADIIA<br/> NYSFKDILRKLAGEKQTEVAPASYDDSYLGSVAAGEFTGDSQQ<br/> ELVAGIPRGAQNFYVSIINSYDMFTIQNFTGEQMASYFGYTVV<br/> VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL<br/> FRDPQILTGTFGRFGSAMAHGLDNLQDGYNDIAIGVPFAGKD<br/> QRGKVLIIYNGKDGNTKPPKFCQGVWASHAVPSGFGFTLRGD<br/> SDIDKNDYPDLVGAFTGKVAVYRARPVVTVDAQLLHMPMIIN<br/> LENKTCQVPDSMTSACFSLRVASVTGQSANTIVLMAEVQLD<br/> SLKQKGAIKRTFLDNHQAHVRPPLVIKQKSHQCDQFIVYLRD<br/> ETFRDKLSPINISLNSLDESTFKEGLEVKPILNYRENIVSE<br/> QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHMLLIINAR<br/> NEGEGAYEAELEFVMIPEEADYVGIERNKNGFRPLSCYEKMENV<br/> RMVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS<br/> NKDNFDSNFSVLQINITAVAQVEIRGVSHPPQIVLPIHWEPEE</p> |

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|------------|--|--|---|
|            |  |  | EPHKEEEVGPLVEHIYELHNIGPSTISDTILEVGWPFSAARDEFL<br>LYIFHIQTLGLPQCOPNPINPQDIKPAASPEDTPELSAFLRNS<br>TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG<br>GESAVLKVRSLWAHTPLQRKNDPYALASLVSEVKMPYTDQP<br>AKLPEGSIAIKTSVIWATPNVSFSIPLWVILAILLGLLVAIL<br>TLALWKCFFDRARPPQEDMTDREQLINDKTPEA  |
| 5959       | 1  | 1166   | GTSGYAAQQLPSLLKEREFLHGLTLNKFASQNLNHRQVCGTRC<br>NTLFVVDVQTSQITKIPILKDREPGGVTOQCGIHAIELNPSRT<br>LLATGGDNPNLSAIYRLPTLDPVCVGGDDGHKDWIFSIAWISDTM<br>AVSGSRDGSMLWEVTDVLTSDARHNVSVPVYAKITHKALK<br>DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL<br>SKLLSTKLKPYCENVCCLAYGSEWVYAVGSQAHVSLDPRQPSY<br>NVKSVCSRERGGSGIRSVSYEHIITVGTGQGSLLFYDIRAQRFL<br>EERLSACYOSKPRLAGENLKLTTG\KGWLNHDETWNRNYFSDIDF<br>FPNAVYTHCYDSSGTLKFVAGGCLPGLHGNAGLWS  |
| 5960       | 2853   | 870  | FWWSDDGPRPRRPAVAGAGAAHLSDPWAMTPTGTANRATNPLNKE<br>LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQWEAIQALT<br>VLETCMKSCGRFHDVGVKPRFLNELIKVVSPLYGSRSTSEKVK<br>NKILELLYSWTVGLPBEVKIAEAYQMLKKQ\IVKSDPKLPDDT<br>TFPLPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE<br>MVQEDQKRMEKISKRVNAIEBVNNVKKLLTEMVMSHSQGGAAAG<br>SSEDL\MKEL\YQRCERMPTLFPTGRVDTEDND\EALAEILQA<br>NDNLTVQVINYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL<br>PPAGTTYPAMPTRPGEQASPEQPSASVSLDDELSGLSDPTP<br>PSGSLDGTGWSFQSSDATEPPAPALAAQAPSMESRFPQTSLP<br>ASSGLDDLLGLKTLQSLPPESQQRWEKQQPTPLRLTLRLDQ<br>NKSSSCSSPSSSATSLHTVSPPEPPRPQPVPTSLASITVP<br>LESIKPSNIPVTVYDQHGFRILFHFARDPLPGRSDVLVVVSM<br>LSTAPQPIRNI VFQSAVPKVMKVLQPPSGTELPAFNPIVHP<br>ITQVLLLANPQKEKVRRLRYKLFTMGDQTYNEMGDVDQFPPEP<br>WGSL   |
| 5961       | 198  | 3147   | SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT<br>GLEVAIKMIDKKAMYKAGMVQVQNEVKIHCQLKHPISILELYNY<br>FEDSNYVYLVLCHNGEMNRYLKNRVKPPSENEARHEFMHQIIT<br>GMILYLSHSHILHRDLTLNLLLRNMNIKIADFGLATQLKMPHE<br>KHYTLCGTPNYISPEIATRSAGLESVWSLGCMPFYTLIGRPP<br>FOTDTVKNTLNKVVADYEMPTFLSIEAKDLIHQLLRNPADRL<br>SLSSVLDHDFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS<br>STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSTDFSSSGDGN<br>FYTQWGNQETSNSGRGRVIQDAERPHSRYLRRAYSSDRSGTSN<br>SQSQAKTYTMRCHSAEMLSVSKRSGGGGENEBRYSPTONNANIF<br>NFFKEKTSSSSGSFERPDNNQALSNIHCPGKTPFPFADPTPQTE<br>TVQQWFGNLQINAHLRKTTEYDSISPNDRFQGHDPDQKDTSKNA<br>WTDTKVKNDSADNAHSVKQNTMKYMTALHSKPEIIQECVF<br>GSDPLSEQSKTRGMEPPWGYQNRILRSITSPLVAHRLKPIROKT<br>KKAVVSLDSEEVCELVKEYASQBYVKEVLQISSDGNITITYY<br>PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA<br>SRFVQLVRSKSPKITYFTRYAKCILMENSFGADFEVWFYDGVKI<br>HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEHGR<br>ICLALESIISEBERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS<br>VDSNYPTRDRASFNRMMHSAASPTQAPILNPSMVTNEGLGLTT<br>TASGTDISSNSLKDCLPKSAQLLKSVPVKNVWGATQ\LTSGAVN<br>VQFNDGSQLVQAGVSSISYTSPNGQ\TTR\YGENEKLPTYIKQ<br>KLQCLSSILLMPSNPTPNFH |
| 5962       | 20   | 2447   | RVCSSASTASQAVMADAWERIRRLAADFQRAQFAEATQRLSER<br>NCIEIVNKLIAQKQLEVHTLDGKEYITPAQISKEMRDELHVRG<br>GRVNIVDLQVINVDLIHENRIGDIIKSEKHVQLVLGQLIDEN<br>YLDRLAEVNDKLQESGQVTISELCKTYDLGNFLTQALTQRLG<br>RIISCHIDLDRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL<br>ISKYGFQQLLYSVLEELVNSGRLRGTVVGGRODKAVFVPDIYS<br>RTQSTWVDSFFRONGYLEFDALSRLGIPDAVSIKKRYKTQLL  |

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|------------|--|--|--|
|            |  |  | FLKAAACVGGQLVDQVEASVEEAISSTGWVDIAPLLPTSLSVEDA<br>AIIQQVMRAFASKOASTVVFSDTVVSEKF\INDCTELFRELMH<br>QKAEKEMKNPNVHLITEEDLKQISTLESVSTSKDKKDERRRKA<br>TEGSGSMRGGGGNAREYKIKKVKKKGRKDDSDDESQSSHTGK<br>KKPEISFMFQDEIEDFLRKHIQDAPEEFISELAEYLIKPLNKTY<br>LEVVRVSFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEGK<br>MKFFADDTQAALTKHLLKSVCTDITNLIFNFIASDLMAVDDPA<br>AITSEIRKKILSKLSEETKVALTCLHNSLNEKSIDFISCLDSA<br>AEACDIMVKRGDKKREKQILFQHRQALAEQLKVTEDPALILHLT<br>SVLLQFSTHSMHLHAPGRCPQIIAFLNSKIPEDQHALLVKYQG<br>LVVKQLVSQSKKTKGQGDYPLNNELDKQEDVASTTRKELQELSS<br>SIKDLVLKSRKSSVTEE  |
| 5963       | 62   | 1130   | PWNPDFFPGRNRLMG\QKGETGFP\GQQGKKGAPGMP\GLMGSN<br>GSPGQPGTPGSKGSKGEPGIQGMPPGASGLKGEFGATGSPGEPGY<br>MGLPGIQGKKGDKNQGEKGIQGGKGENRQGI PGQQGIQGHG<br>AKGERGEKGEPCVRGAIGSKGESVDGLMG PAGPKQGPDPGPGQ<br>GPPGLDGKPGREFSEQFIRQVCTDVIRALPLVLLQSGRIRNCDH<br>CLSQHSGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPLVGVVGRP<br>GVRGLKGLPGRNGEKGSGQFGYPGEQGGPPGPPGEPGPGISKEG<br>PPGDPLGPKGDGHDGKPGIQGQPGPPGICDPSLCFSVIARRDPF<br>RKGPNY  |
| 5964       | 3  | 2147   | SCRTRGRLSPLQPREAGSSRSRARSEFFRFGGMEACQVQTTK<br>RGDPHELNRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSN<br>PKIVQLLAGVADQTKDGLISYQEFALFESVLCAPDSMFIVAFQL<br>FDKSGNGEVT FENVKEIFGQTI IHHHIFPNWDCEFIRLHFGHNR<br>KHLNTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI<br>MVTIRSHMLTPFVEENLVSAGGSISHQVSFSYFNAFNSLLNNM<br>ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYQATPLEIDILYQ<br>LADLYNASGRUTLADIERIAPLAEGALPYNLAEQLRQQSPGLGR<br>PIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKTRMQRGSG<br>SVVGEMLMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAI<br>KLTVNDFVRDKFTRRDGVSPLPAEVLAGGACAGSQVIFTNPLEI<br>VKIRLQVAGEITTGPRVSALNVLRLDLGIFGLYKGAACFLRDI<br>FSAIYFPVYAHCKLLADENGHVGLNLLAAGAMAG\VPAASLV<br>TPADVITRLQVAARAGQTTYSVIDCFRKIL\REEGPSAPWKG<br>TAARVFRSSPQFG\VTLVTYELLQRCFYIDFGGLKPGASEPTPK<br>SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPVA<br>VVQPKAAVAATQ |
| 5965       | 1  | 1498   | MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQCKFLSRG<br>CGSYCAGAKASPLPGKMAMGLMCGRRELLRLQSGRRVHVSAGP<br>SQWLKGKPLTTRLLFPAAAPCCCRPHYLFLAASGPRSLSTSASFA<br>EVQVQAPPVVAATPSPTAVPEVASGETADVQTAAEQSFAELGL<br>GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV<br>TGQREAAARIHNLPEIQKFSSRIREAKLAGDHIEYKASSEMAL<br>YQKKHGIKLYKPLILPVTOAPIFISFFIALREMANLPVPSLQTG<br>GLNWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW<br>MRNVIRMMPLITLPI TMHFPTAVFMYWLSNLFSLVQVSCLRIP<br>AVRTVLKIPQRVVHDLKLPREGFLESFKKGWKNAMETROLRE<br>REQMRNQLELAARGPLRQTFTHNPLQPGKDNPPNIPSS\SSS<br>SSKPKSKYPWHDTLG  |
| 5966       | 102  | 1925   | RSKQVMARLTKRQADTKAIQHLWAAIEIRNQKQIANIDRITK<br>YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQB<br>GYWLPGBEIDWETENHDWYCFECHLPGEVLICDLCPRVYHSKCL<br>SDEFRLRDSSSPWQCPVCRSIIKKNTNKQEMGTYLRFIVSRMKE<br>RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE<br>FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC<br>KNCFYLANARPDNWFYCPICPNHEDWAKMKGFGFWPAKVMQKE<br>DNQVDVRFEGHHQRAWIPSENIQDITVNIHRLHVKRSMGWKA<br>CDELELHQRFLEGRFWKSKNEDRGEAESSISSTSNEQLKVT<br>QEPRAKKGRRNQSVPEPKKEPEPETEAVSSSQEIPTMPQPIEKV<br>SVSTQTKLSASSPRMLHRSQTQTDNGVCQSMCHDKYTKIFNDF  |

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|------------|--|--|--|
|            |  |  | KDRMKS DHKRETERV VREALEKLRSEMEEEKRQAVNKAVANMQG<br>EMDRKCKQVKECKEEFVEEIKKLATQHKLISQTKKKQWCYNC<br>EEEMHYHCCWNTSYCSIKCQEHWAHAKRTCRKR  |
| 5967       | 102  | 1925   | RSKQVMARLT KRRQADTKATQHLWAAIEIIRNQKQIANIDRITK<br>YMSRVGHMHPKETTRQLSLAVKDLIVETLTVGCKGSKAGIEQE<br>GYWLPGEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL<br>SDEFRLRDS SSPWQCPVCRS I K K K N T N K Q E M G T Y L R F I V S R M K E<br>RAIDL N K K G K D N K H P M Y R R L V H S A V D V P T I Q E K V N E G K Y R S Y E E<br>FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHL\DELQLC<br>KNC FYLANARPDNWF CYPCIPNHELDWAKMGFGFWPAKVMQKE<br>DNQVDVRF FGH H H Q R A W I P S E N I Q D I T V N I H R L H V K R S M G W K K A<br>CDELELHQRFLREGRFWKSKNEDRGEEAESSISSTSNELQKVT<br>QEPRAKKGRNQSVPEPKKEPEPEPEAVSSSQEIPTMPQPIEKV<br>SVSTQTKKLSASSPRLHRSTQTNDGVCQSMCHDKYTKIFNDF<br>KDRMKS DHKRETERV VREALEKLRSEMEEEKRQAVNKAVANMQG<br>EMDRKCKQVKECKEEFVEEIKKLATQHKLISQTKKKQWCYNC<br>EEEMHYHCCWNTSYCSIKCQEHWAHAKRTCRKR   |
| 5968       | 81   | 1288   | VRFRRGGAPPTVLT'PGRQGGVFLGPQRPGSEPDIPARGQPHPP<br>RPVGVS TSAQAVQPPAMHRRRLALGLGFCLLAGTSLSVLWVYL<br>ENWLPVSYVPYLLPCPEIFNMKLHYKREKPLQPVVWSQYPQPKL<br>LEHRPTQLLTLPWLAPIVSEGTFNPELLQHIYQPLNLTIGVT<br>FAVGN/HFLESAAEEFFMRYRVHYIYFTDNPAAVPGVPLGPHRL<br>LSSIPIQGHSHWEETSMRRMETISQHIKRAHREVDYLFCLDVO<br>MVFRNPWGPETLGDVLAALHPSYAVPROQFPYERRRVSTAFVA<br>DSGDFYGGAVFGGQVARVYEFTRGCHMAILADKANGIMAAWR<br>EESHLNRHFISNKP SKVLSPEYLDWDRKQPPSLKIRFSTLDK<br>DISCLRS   |
| 5969       | 1126   | 503  | DVGFNKRRKCDLVFLES PRKPSGRDRAPKQRRRIAANKCLC<br>TGVREGEPPS/TTSQVKEAGRDFTYLIVLFGISITGGLEYTI<br>FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTR<br>GRQRHVRFTEYVVDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP<br>GSGEYDFRYIFVEIESYFRRTIIIEDNRSQDD  |
| 5970       | 316  | 4712   | SQDNIGHRLQKHGKLGKGLKSLQGRTDPIPIVVKYDVMGMG<br>RMEMELDYAEDATERRRVLEVEKEDTEELRQYKDYVDKEKAIA<br>KALEDLRANFYCLCDKQYQKHQEFDNHINSYOHAKHQLKDLK<br>QREFARNVSSRSRKDEKKQEKALRRLHBLAEQRKQAECA PGSGP<br>MFKPTTVAVDEEGEDDKDESATNSGTGATASCGLSEFSTDKG<br>GPFTAVQITNTTGLAQAPGLASQGISFGIKWNLGTPLQKLGVSF<br>SFAKAPVKLESIASVFKDAEEGTSEDGTPDKSSDQGLQKV<br>GSDSGSSNLDGKKEDEDPDGGSLASTLSKLKRMKREEGAGATE<br>PEYHYIIPAHCKVKPNFPFLFMRASEQMDGDNTHPKNAPES<br>KKGSSPKPKSCIKAAASQGAETVSEVSEQPKETSMTPEPSEPGS<br>KAEAKKALGGDVSDQSLESHSQKVSETQMCESSNSKETS LATPA<br>GKESQEGPKHTGPFPPVLSKDESTALQWPSELLIFTKAEPSIS<br>YSCNPLYDFDKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE<br>PNKSKEVGGEKIVRSSGGRMDAPASGSACSLNKQEPGGSHGSE<br>TEDTGRSLPSKKERSGKSHRHKKKKXHKSSKHKKRKHADTEEK<br>SSKAESGEKSKRKRKRKRKNKSAPADSRGPKPEPPGSGSPA<br>PPRRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSQDHGGRKH<br>KGELPPSSCQRRAGTKRSSRSSHRSQPSGDESDDASSHLHQ<br>KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSSRSYSSSS<br>DASSDQSCYSRQRSYSDSYSDRSRRHSKRSHDSDSDSYAS<br>SKHRSKRHKYSSDDSYSLSCSQSRSSRSHTRESRSSRGRSRS<br>SSCSRSRSKRRSRSTTAHSWQSRSSRSRDRSRSTRSPSRSGSR<br>KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEQPGKK<br>DDGRGDDSKATGPPSQNSNIGTRGSEGDSPEDKNSVTAKLLL<br>EKIQSRKVERKPSVEEVQATPNKAGPKLKDPPQGYFGPKLPPS<br>LGKPKVPLIGLKLPA TRKPNKKCEESGLERGEQE QSETEEGPP<br>GSSDALFGHQFP\SEETTGPLDDPPPEESKSGEVTADHPVAPLG<br>PPAHFDCYLQDPTISHNYLPDPDGNLTLESLSSSQPGPVSSSL<br>LPAPDLEHFP SYAPPSGDRS IESTDGAEDA\SLAPLESQPIPF |

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|------------|--|--|---|
|            |  |  | TPEEMEKYSKIQAAQHQHIQQQLLAKQVKAFFASAAALAPATPALQPIHIQQPATASATSITTVQHAILQHAAAAAAGIHWPHPHQPLAQVHHIQQPHLTPTISLSHLTHSIIIGHPATFLASHPIHIIPASAIHPGPPTFFHPVPHAAALYPTLLAPRPAATAALHLHPLLHPITFSQQDLQHPPSHCT  |
| 5971       | 53   | 2149   | SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDIIPESVTOERRPPKALFMSRGVGDGSSSHNPKATGSTSDPGNRRNSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSLTENRFHSLPFSLTAKMPNTNGSIGHSPLSLSAQSVMEELNAPVQESPPPLAMPNGSHGLEVGSLAEVKENPFYGVIRWIGQPPGLNEVLAGELEDEBCAG\CTDGT/REGTRYFTCALKKALFVKLKSCRPSDFASLQPVSNQIERCNSLAIWEAYLSEVVEENTPTQKWEKEGLEIMIG\KKKGIGQGHYNSCYLDSTLFLCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTIEVNPLRIYGYVCATKIMKLRLKILEKVEAASGFTSEKDPPEEFLNIFLPHHILRVBPLLKIRSAQKQVQDCYFYQIEMEKNEKVGVPPTIQQLLEWSFINSNLKF AEAPSCLIIQMFRFGDKFLFKKIFPSLELNTDLEDTPRQCRI CGGLAMYECRECYDDPNISAGKIKQFCKTCNTQVHLHPKRLNHKYNPVSLLPKDLPDWDWRHGCIPQNMELFAVLCIETSHYVAFVKYKGDDSAWLFDDSMADRDGGQNGFNIPQVTPCEVGEYLKMSLEDLHLSLDSRRIQGCARRLLCDAIYVPCQTSPTMSLYK |
| 5972       | 440  | 1761   | ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFTTAVVSPAMTQEPFREBLAYDRMPTLERGRQDPASYPADAKPSDLQSKRLPPCFSHKTWVFSVLMGSCLLVTSFGSLYLGNVFPAMDYLRCAAGSCIPSAIVSFTVSRNRANVIPNFQILFVSTFAVTTTCLWFGCKLVLNPSAININFNLI LLLLLLELLMAATVIAARSSEEDCKKKKGSMSDSANILDEVFPFARVLKYSYVVEVIAGISAVLGGI IALNVDDSVSGPHLSVTFFWILVACFPASIAASHVAECNKLCEVLIAISSLTSPLLFTASGYLSFSIMRIVEMFKDY?PAIKPSYDVL LLLLLLLL LLLQA/GPQHGRHRHPVRALQQCKQAAGCILGHPERFAGAPGWGGQGEPPPEGVRQGESLESRRGANGPVTTPRGRNRVAAPSLAPGMETHNP  |
| 5973       | 65   | 2007   | NGDGKDLFGHIWAWRSNGIISNFRSRPHAGMAEEDPAKSPKTGGRAPPGGAEEAGEPTTLQLRLGTISKAVQNKVEGILQDVQKPSDNDKLYLYLQLPSGPTTGDKSSEPTLSNEEYMYAYRWIRNHLBEEHTDCLCPKQSVYDAYRKYCESLACCRPLSTANFGKIIREFPDIKARRLGGRGQSKYCYSGIRKRTLVSMPPLPGLDLKGSESPEMGPEVTPAPRDELVEAACALTCDAERILKRSFSSIVEVARELLQQLHISARSAHAHVLMKAMGLAEDEHAPRERSKPKNGLENPEGGAHKPERLAQPPKDL EARTAGPLARGERKKSVVSSAPGANNLQVNALVARLPLLLLPRAPRSLIPPIPVSPPI LAPRLSSGALKVATLPLSSRAGAPPAAPVPIINMILPTVPALPGPGPGGRAPPGLTQPRGTENREVGIGGDQGHDKGVKRTAEVPVSEASGQAPPAAKQDIEDTASDAKRKRGRPLKKSGSGGERNSTPLKSAAMESAQSSRLPWETWGS GGEGNSAGGAERPGPMGEAEKGAVLAQG\QGDGTVSKGGRPGSGQHTKEAEDKIPLVPSKSVIKGSRSQKEAFPLAKGEVDTAPQGNKDLKEHVLQSSLSQBHKDPKATPP  |
| 5974       | 4293   | 2200   | LGLQMHTTSGRHQAMVTSNLNEDNESVTVIEWIENGDTKGK\BIDLESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIWKNNRTV\ASIKNDPPS\RDNRVVG SARARPSQFPEQFSSAQONGSV\SDISPVOAAKKEFGPPSRKNSNCVKEVEKLQEKREKRRLQOQLEREKRAQVDVATNPNYEIMCMIRDFRGS LDYRPLTTADPIDEHRICVCVRKRPLNKKETOMKDLVITI PSKDVMVMEHPKQKVDLTRYLENQTRFRDYAFDDSDAPNEMVYRFTARPLVETIFERGMATCFAYGQTSGSKTHTMGGDFSGKNQDCSKGIYALAAARDVFLMLKKPNYKKLELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQVQVVGLOREVKCVEDVLKLDIGNSCRTSGQTSANAHSSRSRAVFOILRLRGKLGKGFSLIDLAGNERGADTSSADRQTRLEGAEINKSLALKECIRALGRNKPHTPFRASKLTQVLRDSPIGENSRTCMIATISPGMASCENTLNTLRVYANRVKELTVDP TGAAGDVRIIMHHPNQI\DDLETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTTFFHEAVSQMVEM  |



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|------------|--|--|--|
| 5975       | 4293   | 2200   | EEQVVEDHRAVFQESIRWLEDEKALLEMTEEDVDYDVSATQLE<br>AILEQKIDILTELDRKVKSFRAALQEEQASKQINPKRPRAL<br>LGLOMHTTSGRIHQAMVTSLNEDNESVTVEWENGDTKGR\EID<br>LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR<br>TV\ASIKNDPPS\RDNRVVG SARARPSQFPEQFSSAQNGSV\S<br>DISPVQAAKKEFGPPSRKSNVCVKEVKLQEKREKRLQQQLR<br>EKRAQDVDA TNPNYEIMCMIRD FRGSLDYRPLTTADPIDEHRIC<br>VCVRKRPLNKKETQMKDLVITIPSKDVMVHEPKQKVDLTRYL<br>ENQTRFRDYAFDDSDAPNEMVYFTARPLVETIFERGMATCFAYG<br>QTGSGKTHTMGGDFSGKNQDCSKGIYALAAARDVFLMLKKPNYK<br>LELQVYATPFEIYSGKVFDLJ.NRRTKLRVLEDGKQQVQVGLQE<br>REVKCVEDVLKLDIGNSCRTSGQTSANAHSSRSRAVFQIILRR<br>KGLHKGKPSLIDLAGNSRGADTSSADRQTRLEGAEINKSLALK<br>ECIRALGRNKPHTPPRASKLTQVLRDSFIGENSRTCMIATISPG<br>MASCENTLNTLRANRVKELTVDP TAAGDVRPIMHPPNQI\DD<br>LETQWGVGSSPQRDDLKLLCEQNEEVSPLQFTFHEAVSQMVEM<br>EEQVVEDHRAVFQESIRWLEDEKALLEMTEEDVDYDVSATQLE<br>AILEQKIDILTELDRKVKSFRAALQEEQASKQINPKRPRAL   |
| 5976       | 20   | 2949   | VHHLHLTRVSVVNLDIILRIAQQMGIKTLNLVLG\LKRA\LEF<br>PEVSWMEVKDPNMKGAMLTNTGKYAIP TIDA\EA YAIGKKEKPP<br>FLPEEPSSSSEEDDPIPELLCLICKDIMTDAVVI PCCGNSYCD<br>ECIR TALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNFKNE<br>TGYTKRLRKQLPSPPPIPPRPLIQRLQPLMRSPISRQODPL<br>MIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT<br>ATVSI SVHSEKSDGPFDRSDNKILPAAALASEHSGKTSIIATA<br>LMEKGYQVPVLGTPSLLGQSLHGLIPTTGPRVINTARPGGG<br>RPGWEHSNKLGYLVSP PQQIRRGERSCYRSINRGRHHSERSQRT<br>CGPSLPATPVFVPVPPPLYPPPPHTLPLPPGVPPPPQSPQFP<br>GQP\PPAGYSVPPPGFPAPANLSTPWVSSGVQTAHSNTIPTQ<br>APPLSREEFYREQRLKEEEKKSKLDEFTNDFAKELMEYKKIQ<br>KERRRSFSRSKSPYSGSSYSRSYTYSKSRSGSTRSRSYSRSFS<br>RSHRSYSRSPPYPRRGGRKSNYRSRSRSHGYHRSRSRSPYR<br>RYHSRSRSPQAFRGQSPNKRNV PQGETEREYFNRYREVPPPYDM<br>KAYYGRSVD FRDPFEKERYREWERKYREWEKYYKG YAAGAQR<br>PSANRENFS PERFI.PLNIRNSPFRGRREDYVGGQSHSRNIGS<br>NYPEKLSARDGHNQDNTKSKKESENA PGDGKGNKHKHRKRR<br>KGESEGF LNPELLETSRKSREPTGVEENKTDLSLFLVLP SRDDAT<br>PVRDEPMDAESITFKSVSEKDKRERDKPAKAGDKTKRKNDSAV<br>SKKENIVKPAKG PQEKVDG\DV RDLLDLNL\QLKKPKEETPKDL<br>TILNHLPLRRMKSL\EPF\EKLT LNQOK\TPRNKTSQRGKSE<br>EGLFQRCQIRKANN |
| 5977       | 1363   | 1336   | FLEDRGQVLSHFQCLSLHSINHLHPGAGVAAGPATCW/REYLT<br>PVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEELKV<br>AYLPTGKQFLVTKNVPCYKRCQMEYSDELEAIEEDDGGGWV<br>DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEDEDEG<br>EAADMEEYEEESGLLETD EATLDRKIVEACKAKTDAGGEDAILQ<br>TRTYDLYITYDKYYQT PRLWLFYDEQRQPLTVEHMYEDISQDH<br>VKKTVTIENHPLPPPPMCSVHPCRHA EVMKKI IETVAEGG GEL<br>GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  |
| 5978       | 160  | 3213   | RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRRLRGQTAEAPAGRO<br>RPRREPEAMDEQSVESIAEVFRFCFICMEKLRDARLCPHCSKLCC<br>FSCIRRWLTEQRAQCPCPCRAPLQLREL VNCRWAEVVTQQLD TLQ<br>LCSLTKEEENEKDKCENHHEKLSVFCWTCKKCIHQCALWGGMH<br>GGHTFKPLAEIYBQHVTKVNEEVAKLRRRLMELISLVQEVERNV<br>EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSIT<br>QETELLESLLQVEHQLRSCSKSELISKSSEILMMFQQVHRKPM<br>ASFVTTVPDPDFTSELVPSYDSATFVLENFSTLRQADPVYSPP<br>LQVSGLCWRLKVYPDGNVGVGYLSVLELSAGLPETSKYEYR<br>VEMVHQSCNDPTXNIREFASDFEVGECWGYNRFRDL LLANEG<br>YLNQNDTVILRFQVRSPTFFQKSRDQHWYITOLEAAQTSYIQQ<br>INNKKERLTIELSRTQKSRDLSPPDNHLSPQNDDALETRAKKSA   |

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|------------|--|--|--|
|            |  |  | CSDMLLER\GPYSAS\VREAKEDEEDEEKIQNEDYHHELSGDDL<br>DLDLVYEDEVNQLDGGSSSSASSTATSNTENDIDEETMSGENDV<br>EYNNMELEEGELMEDAAAAGPAGSSHGTVGSSSRISRRLHCSA<br>ATSSLLDIDPLILHLDDLKDRSSIENLWGLQPRPPASLLQPTA<br>SYSRKDKDKQKQAMWRVPSDLKMLKRLKTQMAEVRCKMTDVKV<br>TLSEIKSSSAASGDMQTSLSFSAQAALACGTENSRLQDLGME<br>LLAKSSVANCYIRNSTNKKNSPKPARSSVAGSLSLRRADVDPGE<br>NSRSKGCQTLSEGGSPGSSSGSRHSSPRALIHGSIQDILPKTE<br>DRQCKALDSADVAVFSGLPFAVEKRRKMVTLGANAKGGHLEGL<br>QMTDLENNSETGELQPVLPAGASAAPEEGMSSSDSDIECDTENE<br>CEEHTSVGGFHDSEFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT<br>DENSGR   |
| 5979       | 212  | 3665   | LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE<br>TTTLPSPGSAVISTTTIATTPSKPTCDEKYANITVDLYNKETK<br>LFTAKLVNENVECGNNTCTNNEVHNLTECKNASVSIHNSCTA<br>PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC<br>DTQNIYTRFQCGNMIPDNKEIKLENLEPEHEYKCDSEILYNHSHK<br>FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPQRSFHN<br>FTLCYIKETBKDCLNLDKNLIKDYDLQNLKPYTKYVLSLHAYIIA<br>KVQRNGSAAMCHFTTKSAPPQVNMVMTVSMDSNMHVKCRPPR<br>DRNGPHERYHLEVEAGNTLVNESHKNCDFRVKDLQYSTDYTFK<br>AYFHNGDYPGEPFILHSTSYNSKALIAFLAFLIIVTSIALLV<br>LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVPIHADILLET<br>YKRKIADGRLFLAEFQSI PRVFSKFPKEARKPFNQKNRYVD<br>ILPYDYNRVELSEINGDAGSNYINASYIDGFEKPRKYIAAQGPR<br>DETVDSEFRMIWEQKATVIMVTRCEEGNRNKAHEYWPSMEEGT<br>RAFGECCCKDLTKHKRCP\DYIIQKLNIVNKKKATGREVTHIQ<br>FTSWPDHGVPEPDLHLLKLRNRVNAFNSFFSGPIVVHCSAGVGR<br>TGTIYIGIDAMLEGLEAENKVDVYGVVVKLRQRCLMVQVEAQYI<br>LIHQALVEYNQFGETEVLNSELHPYLHNMKRDPPSEPSPLEAE<br>FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE<br>LEMSKESEHDSDESSDDSDSEPSKYINASFIMSYWKP\EVMI<br>AAQGPLKETIGDFWQMI FQRKVIVMLTELKHGQDQICAQYWG<br>EGKQTYGDIQVLDKDTKSSSTYTLRVFELRHSKRKDSRTVYQYQ<br>YTNWSVEQLPAEPKELISMIQVVKQLPKQNSSEGNKHKSTPL<br>LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKAR<br>GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD<br>KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP<br>ASPALNQGS |
| 5980       | 3  | 2363   | DWAGCKLRLRLFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI<br>PEEDLEVQENNEDAAHDLTELEVMTMHALLQEVDVVVAPCGGLR<br>PTVDVLGDLVNDPLPVITYALHKDELSEDEQEIQEIRKYFSFP<br>VFFFKVPKLGSEIIDSSTRMESERSPLYRQLIDLGYLSSSHWN<br>CGAPGQDTKAQSMLEQSEKLRHLSTFSHQVLQTRLVDAAKALN<br>LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN<br>IANRKQEEKDMIVETLNTMKEELLDDATNMEFKDVIVPENGE<br>VGTREIKCCIRQIQELIISRLNQAVALNLISSVDYLRESFVGT<br>ERCLQSLEKSQDVSVHITSNYLKQILNAAHYHVEVTFHSGSSVTR<br>MLWEQIKQIIQIRITWVSPPAITLEWKRKVAQEAIESLSASKLAK<br>SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK<br>DHAPRLARLSLESRLQDVLLHRRKPLGQELGRGQYGVVYLCN<br>WGGHFPKALKSVVPPDEKHWNDALEFHYMRSLPKHERLVLDLHG<br>SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL<br>DVVEGIRFLHSQGLVHRDIKKNVLLDKQNRKAITDLGFCCKPEA<br>MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGLFWYICSGSVK<br>LPEAFERCASKDHLWNNVRRGARPERLPVDEECWQLMEACWDG<br>DPLKRLPLGIVQPMQLGIMNRLCKS\NSEQPNRGLDDST  |
| 5981       | 1  | 2519   | GRNHSAMERPWGAADGLSRWPHGLGILLQLLPPSTLSQDR<br>DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GAAPRGGRRRSAP<br>G\DEECGRVRDFVAKLANTHQHVFDLGRSSVLSWVGDTGV<br>ILVLTTPHVPLVIMTFGQSKLYRSEYDGKNFKDITDLINNTFIR   |

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|------------|--|--|---|
|            |  |  | TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD<br>LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA<br>VCLAKWGSNTIFFTTYANGSCKADLGALELWRTSLGKSFKTI<br>GVKIYSPGLGGRFLFASVMADKDTTRRIHVSTDOGDTWSMAQLP<br>SVGQEQFYSLAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS<br>KSLDRHLYTTTGGETDFNTVTSRGRVYITSVLSEDNSIQMTIF<br>DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP<br>MAPLSEPNAGVIVIAHGSVGDASVMVDPVYISDDGGYSWTKML<br>EGPHYTYTILDSGGIIVAIEHSSRPINVIKFSSTDEGQCWQTYTFT<br>RDIPIYPTGLASEPGARSMNISWGFESFLTSQWVSYTIDFKOI<br>LERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEQFLRLRKSSVC<br>QNGRDYVVTQKPSICLCSLEDFLCDFGYRPNDSKCVQPELK<br>GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK<br>CTSNFLSPEKQNSKNSVPIILAIVGLMLVTVAGVLIVKVCYVC<br>GGRFLVHLYSVLQQH\A\A\NGVDCVDALDTASHTNKGHYHDDS<br>DEDLLE  |
| 5982       | 56   | 2316   | ATRPGRSSWCRQFSRTASAPGRSNMLRIPVRKALVGLSKSPK<br>CCVRTTATAASNLIIEVFVDGQSVMEPGTTVLQACEKVMQIPR<br>PCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNLITNS<br>EKSKKAREGVMEFLLANHPLDCPI CDQGGECDLQDQSMFMGNDR<br>SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD<br>LGTTRGRNDMQVGTIYEKMFMSLSGNIIDICPVGALTSKPYAF<br>TARPWETRKTESIDVMDAVGSNIVVSTRTEGVMRILPRMHEDIN<br>BEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYSWEDALSRV<br>AGMLQSFQGDVAAIAGGLVDAEALVALKDLLNRVDSOTLCTEB<br>VFPTAGAGTDLRSNYLLNTTIAGVEEADVLLVGTNPRFEAPLF<br>NARIRKSWLHNDLKVALIGSPVDLTITYDHLGDSPKILQDIASG<br>SHFQSQVLKEAKKPMVVLGSSALQRNDGAAIILAAVSSIAQKIRM<br>TSGVTGDWKVMNHLRIASQVAALDLGYKPGVEAIRKNPPKVLV<br>LLGADGGCITRQDLPKDCFIYQGHGHDVGAPIADVILPGAAYT<br>EKSATYVNTGRAQQTQKAVTPPGLAREDNKIIIRALSEIAGMTL<br>PYDTL\DOVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN<br>QQLLADPLVPPQLTMKDFYMTDSISRASQTMKCVKAVTEGAQA<br>VEEPSIC |
| 5983       | 248  | 1763   | EARGDGGRRRHRSAGRRRAGRGEP\AGLKSQGRAPVKRAVARGG<br>RQ\YSAIALLEPAGSBIADLSILYSNRAACYLKEGNCSCGCIQ<br>DCNRALELHPFSMKPLLRAMAYETLEQYKAYVDYKTVLQIDC<br>GLQLANDSVNRLSRILMELDGPWREKLSLIPAVPASVPLQAWH<br>PAKEMISKQAGDSSSHRQQGITDEKTFKALKKEGNCVQNDKNYK<br>DALSKYSECLKINNKECAIYTNRALCYLKLQCFEEAKQDCDQAL<br>QLADGNVKAFFYRRALAHKGLKNYQKSLIDLNKVILLDPISIEAK<br>MELEEVTLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPRPA<br>GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAEYFGQIINAL<br>STRKDKACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNN<br>LIEKDPISLVYQHLLYLSKAERFKMMLTLISKQKELIEQLFEDL<br>SDTPNNHFTLEDIQALKRQYEL  |
| 5984       | 755  | 1193   | SSVCMACTYVSNLGGKQRSVSFLASGLMRVSTGPELRLHHSFVL<br>TGDVGRRICRLLVGLFTKGTSSKRVHPFSPGFCFLLCOLARVG<br>SSPKINVSPFYQN\QTSTQSRCTVFVWQRCSLVGPQVTVPTMY<br>FHSLRSISRFS   |
| 5985       | 22   | 1408   | RRVARPGTAEPKARRTVRRGRARRDLAGAERKAGVSEGRDSOR<br>RRPNPSIPSAAGMSHIQIPPLTELLQGYTVEVLRQPPDLVE<br>FAVEYFTRLREARAPASVLPATPRQSLGHPPPEPGPDRVADAK<br>GDSESEDEDELEVPPSRFNRRVSVCAETYNPDEEEDTDPRVI<br>HPKTDEQRCRLQEAACKDILLKNDQEQLSQVLDAMFERIVKAD<br>EHVIDOGDDGNFYVIERGTIDILVTQDNQTRSVGQYDNRGSFG<br>ELALMYNTPRAATIVATSEGLWGLDRVTFRRIIVKNNAKKRM<br>FESFIESVPLLSLEVSERMKIVDVIGEKIYKR/DGERIITQGE<br>K\ADSFYIIESGEVSIILRSRTKSNKDDGGNQEVEIARCHKQGYF<br>GELALVTNKPRAASAYAVGDVVKLVMDVQAFERLLGPCMDIMKR<br>NISHYEEQLVKMFGSSVDLNLGQ  |

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|------------|--|--|--|
| 5986       | 1806   | 484  | DAWKSTSLTFHWKLWGRHRRGRRRLAHPKNHLSPOQGGATPQVP<br>SPCCRFDSPRGPPPPRLGLLALMAEDGVRGSPVPSPGPPMEED<br>GLRWTPKSPDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI<br>LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AQHSPLE<br>EHVTCVQSILDEFLQT\YGSILPLSTDEVVEKLEDIFQOEFSTP<br>SRKGLVLQLIQSYQRMFGNAMVRGFRVAYKRHVLTMDDLGTLYG<br>QNWLNQVMNMYGDLVMDTVPEK\VHFFNSFF\DKLRTKGYDG<br>VKRWTKNVDIFNKELLLPIHLEVHWSLISVDVRRRTITYFDSQ<br>RTLNRRCPKHIAKYLAQAEAVKKDRDLDFHQGWKGYFKMNVARQNN<br>DSDCGAFVLQYCKHLALSQPFSTQDDMPKLRRIYKELCHCKL<br>TV  |
| 5987       | 1806   | 484  | DAWKSTSLTFHWKLWGRHRRGRRRLAHPKNHLSPOQGGATPQVP<br>SPCCRFDSPRGPPPPRLGLLALMAEDGVRGSPVPSPGPPMEED<br>GLRWTPKSPDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI<br>LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AQHSPLE<br>EHVTCVQSILDEFLQT\YGSILPLSTDEVVEKLEDIFQOEFSTP<br>SRKGLVLQLIQSYQRMFGNAMVRGFRVAYKRHVLTMDDLGTLYG<br>QNWLNQVMNMYGDLVMDTVPEK\VHFFNSFF\DKLRTKGYDG<br>VKRWTKNVDIFNKELLLPIHLEVHWSLISVDVRRRTITYFDSQ<br>RTLNRRCPKHIAKYLAQAEAVKKDRDLDFHQGWKGYFKMNVARQNN<br>DSDCGAFVLQYCKHLALSQPFSTQDDMPKLRRIYKELCHCKL<br>TV  |
| 5988       | 1292   | 410  | FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWVFTCRFQ<br>RLDCIYLNAGIMPNPQNLKALLFGLFS\AEGLLTQGDKITADG<br>LQEVFETDVFHGFILIRELEPLCHSDNPQLIWTSSRNARKSN<br>FSLEDFOHSGKGEPIYSSSKYATDLSVALNRNFNQGLYSNVAC<br>PGTALTNLTGILPPIFTLMLPAIILLRFPANAFITLTPYNGTE<br>ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE<br>KFYQKLELEKHIRVTIQTNDQARLSGSC  |
| 5989       | 194  | 2610   | AMDFPQHSQHVLEQLNQQRQLGLLDCDCTFVVDGVHFKAHKAVLA<br>ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSP<br>NVDDVL\AVATFLQMODIITACHALKSLAEPATSPGGNAEALAT<br>EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGQQAQ<br>SAASGAEQTEKADAPREPPEPVELKPDPTSGMAAAEAALESSE<br>EQEMEVEPARKGEEQKEQEEQEEGAGPAEVKEEGSQLENGEA<br>PEENENEEAGTDSGQELGSEARGLSGTYGDRTESKAYGSVH<br>KCEDCGKEFTHTGNFKRHIRIHTGKPFSCRECSKAFSDPAACK<br>AHEKTHSLPKPYGCECGKSYRLISLLNLRKRHSGEARYRCD<br>CGKLFSTSGNLKRHLVHSGEKPYQCDYCGRSFSDPTSKMRHLE<br>THDTEKHKCPHCDKFNQVGNLKAHLKIHADGPLKCRECGKQ<br>FTTSGNLKRHLRIHSGEKPYVCIHQQRQFADPGALQHRVRIHTG<br>EKPCQCVMCCKAFTQASSLIAHVROHTGKPYVCERCGRFVQS<br>SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLKSHIITHTGKPY<br>LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVS VVT<br>VDDMVTLATEALAATAVTQLTVPVPGAATADETEVLKAEISKA<br>VKQVQEEEDPNTHILYACDSCGDKFLDANSQAQHVRIHTAQALVM<br>FQTDADFYQYGGPGGTWPAGQVLAQAGELVFRPRDGAEGQPALAE<br>TSPTAPECPPPAE |
| 5990       | 2  | 4700   | FGPGPDSGGGARGSGWGSRSQAPYGTGLGAVSGGEQVLLHEEAGD<br>SGFVSLSRGLGPSLRDKLEMEELMLQDETLLGTMQSYMDASLIS<br>LIEDFGSLGEVEMSLPDPSPWDFSPPSFLETSSPKLPSWRPPRSR<br>PRWQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSIPDFP<br>MHLACPEEEDKATAEMAVPAAGDESISLSSELVRAHMPYCLPN<br>LTHLASLEDELQEQPDDLTPPEGCVVLEIVGQAATAGDDLEIPV<br>VVRQVSPGPRPVLLDSSLTSSALQLLMPTESETEAAVPKVTI<br>CSEKEGLSLNSEKLDASCLLKPREVVEPVVPKEPQNPPANAAP<br>GSQARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTVEVTS<br>QVDNLQKQPQELQKESGSPLOGKGPRAWARAWAAALENSSPN<br>LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS<br>PMFVDSVEADPTAVGPVLAGPVPVDPGLVLDLASTSELVEPLPA<br>EPVLINPVLADSAAVDPVAVPISDNLPVDAVPSPGAPVDLALV   |

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|------------|--|--|--|
|            |  |  | DPVPNDLTPVDFVLVKSRTDFRRGAVSSALGGSAPQLLVESES<br>LDPPKTI IPEVKEVVDLSLKIESGTSATTHEARPRPLSLSEYRRR<br>RQQRQAETEERSPQPTGKWPSPETPTGLADIPCLVIPPAPAK<br>KTALQRSPTPLEICLPVPGSPSPSPPEPPVSKPVASSPTEQV<br>PSQEMPLLARPPPVQSVSPAVPTPPSMSAALPFPAGGLGMPPS<br>LPPPPQQPPLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPPGY<br>CLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSTCTY<br>GPLGWGPGQHPFWSVPPPLPPASIGRAVPQPKMESRGTPA<br>GPPENVLPPLSMAPPLSLGLPGHGAPQTEPTKVEVKVPVAPSPHK<br>EKVSALVQSPQMKALACVSAEGVTVEEPASERLKPETQETPRR<br>KPPLPATKAVPTPRQSTVPKLPVAVHAPRLRLKLSFLPTPTQSS<br>DVVQAFISIEIGIEASDLSSLEQFEKSEAKKECPPPAPADSLAV<br>GNSGGVDIPQEKRLDRLQAPELANVAGLTPPATPPHQLWKLPA<br>AVSLLAKAKSPKSTAQEGTLKPEGVTEAKIIPAAVRLQEGVHGGS<br>RVHVGSGDHDYC\VRSTPPPK\MPALLIPEVGSRWNVKRQDI<br>TIKPVLSLGPAAPPPPCIAASREPLDHRTSSEQADPSAPCLAPS<br>SLLSPEASPCRNDMNTTRTPPEPSAKQSRMCRKACRSASPSSQ<br>GWQGRGRNRSVSSGSNRTSEASSSSSSSSSSSSSSSSSSSS<br>HKRWRSSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSSSSSSS<br>PSRRRSRRRRYSYRSHDHYQRQVLOKERAIEERRVVFIGK<br>IPGRMTRSELKQRFVSFEIEECTIHFVQGDNYGFVTRYAEE<br>AFAAIESGHKLQADEQPFDLFCGRRQFCRKSYSDLDSNREDF<br>DPAPVSKFDSLDFDILLKQAQKNLRR |
| 5991       | 334  | 1379   | RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTELQELGLQAR<br>DLRQHVMSITVRNNRIIMRMEYLKAVITPECLLILDYRNLNLK<br>QWLFRELPQLSGEGQLVTYPLPFEFRAIEALLQYWINTLOGKL<br>SILQPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI<br>KIFKESILEILDEEELLEELCVSKWSDPQVFEKSSAGIDHAEEM<br>ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVMM<br>RLNLQLTMTGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITGI<br>MFMGSGLIWRRLLSLFGR/LARSSIASYGMKDMVHGGIVEGL   |
| 5992       | 2  | 609  | AGPDFRLVCGVSGSGFPGRGQATENRPLRPWNGAMEKLRRVL<br>SGQDDEEQLTAQDSQINL/SEVLDASSLSENTRLKWFACFVC<br>GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFMGPVK<br>QLKMMFEATRLLATIVMLLCFIETLCAALWVHKKGLAVLFCILQ<br>FLGNTWYLSYIPYARDAVKKCCSSLS  |
| 5993       | 1650   | 594  | AEGLSWAVWAGLGNAGRHMEAGGATGALGVGCKLPFAFCFFGS<br>SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM<br>EGVPTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ<br>DLKMYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK<br>PQNLLINELGAIKLADFLARAFGVPLRTYTHEVVTLLWYRAPEI<br>LLATRFYTTAVDINSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI<br>FRMLGTPSEDTPGVQTLPDYKGSFPKWRKGLLEEIVPNLEPEG<br>RDLLMQLLQYDPSQRITAKTALAHYPFSSPEPSPAARQYVLRFR<br>RH  |
| 5994       | 394  | 1934   | AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCWTPL<br>PRPEIANQPSKPPPEVPEDLGEKVHTEGRSEPIILLPSRLPEPAGG<br>PQPGILGAVTGPRKGSRRNAGNQSYAELISQAIESAPEKRLT<br>LAQIYEMVVRTVPYFKDKGDSNSSAGWKNSIRHNSLSHSKFIKV<br>HNEATGKSSWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA<br>PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNEEADMWTT<br>FRPRSSSNASSVSTRLSPLRPESEVLAESI PASVSSYAGGVPTT<br>LNEGLELLDGLNLTSSSHLLSRSGLSGFSLQHPGVGTGPIHTYSS<br>SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD<br>PILSQAPTLLLLGLLPSSSKLATGVGLCPKPLBAPGPSSLVPTL<br>SMIAPPPVMASAPIPKALGTPVLTPTTEAASQDRMPQDLDDMY<br>MENLECDMDNIISLDMEDEGLDFNFEPDP   |
| 5995       | 2  | 2437   | RPPGPGPASGAWLCTRARGSAFVPPPLPRPPSRGARRRRRLPGR<br>GVAALRRPGSAPGLPRGRAERSAAGSGRGPSEERGAAGAAAAA<br>AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNQSL<br>CSVGSLSKKEVETPEKKQNDQRNRKRKAEPYETSQGGKTPRGHK  |

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|------------|--|--|---|
|            |  |  | ISDYFERRVEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL<br>DTEQLAQRGAGLCFTFVSAQQNSPSTGSGNTEHSCSSSQQIS I<br>QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLRANCDLR<br>RQI\DEQKMLEKYK\ERLNRCDNEPRNFLEKSKQEKMACRD<br>KSMQDRRLRLGHFTTVRHGASFTEQWTCGYAFQNLIKQQRINSQ<br>REEIERQRKMLAKRKPAMQAPPATNEQKQRKSKTNGAENETL<br>TLAEYHEQEIEFKLRLGHLKKEEAEIQAELERLERVRNLHIREL<br>KRIHNEDNSQFKDHPTLNDRYLLHLLGRGGFSEVYKAPDLTEQ<br>RYVAVKIHQLNKNWRDEKKENYHKKACREYRIHKBLDHPRIVKL<br>YDYFSLDTSFCTVLEYCEGNDLDFYLLKQHLKLMSEKARSIMQ<br>IVNALKYLNIEIKPPIHYDLKPGNILLVNGTACGEIKITDFGLS<br>KIMDDDSYNSVDGMELTSQAGTYWYLPPECFVVGKEPPKISKNS<br>VDVWSVGVIFYQCLYGRKPFPHNQSQQDILQENTILKATEVQFP<br>PKPVVTPEAKAFIRRCCLAYRKEDRIDVQQLACDPYLLPHIRKSV<br>STSSPAGAAIASTSGASNNSSN |
| 5996       | 1612   | 981  | DQOACLLGLMLTLEFGILEFDPWSWIGSWTQR/SWWSWRSRPGCE<br>LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGV<br>AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA<br>FWAFLWFTGDS CYL\ANQWQVSKPKDNPLNEGTDASPGRPSF<br>FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQ   |
| 5997       | 1612   | 981  | DQOACLLGLMLTLEFGILEFDPWSWIGSWTQR/SWWSWRSRPGCE<br>LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGV<br>AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA<br>FWAFLWFTGDS CYL\ANQWQVSKPKDNPLNEGTDASPGRPSF<br>FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQ   |
| 5998       | 1612   | 981  | DQOACLLGLMLTLEFGILEFDPWSWIGSWTQR/SWWSWRSRPGCE<br>LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGV<br>AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA<br>FWAFLWFTGDS CYL\ANQWQVSKPKDNPLNEGTDASPGRPSF<br>FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQ   |
| 5999       | 2  | 1790   | RPMPEKARRGGDGVPRGPVLHVIVVGFHHKKGCOVEFSYPLIP<br>GDGHSHTLPEEWKYLPLFALPDGAHNYQEDTVFFHLEPRNGNG<br>ATVFGISCYR\QIEAKALKVROADITRETQKSVCVLSKPLPLYG<br>LLOAKLQLI\THAYFEEDFSQISILKELYEHMNSSLGGASLEGS<br>QVYLGSLPRDLVLHFRHKGILFLKILLEKKVLFYISPVNKLVG<br>ALMTVLSLFPGMIEHGLSDCSQYRPRKMSSEDDGLQESNCPADD<br>FVSASTADVSHNTLGTIRKVMAGNHGEDAAMKTEEPFQVEDSS<br>KQGEPNNTNQYLPKPSRPSPSSESDWETLDPVLEDPNLKERE<br>QLGSDQTNLPFKDSVPSESLPITVQPPQANTGQVVLIPGLISGLE<br>EDQYGMPLAIFTKGYLCLPYMALQOHHLLSDVTVRGFVAGATNI<br>LFRQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFDY<br>VRHVTENRDDVFLDGTGWEGDEWIRAQFAVYIHALLAATLQLV<br>LFRIVNVAKKIGNVMVT\SRNVVQTGK\AVGQSVGGAFS\SAK<br>TA\MSWLSLTFSTSTSSQSLTEPPDEKP  |
| 6000       | 101  | 1561   | TEPCRTAENCTATMSENNKNLSLESSLRQLKCHFTWNLMEGENSL<br>DDFEDKVYFRTFQNRFPKATMCNLLAYLKLKLGQNEAALECLR<br>KABELIQEHADQAEIRSLVTWGNAYWVYHMGRLSDVQIYVDK<br>VRHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK<br>ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD<br>NQYLVLLALKLHKMREEEGEEGEGEK\LVVEALEKAPG\VTDV<br>LRSAA\KFYRGKDEPDKAIELLKALEYIP\NNAYLHCQIGCCY<br>RAKVQVMNLRBNMGYKRLLELIGHAVHLKKADEANDNLF<br>VCSILASLHALADQYEDAEYFYQKEFSKELTPVAKQLLHLRYGN<br>FOLYQMKCEDKAIHHFIEGVKINQKSREKEMKDKLQKIAKMR<br>SKNGADSEALHVLAFLOQLNEKMQQADEDSERGLSGSLIPSAS<br>SWNGE   |
| 6001       | 176  | 1038   | AFHSPSRGRHRTHTIHTPRHTPRCTMAESHLQSSSLITASQFEEI<br>WLHFDADGSGYLEGKELQNLQELQQARKKAGLELSPMKTFVD<br>YQGORDDGKIGIVELAHVLPTEENFLLFRCCQLKSC\EFMKT<br>WRKYDTHSGFIEEELKNFLKDLLEKANKTVDDTKLAEYTDLM   |

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|------------|--|--|--|
|            |  |  | LKLFDSNNNDGKLELTEMARLLPVQENFLLKFQGIKMGKEFNKA<br>FELYDQDNGYIDENELDALLKDLCEKNKQDLINNITTYKKNIM<br>MALSDGGKLVRTDLALILCAGDN   |
| 6002       | 977  | 81   | LAPPGGGLHIPPRTPLSHSRPPFSSHAPHSPPLPLPPADLHPHS<br>SMAQRSDLLLELDCQLTRDRVVVSHDENLCRQSGLNDRDVGSLDF<br>EDLPLYKEKLEVFYSPGHFAHGSRRMRVLEDFQRFPRTPMSV<br>EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKCKKAANP<br>EMPLSFTISRGFVLLSYLGLLPFIPIPEKFFCFPLNIINRT<br>YFPFSCSCLNQLLAVVSKWLMRKSLIRHLEERGQVQVFWCLNE<br>ESDFEAAFSVGATGVITDYPALRHYLDNHGPAARTS  |
| 6003       | 140  | 4098   | GKLRAFRGMRRLLICKRICDYKSFDDDEESVDGNRPSSAASAFKVP<br>APKTSNGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA<br>FTDVPSIQIYSSRELEETLNKIREILSDDKHWDQORANALKKIR<br>SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVREACITVA<br>HLSTVLGNKFDHGAEAIPTLFNLVPNSAKVMATSGCAAIRFII<br>RHTHVPRLIPLITSNCTSKSVVRRRSFEFLDLLQEWQTHSLE<br>RHA AVL VETIKKGIHDADA EARVEARKTYMGLRNHFPGEAETLY<br>NSLEPSYQKSLQTYLKSSGVSASLPQSDRSSSSSQESLNRPFSS<br>KNSTANPSTVAGRVSGSSKASSLPQSLQRSRSDIDVNAAGAK<br>AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV<br>RAKLSAPLAGMGNADSRGRSRTKMVSQSQPGSRSGSPGRVLT<br>TTALSTVSSGVQRLVNSASAQKRSKIPRSQGCSEASPSRLSV<br>ARSSRI PRPSVSGQCSREASRESSRDTSPVRSFQPLASRHHSRS<br>TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLTGSDVEEA<br>VADALLLGDIRTKKKPARRRYESYGMHSDDDANS DASSAC SERS<br>YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGGLGLQN<br>LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI<br>QVHKDDLQDWLFVLLTQLLKKMGADLLGVSQAKVQKALDVTRES<br>FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD<br>FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFEINTPE<br>FTMLLGLALPKTFQDGATKLLHNHLRNTGNTQSSMSGSPLTRPTP<br>RSPANWSSPLTSPNTSQTLSPSAFDYDTENMNSEDIYSSLRG<br>VTEAIQNFSSFRSQEDMNEPLKRDSSKDDGDSMCGGPG\MSDPRA<br>GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPNYSDSIS<br>PFNKSALEAMFDDADOFDDLSLDHSDLVABLLKFI-SNHNER<br>VEERKIALYELMKLTQEEFSVWDEHFKTILLLLETLGDKE?T<br>IRALALKVLEIRLHQPARFKNYAELTMKTLAHDKDPHKEVVR<br>SAEEAAV\LATSI\SPEQCIKVLCP\IIQTADYPINLAAIKMQT<br>XVIERVSKETLNLPLPEIMPGLIQGYDNSESSVRKACVFCLVAV<br>HAVIGDELKPHLSQLTGSKMMLNLYIKRAQTGSGGADPTDVS<br>GQS |
| 6004       | 140  | 4098   | GKLRAFRGMRRLLICKRICDYKSFDDDEESVDGNRPSSAASAFKVP<br>APKTSNGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA<br>FTDVPSIQIYSSRELEETLNKIREILSDDKHWDQORANALKKIR<br>SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVREACITVA<br>HLSTVLGNKFDHGAEAIPTLFNLVPNSAKVMATSGCAAIRFII<br>RHTHVPRLIPLITSNCTSKSVVRRRSFEFLDLLQEWQTHSLE<br>RHA AVL VETIKKGIHDADA EARVEARKTYMGLRNHFPGEAETLY<br>NSLEPSYQKSLQTYLKSSGVSASLPQSDRSSSSSQESLNRPFSS<br>KNSTANPSTVAGRVSGSSKASSLPQSLQRSRSDIDVNAAGAK<br>AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV<br>RAKLSAPLAGMGNADSRGRSRTKMVSQSQPGSRSGSPGRVLT<br>TTALSTVSSGVQRLVNSASAQKRSKIPRSQGCSEASPSRLSV<br>ARSSRI PRPSVSGQCSREASRESSRDTSPVRSFQPLASRHHSRS<br>TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLTGSDVEEA<br>VADALLLGDIRTKKKPARRRYESYGMHSDDDANS DASSAC SERS<br>YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGGLGLQN<br>LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI<br>QVHKDDLQDWLFVLLTQLLKKMGADLLGVSQAKVQKALDVTRES<br>FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD<br>FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFEINTPE   |

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|------------|--|--|---|
|            |  |  | FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP<br>RSPANWSSPLTSPNTSQTNTLSPSAFDYDTENMNSEDIYSSLRG<br>VTEAICNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA<br>GGDATDSSQTAL\DNKASLLHSMPTHTSSPRSDYNPYNYSDSIS<br>PFNKALKEAMFDDADQFPDDLSDHSDLVAEELLKELSNHNER<br>VEERKIALYELMKLTQEEFSFVWDEHFKTILLLLLLETLGJKEPT<br>IRALALKVLRILRHQPARFKNYAELTVNKTLEAHKDPHKEVVR<br>SAEEAASV\LATSI\SPEQCIKVLCPPIQTADYPINLAAIKMQT<br>KVIERSKETLNLPLPEIMPGLIQGYDSESVRKACVFLVAV<br>HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDS<br>GQS  |
| 6005       | 133  | 5955   | RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEDMDALL<br>NNSLPPPPHNEEDPEEDLSETETPKLKKKKPKKPRDPKPKS<br>KRQKERMMLCRQLGDSGEGPEFVEEEBEVALRSDSEGSYTP<br>GKKKKKLGPKKEKKS KRKEEEEDDDDDDSKEPKSSAQLL<br>BDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS<br>KMMVLGAKWREFSTNNPFGSSGASVAAAAA AVVESMVT<br>TEVAPPPPPVEVPIRAKTKEGKOPNARRKPKGSPRVDAKKPK<br>PKKVAPLKI KLGGFGSKRRSSSEDDDLDESDFDDASINSYSV<br>SDGSTSRSSSRKKLRTTKKKKKGEEVTAVDGYETDHQDYCEV<br>CQQGGEIILCDTCPRAYHMCVLDPMDEKAPGKWSCHCEKEGI<br>QWEAKEDNSEGEEILBEVGGDLREEDDHMEFCRVCKDGGELLC<br>CDTCSSYHIIHCLNPLPEIPNGEWLCPRCTCPALGKVKQKILI<br>WKWQPPSPPTPVPRPPDADPNTSPKPLEGRPERQFFVKWQMS<br>YHCSWVSELQLELHC\QVMFRNYQRKNDMEPPSGDFGGDEBK<br>S\RRRKNKDPKFAEMEERFPRYGIKPEW\MMIHRILNHSVDKKG<br>HVHYLIKWRDLPYDQASWESEDEVIQDYDLFKQSYWNHRELMRG<br>ERGRPGKLLKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG<br>TLHPYQMEGLNWLRFSAWQGTDTILADEMLGKTQVAVFLYSL<br>YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGD<br>DSRAIIRENEFS\FEDNAIRGGKASRMKEASVKFHVLLTSYE<br>LITIDMAILGSDWACLIVDEAHLKNNQSKFFRVNLNGYSLQHK<br>LLLTGTPLQNNLEELFHLNFLTPTFRFHNLEGFLEEFADIAED<br>QIKKLHDMLG\PHMLRRKADVFKNMPSKTELIV\RVLSPM/Q<br>KYYK\YILHSKFLKALN\ARGGGNQVSLNNVMDLKKCCNHPY<br>LFFVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH<br>RVLIFSQMTKMLDLEDLEHEGYKYERIDGGITGNMRQEAIDR<br>FNAPGAQQCFLLSTRAGGLGINLATADTVIIYDSWNPHNDIQ<br>AFSRAHRIGONKKVMIYRFVTRASVEERITQVAKKMMMLTHLVV<br>RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGED<br>SSVIHYDDKAIERLLDRNQDETEDELQGMNBYLSSFKVAQYVV<br>REEEMGEEEVEREIIKQEEVDPDYWEKLLRHHYEQQEDLAR<br>NLGKGRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE<br>DFDERSEAPRRPSRKGLRNDKDKPLPLLARVGGNIEVLGFNAR<br>QRKAFLNAIMRYGMPPODAFTQWLVRDLRGKSEKEFKAYVSLF<br>MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ<br>EFEHVNGRWSMPELAEVEENKMSQFGSPSPKPTPTSTPGDTQP<br>NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT<br>QAPAPASEDEKVVEPEGEKEKVEAEVKERTEPEMETEPKGGK<br>AADVEKVEEKSAIDLTPIVVEDKEEKEEKEEKEVMLQNGETPK<br>DLNDEKQKKNIKQRFMENIADGGFTLHSLWQNEERAATVTKKT<br>YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFGKEM<br>NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSDDPSH<br>PSMALNTRFAVECLAESHQHLKESMAGNKPANAVLHKVLKQL<br>EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRANRAP<br>EPTPOQVAQQQ |
| 6006       | 1  | 965  | DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVDKPSIPVHPC<br>GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAUVS<br>ERIHEQVRDRQLEKEYVCRVEGEFPTEVTCKEPILVVSYKGVG<br>CRVDPRGKPCETVFQRLSYNGQSSVRCRPLTGRTHQIRVHLQF<br>LGHPILNDPIYNSVAVGSPSRGRGGYIPKTNEELLRLDLVAEHQAK  |



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|------------|--|--|--|
|            |  |  | QSLDVLDLCEGDLSPGLTDSAPSSSELGKDDLEELAAAA\QKME<br>EVAEAPQELDTIALASEKAVETDVMNQ\ROQT\TLCRVPAGATG<br>SLAPRPCDVPTCPTL  |
| 6007       | 3  | 2351   | HELQVEVVFDTKTGTLENEMQFRECSINGKHYQEIINGRLVPE<br>GPTPDSSEGNLSYLSLSHLNNLSHLTSSSFRTSPENETELIK<br>EHDLFPAVSLCHTVQINNVDCTGDPWQSNLAPSOLEYYAS<br>SPDEKALVEAARIGIVFIGNSEETMEVKTLGKLERYLKLLHILE<br>FDSRRRMSVIVQAPSSEKLLFAKGAESSILPKCIGGETEKTTRI<br>HVDEFALKGLRTLCAIYRKFTSKEYEEDKRTFEARTALQOR\B<br>EKLAAVFPQIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKV<br>WVLTGDKHETAVSVLSLSCGHFRTMNIILELINQKSDSECAEQLR<br>QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV<br>LCCRMAPLQKAKVIRLIKISPEKPIITLAVGDGANDVSMIQEAHV<br>GIGIMGEGRAARNSDYAIARFKFLSKLLFVHGHHFYIIRIATL<br>VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTL\NICFT<br>SLPILYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT<br>ILGFSAHAFIPFFGSYLLIGKDTSLGNGQMFNGNWTFTLVFTVM<br>VITVTVMALETHFWTWINHLVWGSIIIFYFVSLFVGGLWPP<br>LGSQNMVVFVLIQLSSGSAAWFAIILMVVTCFLDIKKVFDRLH<br>HPTSTEKALQTLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI<br>GRCSPTHSRSWSASDPFYTNDRSILTLSTMDSSTC   |
| 6008       | 4554   | 1089   | AGVRRAGARRGPGRALPAGATAVPPPSARRRRRCPEAHAGPAR<br>ASRPSQETMFQLPVNNLGLSLRKARKTVKKILSDIGLEYCKEHIE<br>DFKQEPNDFYLNKTTWEDVGLWDPSTLTKNQDYRTKPFCCSACP<br>FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH<br>IKIFHAPNASAPSSSLSTFKDKNKNQDGLKPKQADSVEQAVYYCK<br>KCTYRDPLEYEIVRKHIYREHFQHVAAPIYAKAGEKSLNGAVPLG<br>SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG<br>HTNVVVPKSLPLMLIAPKPDKKSMLPPRIGSLASGNV\RLSP<br>SQQMVNRLSIPKPNLSTGVNMSSVHLQNNYGVKSVGGQYSV<br>GQSMRLGLGNAPVSIPOQSQSVKQLLPSGNGRSYGLGSEQRSG<br>APARYSLQSANASSLSGQLKSPSLSQSQASRVLGQSSSKPAAA<br>ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFKEHKAKEKVP<br>AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHLIHLGLSCPYCRS<br>TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQGSHTNIH<br>LLVTTYNLRLDAPAESVAYHAQNPPVPPKPKQVQEKADIPVKS<br>SPQAAVPYKDKVGTLCPLCFSILKGPISDALAHHLRERHQVIO<br>TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN<br>GQDKTNAPSRNLQSPSLAPVKTVEQMEFLLKRRKLDSDSDSP<br>SPFEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPY<br>TRREIEKLAASLWV\WK\SDIASHFNSKRKKVRDCEKYKPGVL<br>LGFNMKELNKKVHENDF\AEGLFENHDEKDSRVNASKTADKKLN<br>LGKEDDSSDSFENLEESNESGSPFPDVFVEPEPKISNDNPEEH<br>VLKVIPEDASESEKLDQKEDGSKYETIHLTEPTKLMHNASDS<br>EVDQDDVVEWKDGASPSSEGPSQVSDFDNTCEMKPGTWSDE<br>SSQSEARSSKPAKKKATMQGDREQLKWNSSYGVKVEGFWSKD<br>QSQW\NASENDERLSNPQIEWQNSTIDSDEGEQFDMNTDGAEP<br>MHGSLAGVKLSQQA |
| 6009       | 4272   | 1534   | CHGLQHLTPFRENLNLSLQ*EPH*AA*QAVRSEKSI*GSPSC<br>HLVLGLVLPVARQSSHSAGPAQSAFR*TGTSGETPKAAEQSGYW<br>EAYTLGHQHWMPPIQRPLVMKRRIMCGKCEK*VSDSVTGG<br>RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL<br>NGKRGGCFESGYLFGFIVIGKIQSLKAVLPVNGQTGERASPG<br>NCRIHIVDAVC*SEHH*DHFLAAFLNSTIIS*VAPGSWQDHA<br>VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL<br>FVLAPQDGEVFFVEGQLVTVLGLVVPQSIHRTFVHTQLFLHP<br>I*KLGAADVAFHLHLLTVCSSEFNAYG*GKNGGTTLHQLFAEVN<br>AVTRGSVQRRPSITISSIHVDTKIQQLHDVVMVAGADGVVQWG<br>DPFVVLGAGIFHLIDDPLHQIELSFQRRV*EQCGVKPDSQVVP<br>PLRVGLLQVGPLVRGGRRVAGRGKRCWRDLFPWRWGLSHRT<br>RDLLRGDRGHVVIVLCRLGSLVGGTDELLWFGGR*LIIG   |

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|------------|--|--|--|
|            |  |  | I*RGRLSGEWGCGLGRGELFQVSIIGVSIHIGQGDHEVLGG<br>AGLVERGALHATGGQVEALVQQLLDVGPAGALGLCDGAALFQGP<br>GRVGQLPAEGLQVCITLVAQWRMHGRELGGAEWPQALHGAAI<br>CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRWRG*TR<br>R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLLEVHGVYGT*IHCL<br>GSFPGRLLWP*PFISQERPNGHCQWEFRLAVPSWKCRRSRWRVRG<br>TWRYGNPLNLL*GAWLGGACGGQGGPLSTWQACTGPGQAAP<br>LPPFQACRPRTRQRCRTWVCPIAWRQLLAYTRD   |
| 6010       | 1  | 3533   | IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM<br>AGISQNAKTGDLPAFGCECVGIASKALCGLTEAAAQAAVLVGI<br>PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA<br>TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL<br>VKTIKALDGDPSFEDNRNKCRIATAPLIEAVENLTAFASNPEFVS<br>IPAQISSBGSQAQEPILVSAKPMLESSSYLIRTARSLAINRDP<br>PTWSVLGHSHTVSDSIKSLITSIRDKAPGGRECDYSIDGINRC<br>IRDIEQASLAAVSQSLATRDDISVEALQEQLTSSVVOEIGHLIDP<br>IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM<br>TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK<br>EAVDDIMVTINFAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG<br>TFVDYQTTVVVKYSKAIATAQEMMTKSVTNPBELGGLASQMTSD<br>YGLAFQGMMAAATAEPEEIGFQIRTRVQDLGHGCI FLVQKAG\  |
| 6011       | 446  | 1835   | ALQVCPTDSYTKRELIECARAVTEKVS LVL SALQAGNKGTOACI<br>TAATAVSGIIADLDTTIFATAGTLNAENSETFADHRENILKTA<br>KALVEDTKLLVSGAASTPDKLAQAQSSAATITOLAENVVLGSA<br>SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM<br>YQLKGAAKVMVTNVTSLKTVKAVEDEATHGTRALEATIBCIKQ<br>ELTVFQSKDVPKTSPPBESIRMTKGITMATAKAVAAGNSCRQE<br>DVIATANLSRKAVSDMLTACKQASFPDVSDEVTRALRFGTETC<br>TLGYLDLLEHVLVILQKPTPELKQQLAAAFSKRVAGAVTELIQAA<br>EAMKGTWVDPEDPTVIAETELIGAAASIEAAKKLEQLKPRAK<br>PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGG<br>VGSIPANAADDGQWSQGLISAARMVAAATSSCEAANASVQGH<br>SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV<br>KRASDNLVRAAQKAAFGKADDDDVVVKTFVGGIAQIIAAQEE<br>LKKERELBEEARKKLAQIRQQYKFLPTELREDEG   |
| 6012       | 351  | 5013   | LLQAPAMRKSPGLSDCLWAWILLSTLTGRSYGQPSLQDELKNDT<br>TVFTRILDRLLDGYDNRLRPLGERVTEVKTDIFVTSFGVPVSDH<br>DMEYTTIDVFRQSWKDERLKFKGPMTVLRLNNLMASKIWPDTF<br>FHNGKKSVAHNMTPNKLRLITEDGTLTYMRLTVR\AECPMF<br>GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTRPARSVVVAED<br>GSRLNQYDLGQTVDSGIVQSSSTGEYVVMTHFHLKRIKGYFVI<br>QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTLISIS<br>ARNSLPKVAYATAMDWFIACVYAFVFSALIEFATVNYFTKRGYA<br>WDGKSVVPEKPKVKDPLIKKNNTYAPTATSYTPNLARGDPGLA<br>TIAKSATIEPEVKPKETKPPPKTFNSVSKIDRLSRIAPPLLF<br>GIFNLVYWATYLNREPQLKAPTPHQ<br>PAELFQSFAIWHKELYDWRLGPWNOCOPVISKSLEKPLECTKGE<br>EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQAQLIPCOQD<br>CIVSEFSAWSECSKTCGSLQHRTRHVVPQFGGSGCPNLTEF<br>QVCQSSPCEAEELRYS LHVGPWSTCSMPHSRQVRQARRRGKNKE<br>REKDRSKGVKDPAREELIKKRNRRNRQNRQENKYWDIQIGYQTR<br>EVMCINKTGKAADLSFCQKEKLPMTFQSCVITKECQVSEWSEWS<br>PCSKTCHDMVSPAGTRVTRTRIROPPIGSEKECEPEFEEKEPCLS<br>QODGVVPCATYGWRTTEWTECRVDPILLSQDQKRRGNQ TALCGGG<br>IQTREVVYCVQANENLLSQLSTHKNEASKPMDLKLTGPIPNNT<br>QLCHIPCPTCEVSPWSAWGPCTYENCNDQGGKGFKLKRRRIT<br>NEPTGGSGVTGNCPHLEAIPCEEPAICYDWKAVRLGDCEPDNGK<br>ECGPCTQVQEVVCINSDEGEVDRLCRDAIFPIPVACDAPCPKD<br>CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP<br>NSSALQEVRS CNEHPCTVYHWQTGPWGGQCIEDTSVSSFNNTTTT<br>NGEASCSVGMQTRKVICVRVNVGVQVGPKKCPESLRPETVRPCLL |

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|------------|--|--|--|
|            |  |  | PCKKDCIVTPYSDWTSCTSPS\SCREGDSSIRKQSRHRVIIQLPAN<br>GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS<br>VQDQSP\GAQEGCGPGRQARAITCRKQDGGQAGIHCECLQYAGPV<br>PALTQACQIPQDDCQLTSWSKFSSCNGDCGAVRTRKRTLGVGKS<br>KKKEKCKNSHLYPLIETQYCPCKDYNAQPVGNWSDCILPEGKVE<br>VLLGMKVQGDIKECGQGYRQAMACYDQNGRLVETSRNSHGYI<br>EEACIIPCPSDCKLSEWSNWSRCSKSCSGSVKVRKWLREKPYN<br>GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV<br>NMRENCGEVQTRKVRMONTADGPSEHVEDYLCDEEMPLGSR<br>VCKLPCPEDCVISEWGPWTQCVLPNCQSSFRQRSADPIRQPADE<br>GRSCPNAVEKEPCNLNKNCHYDYNVTDWSTCQLSEKAVCGNGI<br>KTRMLDCVRS DGSKVDLKYCEALGLEKNWQNTSCMVECPVNCQ<br>LSWSPWSECSQTCGLTGKMRRTVTQPFQDGRPCPSLMDQS<br>KPCPVKPCYRWQYQGWSPCQVQEAQCCEGTRTRNISCVVSDGSA<br>DDFSKVVDREFCADIBLIIDGNKNMVLBEESCSQPCPGCYLKDWS<br>SSWSLCQLTCVNGEDLFGGCIQVRSRPVIIQELNQHLCPEQML<br>ETKSCYDQCCEYKWMASAWKSSRTVWCQRSDGINVTGGCLVM<br>SQPDADRSCNPPCSQPHSYCSBTKTCHCEEGYTEVMSSNSTLEQ<br>CTLIPVVVLPMTMEDKRGDVKTSRAVHPTQPSNPAGRGRTWFLQ<br>PFGPDGRLKTVVGYGAAGAFVLLIFIVSMIYLACKPKPKPQRQ<br>NNRLKPLTLAYDGDADM |
| 6013       | 1161   | 710  | GAFIAGVPVQPVLIIRYPNSLDTTSAWVRGPGVLKVLWTASQPC<br>SIVDVEFLPVYHSPSESRDPTLYANNVQRVMAQALGIPATECE<br>FVGSPLPVIVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR<br>ARPESNDQPGRVCAATAL  |
| 6014       | 2857   | 613  | EA VAGGMEKSRMNLKPGPDTLCFDKDEFMKEDFDVDHVFVSDCRK<br>RVQLEELRDDLELYKLLKTAMVELINKDYADF\VNLSNVLVGM<br>DKALNQLSVPLGQLREBVLRLSSVSEGI RAVDERMSKOEDIRK<br>KMCVLRLLIQVIRSVKEIEKILNSQSSKETSALASSPLLTGQI<br>LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE<br>GLLLEGLQTSDDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI<br>DEVIIIEQFVESHNPGLQVMYNKLEFVPHHCRLLREVTTGGAISS<br>EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAPHEKY<br>TISMDFVRRLERQCGSSQASVKRLRAHPAYHSFNKKWNLVVFQI<br>RPREIAGSLAALTUVLEDAPAESPYCLASHRTWSSLRRCWSD<br>EMFLPLLHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPK<br>IKKPLVTGSKEPSITQGNTEQDQSGSPSETKPVVSISRTQLVYV<br>ADLDKLEQLPELLEIIKPKLEMIGFKNFSSISAALEDSSQSSFS<br>ACVPSLSSKIIQDLSDCFCGFLKSALEVPRLYRRTNKEVPTTAS<br>SYVDSALKPLFQLQSGHKDKLQAI IQQWLEGLTSESTHKYYET<br>VSDVLNSVKKMEESLRLKQARKTTPANPVGPSGGMSDDDKIRL<br>QLALDVEYLGEOIQKLGLOASDIKSFSAALAEVAAAKDQATAEQ<br>P   |
| 6015       | 13   | 2237   | ABGCAERRGTEPVVELSMSWESGAGPGLGSGQMDLVWSAWYKGC<br>VKGKGSPLSAHGIVVAWLSRAEWDQVTVYLFCDHKLQRYALN<br>RITVWRSRSGNELPLAVASTADLIRCKLDDVTGGGLTDELRLLY<br>GMALVRVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT<br>HKKMPHINDCRRGCYFVLDWLQKTYWCRLQENSLRETWELEEF<br>EGIEEEDQEEEDKNIVDDITEQKPEPQDDGKSTESDVKADGDSK<br>GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP<br>KAIAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT<br>FEQLAALQIEYEENVLDNDVLVLPKPFQFQWQPLRLGLHSQNFQ<br>ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARR<br>SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPOLLRII<br>F\KAMGQGLQDE\EQEKLRLICSIYTQSGENSLVQEGSEASPIG<br>KSPYTLDSLYWSVKPASSSFGSEAKAQOQEEQGSVNDVKEEKE<br>EKEVLDPQVEEENDDQEEEEEDEDEDEDEEDRMEVGFSTG<br>QESPTAENARLLAQKRGALQGSANQVSSSEDVRWDTFP\LGRMPR<br>SRPRTPAELMLENYDTHVIFWTKPV\EQRLEPSTCK\TDTLGL<br>\SCGVGS\GNCNSSSSNFRGAPLLEARGSLH\GL\KTGLQLF  |
| 6016       | 13   | 2237   | ABGCAERRGTEPVVELSMSWESGAGPGLGSGQMDLVWSAWYKGC   |

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|------------|--|--|---|
|            |  |  | VKGKGS LPLSAHGIVVAVLSRAEWDQVTVVYLPCCDDHKLQRYALN<br>RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY<br>GMALVRFVNLISERKTKFAKVPKCLAEVNIPODWIVDLRHET<br>HKMPFINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEF<br>EGIEEDQEEDKNIVVDITEQKPEPQDDGKSTESDVKAQDGSK<br>GSEEVDSHCKKALSHKELYBRARELLVSYEZEQFTVLEKFRYLP<br>KAIAKANNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT<br>FEQLAALQIEYEENVLDNDLVLPKPFQFWQPLLRLGLHSQNFQ<br>ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARR<br>SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASQQLRII<br>F\KAMGQGLQDE\BQEKLLRICSIYTQSGENSLVOEGSEASPIG<br>KSPYTLDSLYSVKPASSFGSEAKAQQEEQGSVNDVKEEKE<br>RKEVLDPQVEEEENDDOEEDDEDEDEDEDRMEVGPFSFG<br>QESPTAENARLLAQKRGALQSSAQVSSDEVWDTFP\LGRMPR<br>SRPRTPAELMLENYDTHVIFWTKPVL\EQRLPESTCK\TDTLGL<br>\SCGVGS\GNCSSSSSNFRGAFLEARGSLH\GL\KTGLQLF  |
| 6017       | 203  | 3469   | SHQETEQNSAMAPRKRGGGSGISFIFCCFRNNDHPEITYRLRND<br>NFALQTMEPALPMPPVEELDMFSELVDELDLTDKHEAMFALP<br>AEKKWQIYCSKKKQDENKGATSWPEFYIDQLNSMAARKSLAL<br>EKEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLK<br>TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLASHSINVIAQ<br>SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER<br>TRFQTLINDLDXSTGRYRDEVSLKTAIMSFINAVLSQAGAVESL<br>DFRLHLRYE\FMLGIHPVMDKLRKHENSTLDRHLDPFPEMLRNE<br>DELEFAKRFELVHIDTKSATQMFELTRKRLTHSEAYPHFMSILH<br>HCLQMPYKRSNGTVQYWLLDRIIQQIVIQNDKGQDPDSTPEN<br>FNINNVVRLMVNEVVKQWKEQAKMRKEHNELOQKLEKKEREC<br>DAKTQEKEMMQTLNKKMEKLEKETTEHKQVQVQVADLTAQLHE<br>LSRAVACASIPGGPSPGAPGGPFPSSVPGSLLPPPPPPPLPGGM<br>LPFPPLPLPGGPPPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ<br>PTNALKSFNWSKLPEKLEGTVMTEIDDTKVFKILDLEDLERTF<br>SAYQRQDDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRR<br>QNCNILLRSLKLSNDEIKRAILTMDEQEDLPKDMLEQLKFVPE<br>KSIDIDLEEKKHELDMAKADRFLFEMSRINHYQQRQLQSLYFKK<br>KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNMYN<br>KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP<br>SVNLNNEELRDIPQAAKVMTELDKEISTLRSGLKAVETELEYQ<br>KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV<br>KHFGFEAGKIQPDFFGIFDQFLQAVSEAKQENENMRKKKEEE<br>RRARMEAQLKEQREERERKMRKAKENSEESGEFDDLVSAALRSGEV<br>FDKDL SKLKRNRKRITNQMTDSSRERPI TKLNF |
| 6018       | 13   | 2510   | TISQSGGIRRRREAVWFVNNMDFSRLLHMYSPPOCVFENTGYTY<br>ALSSSYSSDALDFETEHKLDVPVDSPRMSRRSLRLATTACTLGD<br>GEAVGADSGTSSAVSLKNRAARTTKORRSTNKSASFVSNHVSQV<br>TSAGVSYGGTVSLQDAVTRRPPVLDESIREQTTVDHFWGLDDD<br>GDLKGNKAAIQGNGDVGAGAATGHNGFFCSNCLMSERKDVLT<br>AHPAAGPVSrvysRDRNQKDDCKGKRHLDAHPRAGTLWHIN<br>ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF<br>WNLGIGWYQFVTLSISLNVFLTRCLRNICKFLVLLIPLFLLLG<br>LSLRGQG\NEFFSPLPVLNWSMHRTOQVDDPDQVFKPTTSRLKQ<br>PLQGDSEAFPMHWSGVEQQVASLSGQCHHHGENLRELTLLQK<br>LQARVDQMEGGAAGPSASVRDAVGOPPRETDFMAHQEHEVRMS<br>HLEDILGKLEKSEAIQKELEQTQKTI SAVGEQLLPTVEHLQL<br>ELDQLKSELSSWRHVKTGCETVDAVQERVVDVQVREVMKLLFS<br>QGGSLQQLQRFSSQFVSKGDLQTLMLDLQLILRNVTTHVSV<br>TKQLPTSEAVVS AVSEAGASGITEAQARAIVNSALKLYSQDKTG<br>MVDFALESGGGGILSTRCSETYETKTALMSLFGIPLWYFSQSPR<br>VVIQPDIIYPGNCWAFKGSQGYLVRLSMHIHPAFTLEHPIKTL<br>SPTGNISSAPKDFAVYGLFNEYQREGQLLGQFTVDQDQESLQMF<br>QALKRPDDTA FQIVELRIFSNWGHPEYTCLYRFRVHGEPPV<br>K  |
| 6019       | 2  | 1066   | TPNDREPPFPQRPSSRRASHLAQBITSAASLGDTQILGSLTTA   |

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|------------|--|--|---|
|            |  |  | PVITSAIRSMFGISSQILTNAGQVIGTLPWVNSASVAAPAPA QSLQVQAVTPQLLNAGQVIATLASSPLPPVAVRK\PTSPES LLKSEVQPIKPTPTVPQPAVVIASPAAPAKPSASAPIITCSET PTVSQLVSKPHTPSLDEEDGINLEEIREFAKNFKIRRLSLGLTQT QVQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN EABLNRQEQQLMEFVGGEPSSKKRRRTSFTPAIEALNAYFE KNPLPTGQEITEIAKELNYDREVVRVWFVFNRRQTLKNTSKLNVF QIP  |
| 6020       | 4953   | 549  | <p>             EAIQFEVSIIGNYGKFDTTCKPLASTTQYSRAVFDGNYYYLFW<br/>             AHTKPVVTLTSYWEDISHRLDAVNLTLLAMAERLQTNIEALKSGI<br/>             QGKIPANQLAELWLKLIIDEVIEDTRYTLPLTEGKANVTVLDTQI<br/>             RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE<br/>             EPQNSMPDIIIMIRGEKRLAYARIPAHQVLYSTSGENASGKYC<br/>             GKTQTI FLKYPQEKNNGPVKPVVELRVNIWLGLSAVEKKFNSFAE<br/>             GTFTVFAEMYENQALMFGKWTSGLVGRHKFSQVDTGKI KLKREF<br/>             FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP<br/>             GGDWKPADTYTDANGDKAASPSELTCPGWEWEDDAWSYDINR<br/>             AVDEKGWEYGITIPPDHKKPSWVAEKMYHTRRRRLVRKRKDD<br/>             LTQTASSTAGAMEELQDQEGWEYASLIGWKFWKQSSDTFRRR<br/>             RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQKHA<br/>             TTVFGANTPIVSCNFDRDYIYHLRCVYQARNLLALDKDSFSDP<br/>             YAHICFLHRSKTTEIIHSTLNPWDQTIIFDEVEIYGEPTVLQ<br/>             NPPKVI MELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW<br/>             HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP<br/>             QGIRPVVQLTAIEILANGLRNMKNFQMASITSPSLVVECGGERV<br/>             ESUVIKNLKKTNPFPSSVLFMKVFLPKKELYMPLVIKVIDHRQ<br/>             FGRKPVVQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR<br/>             DIVIEMEDTKPLASKCLSSMSTALSKMASPATVHLTEKEEIV<br/>             DWWSKFYASSGEHEKCGYIQGYSKLKIYNCELENVAEPEGLT<br/>             DFDSTFKLYRGKSDENEDPSVVGEPKGSFRIYPLPDDPSVPAPP<br/>             RQPRELPDSVPQECTVRIYIVRGLELQPDNGLCDPYIKITLG<br/>             KKVIE\DRDHYIPNTLNPVFGRMYSCLYPQEKDLKISVYDWD<br/>             TFTRDEKVGETIIDLNP\LSRFG\SHCG\IPEEYCVSGVNTW<br/>             RDSLR\PTQ\LLQNVARFKGFPQPILEDGSSRIRYGRDYSLDE<br/>             FEANKILHQLGAPEERLALHILRTQGLVPEHVETRLHSTFQP<br/>             NIS\RYLRLVIWNTKDVLDEKSITGEEMSDIYVKGWIPGNE<br/>             NKQKTDVHYRSLDGEENFNWRFVFPFDYLPALQCLIVAKKEHFW<br/>             SIDQTEFRIPPR\LIQIW\DNDFKS\LDYLGFPRTLTCRHTI<br/>             HFLQKSPGGNC/RGLDMIPLDKAMNPLKAKTASLFEQKSMKGW<br/>             PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP<br/>             KLDLPNRPETSLWFTNPKCTMKFIVWRRFKWVIIGLLFLILL<br/>             LFAVALLYSPLNYSMLKIVKPNV           </p> |
| 6021       | 4953   | 549  | <p>             EAIQFEVSIIGNYGKFDTTCKPLASTTQYSRAVFDGNYYYLFW<br/>             AHTKPVVTLTSYWEDISHRLDAVNLTLLAMAERLQTNIEALKSGI<br/>             QGKIPANQLAELWLKLIIDEVIEDTRYTLPLTEGKANVTVLDTQI<br/>             RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE<br/>             EPQNSMPDIIIMIRGEKRLAYARIPAHQVLYSTSGENASGKYC<br/>             GKTQTI FLKYPQEKNNGPVKPVVELRVNIWLGLSAVEKKFNSFAE<br/>             GTFTVFAEMYENQALMFGKWTSGLVGRHKFSQVDTGKI KLKREF<br/>             FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP<br/>             GGDWKPADTYTDANGDKAASPSELTCPGWEWEDDAWSYDINR<br/>             AVDEKGWEYGITIPPDHKKPSWVAEKMYHTRRRRLVRKRKDD<br/>             LTQTASSTAGAMEELQDQEGWEYASLIGWKFWKQSSDTFRRR<br/>             RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQKHA<br/>             TTVFGANTPIVSCNFDRDYIYHLRCVYQARNLLALDKDSFSDP<br/>             YAHICFLHRSKTTEIIHSTLNPWDQTIIFDEVEIYGEPTVLQ<br/>             NPPKVI MELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW<br/>             HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP<br/>             QGIRPVVQLTAIEILANGLRNMKNFQMASITSPSLVVECGGERV<br/>             ESUVIKNLKKTNPFPSSVLFMKVFLPKKELYMPLVIKVIDHRQ<br/>             FGRKPVVQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR           </p>   |

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|------------|--|--|--|
|            |  |  | <p>DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV<br/> DWNSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT<br/> DFSDTFKLYRGKSDENEDPSVVGFEKGSFRIYPLPDDPSVPAPP<br/> RQFRELPSVVPQECTVRIYIVRGLELQPDNNGLCDPYIKITLG<br/> KKVIE\DRDHYIPNTLNPVFGMYELSCYLPQEKDLKISVYDYD<br/> TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW<br/> RDSLR\PTQ\LLQNVARFKGFPPQILSEDSRIRYGGRDYSLDE<br/> FEANKILHQHGAPEERLALHILRTQGLVPEHVETRTLHSTFQP<br/> NIS\RYYLRLVLIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE<br/> NKQKTDVHYRSLDGEENFNWRFVFPFDYLPAEQLCIVAKKEHFW<br/> SIDQTEFRIPPR\LIQIW\DNDFKS\LDDYLGFPRTLTCRHTI<br/> HFLQKSPGGNC/RGLDMIPLKAMNPLKAKTASLFEQKSMKGWW<br/> PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP<br/> KLDLPNRPETSFLWFTNPCKTMKFIWRRFKWVIIGLLFLLILL<br/> LFVAVLLYSLPNYLSMKIVKPNV</p>   |
| 6022       | 4953   | 549  | <p>EAIQFEVSGNIGYGNKFDFTCKPLASTTQYSRVFDGNYYYLWLP<br/> AHTKPVVTLTSYWEDISHRLDAVNTLLAMERLQTNIEALKSGI<br/> QKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI<br/> RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLKLMQLTE<br/> EPQNSMEDIIWIMIRGEKRLAYARIPAHQVLYSTSGENASGKYC<br/> GKTQTIPLKYPQEKNGPKVPVELRVNIWGLSAVEKKFNSPAE<br/> GTFTVFAEMYENQALMFGKNGTSGLVGRHKFSVDTGKIKLKREF<br/> FLPPKGEWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRY<br/> GGDWKPAEDTYYTDANGDKAASPELTCPPGWEWEDDAWSDINR<br/> AVDEKWEYGITIPFDHKPKSWAAEKMYHTRRRRLVRKRKXD<br/> LTQTASSTAGAMEELQDQEGWEYASLIGWKFWHKQRSSDTFRRR<br/> RWRKMAPSETHGAAAIKLEGALGADTTEDGDEKSEKQKHS<br/> TTVFGANTPIVSCNFRDRIYVHLRCYVYQARNLLALDKDSFSDP<br/> YAHICFLHRSKTTETIESTLNPWTQDIIIFDEVEIYGEPTQVLQ<br/> NPPKVIEMELDNDQVGKDEPLGRSIFSPVVKLNSEMDITPKLLW<br/> HPVMNGDKACGDVLVTAEILRGKDGSSNLPILPPQAPNLYMVP<br/> QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV<br/> ESVVIKNLKKTPNFPSSVLFMKVFLPKEELVMPPLVIKVIDHRQ<br/> YGRKPVVGQCTIERLDRFCRDPYAGKEDIVPQLKASLLSAPP<br/> DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV<br/> DWNSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT<br/> DFSDTFKLYRGKSDENEDPSVVGFEKGSFRIYPLPDDPSVPAPP<br/> RQFRELPSVVPQECTVRIYIVRGLELQPDNNGLCDPYIKITLG<br/> KKVIE\DRDHYIPNTLNPVFGMYELSCYLPQEKDLKISVYDYD<br/> TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW<br/> RDSLR\PTQ\LLQNVARFKGFPPQILSEDSRIRYGGRDYSLDE<br/> FEANKILHQHGAPEERLALHILRTQGLVPEHVETRTLHSTFQP<br/> NIS\RYYLRLVLIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE<br/> NKQKTDVHYRSLDGEENFNWRFVFPFDYLPAEQLCIVAKKEHFW<br/> SIDQTEFRIPPR\LIQIW\DNDFKS\LDDYLGFPRTLTCRHTI<br/> HFLQKSPGGNC/RGLDMIPLKAMNPLKAKTASLFEQKSMKGWW<br/> PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP<br/> KLDLPNRPETSFLWFTNPCKTMKFIWRRFKWVIIGLLFLLILL<br/> LFVAVLLYSLPNYLSMKIVKPNV</p> |
| 6023       | 102  | 916  | <p>SQELGMFVELNNLLNTTPDRAEQGKLTLLCAKTDGSLVHHFL<br/> SFYLANCKVCFVALIQSFSHYSIVGQKLGVSILMARERGQLVF<br/> LEGL/IVCSGR\VFQAQKEPHPLQPLREANAGNLKPLFEFVREA<br/> LKPVDSGEARWTPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT<br/> VCWELKGNMVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL<br/> ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF<br/> AKGMSPAVL</p>  |
| 6024       | 3  | 3260   | <p>FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEAE<br/> LPAELFQKKVVASFPRTVLSTGNDNRYLVLANVTQVQKEGNCCK<br/> RLVITASQSLENKELCILRNDWCSPVPEPGDIIHLEGDCTSDTW<br/> IIDKDFGYLILYPDMLISGTSIASSIRCMRRVILSETFRSSDDPA<br/> TRQMLIGTVLHEVFQKAINNSFAPEKLQELAFQTIQIRHLKEM</p>   |

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|------------|--|--|--|
|            |  |  | YRLNLSQDEIKQEVEDYLPSCFKWAGDFMHKNTSTDFPQMQLSL<br>PSDNSKDNSTCNIEVVKPMDIEESIWSRFGKLGKIDVTGVVKI<br>HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLTYLLSQERRADP<br>RAGLLLYLKTGMYPVPANHLDKRELLKLRNQMAFSLFHRISKS<br>ATROKTQLASLPQIIIEEKTCKYCSQIGNCALYSRAVEQOMDCS<br>SVPIVMLPKIEEETQHLKQTHLEYFSLWCLMLTLESQSKDNKKH<br>HQNIWMLPASEMEKSGSCIGNLIRMEHVKIVCDGQYLHNFQCKH<br>GAIPVTNLMAHDRVIVSGEERSLFALSRGYVKEINMTTVCLLD<br>RNLSVLPBESTLFRLDQEEKNCDIDTPLGNLSKLMNTFVSKKLR<br>DLIIDFREPOFISYLSVLPDADKDTVACILKGLNKPQRQAMKK<br>VLLSKDYTLIVGMPGTGKTTTICTLVRLIYACGFSVLLTSYTHS<br>AVDNILLKLAFKIGFLRSR/QIKVHPAIQQFTEHEICRSKSI<br>KS/LALLEELYTSQILIDATTCMGINHPISRKIFDFCIVDEASQ<br>ISQPICLGPLFFSRRFVLVDHQQPLPLVLNREARALGMSESLP<br>KRLEQNKSAVVQLTVQYRMNSKIMSLNKLTYEGKLECGSDKVA<br>NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD<br>KVPAPQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIAP<br>YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN<br>KDGTVGELLKDWRRINVAITRAKHLKILLGCVPSLNCPYPLEKL<br>LNHLNSEKLIIDLPSREHESLCHILGDFQRE  |
| 6025       | 3977   | 89   | GGFPAQSDHLPVPFPLRSDLLITMSTLYVSPHPDAFPSLRALYA<br>ARYGEAGEGPGWGAHPRIQLQPPPTSRTSFPPLPALEGQPG<br>GLWVWGATAVAQLLWPAAGLGGPGGSRAAVLQQWVSADTELIP<br>AACGATLPALGLRSSAQDPQAVLGALGRALSPLIEWLRHTYLA<br>GBAPTADLAAVATALLLPFRYVLDPPARRIWNVTRWFTCVRO<br>PEFRAVLGEVVLVSGARPLSHQPGPEAPALPKTAAQLKKEAKKR<br>EKLEKFKQKQKIQQQQPPPEKKPKPEKREKRDPGVITYDLPTP<br>PGEKKDVSQPMPSYSPRYVEAAWYPWWEQQGFYKPEYGRPNVS<br>AANPRGVFMCIIPPNTVGSLLHGHALTNAIQDSLTRWHRMRGE<br>TTLWNPSCDHAGIATQVVVEKKLWREQGLSRHQLGREAPLQEVW<br>KWKEEGKDRIYHQLKKGSSLDWDRACTMDPKLSAAVTEAFVR<br>LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG<br>YKEKVEFGVLVSFAYKVQGSDDSEVVVATRIETMLGDVAVAV<br>HPKDTRYQHLKGRNVIHFFLSKSLPIVDFEVDMDFGTGAVKIT<br>PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPFLGLPRFEAR<br>KAVLVALKERGLFRGIEDNPMVVLNCRSKDVVEPLLRPQWVR<br>CGEMAQAASAATRGDLRILPERHQTWHAWMDNIRE\WCMFPG<br>KLWWG\HR\IPAYFVTVDPAVPPGEDPDGRYVWVSGRNEAEARE<br>KAAKEFGVSPDKISLQDEEDVLDTWFSGLFPLSILGWPNQSED<br>LSVFYPTLLETGHDILFFWARMVMLGLKLTGRLPFREYVLLHA<br>IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS<br>EVEKAKEGQKADFPAGIECGTDALRFGLCAYMSQGRDINLDVN<br>RILGYRHFCKNLWNATKFAIRGLGKGFVPSPTSQPGGHESLVD<br>WIRSLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC<br>LKPVLNCGVDQAAECARQTLTYTCLDVGRLRLSPFMPFVTEELFQ<br>RLPRMPQAPPSSLCVTPYPEPSECSWKDPEAEAALELALSITRA<br>VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGGP<br>QAQVVVAEAPWGLPAP\QGCALASDRCSI\HLQLQG\LLDP<br>ARELG\KLQ\AKRVEAQ\ROAQ\RLR\ERRA\ASGNPVKVP\E<br>VQEADAEKQQTEAELEKVDDEALFQKML |
| 6026       | 2674   | 514  | GPITFLKKKAKMDMPLRIHVLLGLAITTLVQAVDKKVDPCRLC<br>TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQIILLQ<br>TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKMPQLLSV<br>YLEENKLTPEKCLSELSNLQELYINHNLSTISPGAFIGLHN<br>LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK<br>PLINLRSLVIAGINLTIIPDNALVGLLENLISISFYDNRLIKVPH<br>VALQKVNLKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPEL<br>ISIDSLAVDNLPLDKIEATNNPRLSYIHPNAPFRLPKLESML<br>NSNALSALYHGTIESLPNLKEISIHNSPIRCDCVIRWMMNKTN<br>IRFMEPDSLPCVDPEFQGNVRQVHFRDMMEICLPLIAPESFP<br>SNLNVAGSYVSHCRATA\EPQPEIYWITPSGQKLLPNT\LTD  |

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|------------|--|--|--|
|            |  |  | KFYVHSEGLTDINGVTPKEGGLYTCIATNLVGADLKSMIKVDG<br>SFPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVK<br>TENSAAQASARIPSDVKVYNLTHLPSTBYKICIDIPTIYQNR<br>KXCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLGIGVICLIS<br>CLSPMNCDGGHSYVRNYLQKPTFALGELYPPLINLNEAGKEKS<br>TSLKVKATVIGLPTNMS  |
| 6027       | 5254   | 4148   | GGRRAPGRPRGRSICKDEEBETVFREVVSFSPDPLFVRYDKDITTK<br>PISFYLSLEELLAWKPRLEDGFNVALEPLACRQPLSSQRPRT<br>LLCHDMMGGLDDRFIQGSVVQTPYAFYHWCIDVFYFSSHHT<br>TIPPVGWTNTAHRHGVCLGTFITWNEGGRLCEAFLAGDERSY<br>QAVADRLVQIT\RRFRFDGWLINIENSLAAGVNMPPFLRYLT<br>TQLHRQVPGGLVLWYDSVVQSGQLKQDELNQHNRFVFDSCDGF<br>FTNYNWREHLEMLRGQAGERRADVVGVDVFARGNVVGGFRDT<br>DKVGGGFRPRASGPVPLPGPHFLMDLPFSPAPQRNDSSCSSQSG<br>DPVALNRNRCAPAKLCPH   |
| 6028       | 120  | 3432   | NCLLLQAKGFHGETIEDLQOWLTDTERHLLASKPLGGLPETAKEQ<br>LNVHMEVCAAFEAKEETYKSLMQKQQLARCPKSAETNIDQDI<br>NNLKEKESVETKLNRR\KT\KLEALNLA\MEFHNSL\QDFIN<br>VLTQAEQTLNVASRPSLILDTVLFIQIDEHKVPANEVNSHREQUI<br>ELDKTGTHLYFSQKQDVVLKNNLISVQSRWEKVVQRLVERGR<br>SLDDARKRAKQFHEAWSKLEWLESEKSLDSELEIANDPKIK<br>TOLAQHKFQKSLGAKHSVYDNTNRGSLKEKTSLADNKLKD<br>DMLSELRDKWDITICGSVERQNKLEEA\LLFSGQFTDALQALID<br>WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ<br>ALKRSARELIEGSRDDSSWVKVQMQLSTRWETVCALSIKQTR<br>LEAALRQAEFFHSVVHALLLEWLAEEQTLRFHGVLPDDEDALRT<br>LIDQHKFEMKLEEKRAELNKATMGDTVLAICHDPDSITTIKHW<br>ITIRARFEEVLAWAKHQQRLLASALAGLIAQZELLEALLAWLO<br>WAEETLTDKDKKEVIPOEIEEVKALIAEHQTFMEEMTRKQPDVDK<br>VTITYKRRADPSSLSQSHIPVLDKGRAGRKRFPASSLYPSGSQT<br>QIETKNPRVNLVSKWQVWLLALERRRKLNDALDRLEELREFA<br>NEDFDIWRKKYMRWNHKKSRVMDFFRIDKDDGKITRQEPID<br>GILSSKFPTSRLEMSAVADIFDRDGDGYIDYEFVAALHPNKDA<br>YKPIITDADKIEDEVTRQVAKCKAKRFQVEQIGDNKYRFFLGNO<br>FGDSQQLRLVRIIRSTVMVRVGGGWMALDEFVKNDFCRAGRT<br>NMELREKFILADGASQGMMAFRPRGRSRPSRSGASPNRSTSVS<br>SQAAQAASPOVPATTPKILHPLTRNYGKPLTNSKMSPTCKAA<br>ECSDFPVPSAEGTPIQGSKLRLPGYLSGKGPHSGEDSLITTAA<br>ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRSGSDASDFDISE<br>IQSVCSDEVETVPQTHRPTFRAGSRPSTAKPSKIPTPQRSKSPAK<br>LDKSSKR |
| 6029       | 1  | 3533   | IMPCGSSRLRGWTHPNEFVSDLSYFDCIESVMENSKVLGESM<br>AGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAYLVGIFD<br>PNSQAGHQGLVDP IQFARANQAIQMACQNLVDPGSSPSQVLSAA<br>TIVAKHTSALCNACRIASSKTANPFAKRFVQSAKEVANSTANL<br>VKTIKALDGDSEDNRNKCR IATAPLIEAVENLTAFAENPEFVS<br>IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP<br>PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC<br>IRDIEQASLAASVQSLATRDDISVEALQEQLTSVVQIEGHLIDP<br>IATAARGEAAQLGHKGTQLASYFEPLILAAGVASKILDHQQM<br>TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAQLMK<br>EAVDDIMVTLINEASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG<br>TFVDYQTTVVYKSKAIAVTAQEMMTKSVTNPEELGLASQMTSD<br>YGHAFQGMMAATAEP E EIGFQIRTRVQDLGHGCI FLVQKAG\<br>ALQVCPTDSYTKRELIECARAVTEKVSVL SALQAGNKGTOACI<br>TAATAVSGIIADLDTT IMFATAGTLNBNSETFADHRENILKTA<br>KALVEDTKLLVSGAAS TPDKLAQAQSSAATITQLAEVVKLGAA<br>SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM<br>YQLKGAAKVMVTVNTSLKTVKAVEDEATRGTRALEATIECIQ<br>ELTVFQSKDVPKTSPEESIRMTKGITMATAKAVAAGNSCRQE<br>DVIATANLSRKAVSDMLTACKQAS FHPDVSDVVRTRALRFGTEC  |



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|------------|--|--|--|
|            |  |  | TLGYLDLLEHVLVILQKPTPELKQQLAASFKRKRVAGAVTELIQAA<br>EAMKGTWVDPEDPTVIAETELLGAAASIEAAKLEQLKPRAK<br>PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQCK<br>VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGH<br>SEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV<br>KRASDNLVRAAQKAAFGKADDDVVVTKFVGGLIAQIIAAQEE<br>LKKERELEEARKKLAQIRQQQYKFLPTLELREDEG   |
| 6030       | 3  | 1777   | FPGRGSPALQLEVLICGLMGLERALNVLAPIFYRNIVNLLTEN<br>APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQOF<br>TSRRVELLIFSHLHLSLRWHLGRRTGEVLRIADRGTSSTVGLL<br>SYLVFNVIPTLADIIIGIYFMSFFNAWFLIVFLCMSLYLTLT<br>IVVTWRTKFRAMNTQENATRAVAUSDLLNFETVKYNAESYE<br>VERYREALIKVQGLEWKSSASLVLLNQTNLVIGLGLAGSLLC<br>AYFVTEQKLQVGDYVLFGTYYIQLYMLNWFGTYYRMIQTNFID<br>MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR<br>ETLQDVSTPVMGPQTALVGPSPGAGKSTILRLFRFYDISSGCI<br>RIDGQDISQVTOALFRFSHWELCPKDTVLNDTIADNIRYGRVT<br>AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR<br>VAIARTILKAPGIIILLDEATSALDTSNERAIQASLAKVCANRTT<br>IVVAHRLSTVVDADQILVIKDCIVERGRHEALLSRGGVYADMW<br>QLQQQEETSSEDTPKQTMER   |
| 6031       | 160  | 1694   | LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKATKS<br>DSSSPQRVQRPHSSPFRFVTEELLEETARGVTNMLAHEIVVNG<br>DFQIKPVELPENSLLKRVKEIVHKAFWDCLSVQLSEDPAYDHA<br>IKLVGEIKETLLSFLPGHTRLRNQITEVLDDLKQAEANGAL<br>DISKLAEFIIGMMGTLCAPARDEBVKLLDKIKEIVPLFREIFSV<br>LDLMKVDMAFNAISSIRPHLMQSQSVYERKKFQEIILERQPNLSD<br>FVTQWLEEASEDLMTQKYKHALPVGGMAGSGDMPRLSPVAVQN<br>YAYLKLKLDHQLRPFPEVTVMQDQSRFHQLQ\REQLTILGAV<br>LLVTFMSMAAPGISSQADFAEKLKMIKILLTDMHLPSPFHLKDV<br>TTIGKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPD<br>IRRIMESRILTFLETYLAGSHQKPLPTVPGGLSPVQRELBVAI<br>KFARLVNKNMVFCEPYDAILSKILVRS   |
| 6032       | 39   | 2415   | AARLCRAQPTKSANMIRDLKSMYPQTRHPAPHQPAQPFKFTISE<br>SCDRIKEEFQFLQAYHSLKLECEKLAASEKTEMQRHYVMYEMS<br>YGLNIEMHKQAEIVKRLNAICAVIPFLSQEHQQQVQAVERA<br>QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP<br>PIGSSAGLLALSSALGGQSHLPKDEKKHNDHQRDRDSIKSS<br>SVSPSASFRGAEKHRNSADYSSSESKKQKTEEKEIAARYDSG<br>SDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP<br>ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPTDAPT<br>NTPGLRPVPGKPPGVDPPLASSLRTPMAVPCPYPTFGIVPHAG<br>MNGELTSPGAAYAGLHNISPQMSAAAAAAYGRSPVVGFD<br>PHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMPPVPPPDAL<br>IGPGIPRHRQINTLNHGEVCAVTISNPTRHVYTGKGCVKVW<br>DISHPGNKSPVSQLDCLNRDNYIRSCRLPDGRTLIVGGEASTL<br>SIWDLAAPTPIKAELTSSAPACYALAIAPDSKVCFCSSDGN<br>AVWDLHNQTLVRQFQGTGASCIDISNDGTCLWTGGLDNTVRS<br>W\DLREGRLQHQD\FTSPVFSGLGCP\TEEWLAVGMENSN\V<br>EVLHVTKPDQYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA<br>W\RTPYG\ASIF\QSKSSSS\VLSCDI\SVDDKYIVTGS\GDK\<br>RATVYEVII |
| 6033       | 39   | 2415   | AARLCRAQPTKSANMIRDLKSMYPQTRHPAPHQPAQPFKFTISE<br>SCDRIKEEFQFLQAYHSLKLECEKLAASEKTEMQRHYVMYEMS<br>YGLNIEMHKQAEIVKRLNAICAVIPFLSQEHQQQVQAVERA<br>QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP<br>PIGSSAGLLALSSALGGQSHLPKDEKKHNDHQRDRDSIKSS<br>SVSPSASFRGAEKHRNSADYSSSESKKQKTEEKEIAARYDSG<br>SDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP<br>ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPTDAPT<br>NTPGLRPVPGKPPGVDPPLASSLRTPMAVPCPYPTFGIVPHAG  |

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|------------|--|--|---|
|            |  |  | MNGELTSPGAAYAGLHNIS PQMSAAAAAAAAAYGRSPVVGFD<br>PHHIMRVPAIPPNLTGIPGGKPAYSFHVSA DGMQPVFPFPPDAL<br>IGPGIPRHARQINTLNHGEVVCVITISNPTRHVYTGGKGCVKVW<br>DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL<br>SIWDLAAPTPIKAELTSSAPACYALAI SPDSKVCFSCCSDGNI<br>AVWDLHNQTLVRQFGHTDGASCIDISNDGTLKLTGGLDNTVRS<br>W\DLREGRLQQHD/FFTSPVFSGLGYCP\TEWLAVGMENSN/V<br>EVLHVTKPKDYQLHLHESCVLSLKFACGKWF\VSTGKDNLLNA<br>W\RTPYG\ASIF\QSKSSS\VLSCDI\SVDDKYIVTGS\GDK\<br>RATVYEVIV   |
| 6034       | 2683   | 714  | ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAAM<br>EIAPOEAPPVPGADGDI EEPAPAEAGSPSPASPPADGRLKAAAKR<br>VTFFSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNK<br>RQIPKLLRQLQEFDTLGHRLDCLDKGEKLDYKTCALAEVFKR<br>LQFKVVDLEQTNLDEGDGASALFDMIEYYESATHLNISFNKHIGT<br>RGWQAAAHMMRTKSCLOYL\ DARNTPLLDHSAFFVARALRIRSS<br>LAVLHLENASLSGRPLMLLATALKMNMLRELYL\ADNKLNGLO<br>DSAQLGNLLKFNCSLQILDLRNNHVLD SGLAYICBGLKEQRKGL<br>VTL\VLWNNQLTHTGMAFLGMLTLPHTQSLLETNLGHNPIONEGV<br>RHLKNGLISNRSVLRGLASTKLTCGAVAVASFI AESPRLLRL<br>DLRENEIKTGGLMALS LALKVNHSLRLDLDRPKKEAVKSFIE<br>TQKALLAEIQNGCKRNLVLAREEKEQPPQLSASMPETTATPE<br>QPDDEPAAGVQNGAPSPAPSPDSDSDS DSGEEEEEEGERDET<br>PSGAIDTRDTGSSEPPPPPPPPRSGPPLPNGLKPEFALALPPEP<br>PPGPEVKGSGSCGLEHLSCKNEKELEELLLEASQESQGETL |
| 6035       | 19   | 404  | SVTYLGIILHKN TGALPADPVQLISQTPTPTKQQLSFLGMVG<br>YFYLWIPGFALTKPLCKLTENLADAI DPKSFSSSFRSLKTA<br>LENASTLALPDSSQPF\SLHTABVQGCVEILTQGLGPLPV   |
| 6036       | 1745   | 356  | LFDVEKLRGRGRKMD SVEKGAATSVSNPRGRPSRGRPFKLQRN<br>SRGGQGRGVKPPHLLAALI LARGGSGKIPLKNI KHLAQVPLIGW<br>VLRALD SGAFQSVWVSTDHDEIENVAKQFGAQVHRSSSEVSKD<br>SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQVAEMIR<br>EEGYDSVFSVRRHQFRWSEIQKGVREVTPLNLNPAKRPRQD<br>WDGELYENG SFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV<br>DIDWPIAEQVRVLYGYFGKEKLKEIKLLVCNIDGCLTNHGIYVS<br>GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK<br>LDCRMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDDECLK<br>RVGLSGAPADACSTAQKAVGYICKNGGGA\IREFAEHIC\LL<br>MEKGLINFMPKNNRLAVNIGEEK  |
| 6037       | 2936   | 1919   | WTSWMMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTFA<br>GGGFPRRHVTLPSKSKFRONQLLSSLKGEPA PALSSRDSRFRDR<br>SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEEENGACKYG<br>DKCQFAHGIHELRLSLTRHPKYKTEL CRTFHTIGFCPYGPRCHFI<br>HNAEERRALAGARDLSADRPR LQHSFSFAGFP SAAATAAATGLL<br>DSPTSITPPPI LSADDLGSPTLPDGTNNPF\AFSSQELASLFA<br>PSMOLPGGGSFTTFLFRMSES PHMEDSPSPQDLSLQEGYLS<br>SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD   |
| 6038       | 1450   | 426  | SSALQEFGRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAA<br>YKGTKHAKKLKALEAMKNKQSVTAKDSAKTTFTSITNTINTS<br>SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG<br>NSSCPSTETE EBAKRL\YCSLCKVAVNSASQLEAHNSGTHKH<br>TMLEARNSGTIIKAPPRAGVKGKGVNKGNTGLQNKTFHCICD<br>VHNSETQLKHISRRHKDRAAGKPPKPKYSPYNKLOKTAHPL<br>GVKLVFSKEPSKPLAPRILPNLAAAAAAAVAVSSPFLRTAP<br>AATLFTQTSALPALLRPAGPIRTAHTPVLFPAPY   |
| 6039       | 4073   | 1000   | LDEYEARTLANLDDFEEDNEDDENRVNQEEKAAKITELINKL<br>NFLDEAEKDLATVNSNPFDDPDAELNPFDPDSEEPITETASP<br>RKTEDSFYNNYNPFKEVQTPOYLNPDEPEAFVTIKDSPPQST<br>KKKNIRPVDMSKYLADSSKTEEEELDES NPFYEPKSTPPNNL<br>VNPVQELETERRVKRA PAPPVLSPKTGVLNENTVSAGKDLSTS   |

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|------------|--|--|---|
|            |  |  | PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNFTTSW<br>RNGLSFCAILHHRPDLIDYKSLNPQDIKENNKKAYDGFASIGI<br>SRLLPSPDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN<br>SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPQLQPPISGA<br>VDFLSQDDSVFVNDSGVGSESEHQTPDDHLSPTASPYCRRTK<br>SDTEPQKSQSSSGRTSGSDDPGICSTNDSQTAQVLLGKKRLLKA<br>ETLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK<br>LENSRSLRCRSDPESPIKKTSLSPSTSKLGYSYSRDLDAKKKHA<br>SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL<br>LEQARDAALKAGNKHNTNTAAPPENRQLSDQDEERRRQLRER<br>ARQLIAEARSGGKMSLPSYGERAAEKLKERSKASGDENDNIEI<br>DTNEIPEGFVVGGLDNLNENDLDTPEQNSKLVDLKLKLLLE<br>VQPQVANSPPSAAQKAVTESSEQDMKSGTEDLRTERLQKTERF<br>RKPVVFSDSTVRKTQLQSFQYIENRPEMKRQSIQEDTKKGN<br>EKKAAITETQRKPSDEVLNKGFKDS\SQYVVGELAALENEQKQ<br>IDTRAALVEKRLRYLMDTGRNTEEEAMMOEWFMVNNKNALIR<br>RMNQLSLLEKEHDLERRYELLNRELRLMLAI EDWQKTEAQKRRE<br>QLLLDELVALVNRDALVRDIJAEQEKQAEEDHEHLERTLEQNGK<br>KMAKKEKCVLQ  |
| 6040       | 475  | 1052   | PTALMTAPSCAFFVQFRQPSVSGLSQITKSLYISNGVAANNKLM<br>LSSNQITMVINVSVEVNTLYEDIQYMQVPVADSPNSRLCDFFD<br>PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHMSL<br>LDAHTWTKSCRPIIRNSGFWEQLIHYEFQFGKNTVHMVSSPV<br>GMIPDIYEKEVRLMIPL   |
| 6041       | 2  | 3886   | TEKDEKTAHNLENVLIHFWERLSEICVAKISEFEADVESVLGVS<br>NLQVLQKPKGSLKSSKKKNGKVRPADEILESNNKENEKCVSSEG<br>EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY<br>VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIQAKPLE<br>IAKLQKNPVAVQFLYQKLIGWLNEDQKDFGLVDILYSALRCC<br>DNDMERKKVLDLTKVDLKWNSLLKIEKACPSDDKHALVTPWL<br>KGDILGEKLVNLADCLCNEDLESRVSSSEHSERWTLISLVLSQ<br>HVKNDYLIGDVYVERIIVRLHETLFTKKLSEAESSDSVSFIC<br>DVAYNYFSSAKGCLLMPSSDLLLLTLFQLCAQSKETHLPDFLI<br>CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL<br>DINSLOVLLSAVDDLNTLLESEDSYLMGVYIGSVMPNDSEWEK<br>MRQSLPMQWLHRLPLEGRSLNLYECFKTDFKEQDIKTLPSHLCT<br>SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP<br>IFLIGFCEILQKMNIITYDNLRVLGNMSSLQLLFNRSREHGTW<br>SLIIAKLILSRSSISSEVKPHYKRKESFFPLTEGNLHTIQSLCP<br>FLSKEEKKESFAQCIPALLGWTKKDLCTNGGFGHLAIFNSCLQ<br>TKSIDDGELHGLIKIIISWKEHEDIPLFSCNLSEASPEVLGV<br>NIEIRFLSLFLKYCSSPLAESWDFIMCSMLAWLETTSENQAL<br>YSIPLVQLFACVSCDLACDLAFAFDSTLDTIGNLPVNLISEWK<br>EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCELTLY<br>ISKEQLLSHKLPARLVADQKTNLPEYLQTLNLTAPLLLFRARP<br>VQIAVYHMLYKLMPELPOYDQDNLSYGEDEEPPALSPPAALMS<br>LLSIQEDLLENVLGCI PVGOIVTIKPLSEDFCYVLGYLLTWKLI<br>LTFKAASSQLRALYSMLRKTSLNKLKLYHLFRLMPENPTYAB<br>TAVEVPNKDPKTFTEELQLSIRETTMLPYHIPHLACSUYHMTL<br>KDLPAVRLWVNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT<br>STQFNGMTVKARATTREVMATYTIEDIVIELIQPLSNYPGLS<br>IIVESGKRVGVAVQQRNWMQLSTYLTHTQNGSIMEGLALWKNN<br>VDRFEGVEDCMICFSVIHGFNYSPLPKACRTCKKKFHSA\CLY<br>KWTSSNKSTCSLCRETF |
| 6042       | 1306   | 253  | MAELAPASPSDIKASVSNQDTLLCSRROSCGMNEVRQVSLTYP<br>GSPAPSHSLPQPRSGSLCPSRAW/PDPHQLFDDTSSAQSRGY<br>GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAQQKE<br>LVKDNIDRFIPITKLKYFAVDTHYVGRKLGLLFFPYLHQDWEV<br>QYQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS<br>PDLGLQASSALAWLTLEVLAILLSLYLVTNTDITDILVAF<br>GYKYVGMIGVLMGLLFGKIGYLVLGWCCVAIFVMIRTLRLK   |

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|------------|--|--|---|
| 6043       | 403  | 599  | ILADAAAEVGPVRGARNQLRMYLTMAVAAQPMIMYWLTFHLVR<br>LCLFFFFPCATPVLPPLSLISAL/CLSHLSVSSWFCPCQPPPLFC<br>PLPPLQNKTAKGSLSTEQSERG  |
| 6044       | 793  | 412  | KLEMMNFTLISKVKISREVTMIASKEFGIGQQVRHSLGVLGVVV<br>DIDPVYLSLSEPSDELAVNDELRAAPWYHVMMEDDNLGPVHTYL<br>AEAQLSSELQDEHP/EQPSMDELAQTIRKQLQAPRLRN  |
| 6045       | 155  | 2299   | SPLPQVAAMNYLRRRLSDSNFMANLFPNGYMTDLQRPQPPPPPPG<br>AHSFGATPGPGTATAERSSGVAPAAPSPGSSGGGGFFSSSL<br>SNAVKQTAAAAATFSEQVGGSGGAGRGGAASRVLLVIDEPHT<br>DWAKYFKGKKIHGEIDIKVEQAEFSDNLVAHANGGFSVDMVEL<br>RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS<br>VNSLHSVYNFCDKPWFVFAQMVRHLKHLGTEEFPLIDQTFYPNHK<br>EMLSS\TTPVVKMGHGTWGWGKVKVDNQHDFQDIASVVALT<br>KTYATAEPFIDAKYDVRVQKIGONYKAYMRTSVSGNWKNTGSA<br>MLEQIAMS DRYKLWVDTCEIFGGLDICAVEALHGDGRDHIIE<br>VVGSSMPLIGDHQDEDKQLIVELVNMMAQALPRQRORDASPGR<br>GSHGQTPSPGALPLGRQTSQQPAGPPAQORPPPPQGGPPQPGPGP<br>QRQGPPLQORPPPGQOHLGSLGPPAGSPLPQRLPSPTSAPQPP<br>ASQAAPPTQGGQRQSRPVAGGPGAPPAARPPASPSQRQAGPPQ<br>ATRQTSVSGPAPPKASGAPPGGQQRQGPQKPPGPAGPTRQASQ<br>AGPVPTGPPTTQQRPSGPGPAGRPKPQLAKXPSQDVPPPPATA<br>AAGGPPHPQLNKSQSLSLNAFNLPEPAPPRPSLSQDEVKAETIRS<br>LRKSFASLFS  |
| 6046       | 212  | 1075   | EGLTGPCERVFFLLGRGPPHGATRAGHRAVRWAGPESLPPLPR<br>SLIMDS PRAGTHQGPLDAETE VGADRCTSTAYQEQRPQVEQVGK<br>QAPLS PGLPAMGGPGPGPCEDPAGAGGAGAGGSEPLVTVVQCA<br>FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH<br>WVPIPEEESLQRAWQDAACPRGLQLQCRGAGGRPVLYQVVAQH<br>SYSAQGPEDLGRQDQTVVLCVQDQAWLEGHCDGRIGIFPKCF<br>VVPAGPRMSGAPGRRLRSQQGDQP  |
| 6047       | 49   | 1405   | PVLVTSLRMREADTLRPPQLMESADIIISTVEFNHTGELLATGD<br>KGRGVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLSLE<br>IEBKINKIKWLPOQNAHSLSTNDKTIKWKITERDKRPEGYN<br>LKDEGKLDLSTVTSLQVPVLKPMMLMVEVSPRIIFANGHTYH<br>INSISVNSDCETYSADDLRINLWHLAITDRSFTP\NIVDIKPA<br>NMEDLFEVITASEFHPHCNLFVYSSSKGSLRLCDMRAALCDK<br>HSLFEEPEPDSNRSEFFSEIIS\SVSDVKFSDRYMLTR\DYL<br>TVKVWDL\NMBARPIETYQVHOYLSKLCSLYENDCIFDKFECA<br>WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV<br>LKERRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA<br>TNNLYIFQDKVNSDMH  |
| 6048       | 1  | 3194   | GIRTPKFCDSPTSLEMRNGRGRKMRPNSTPNVNETATASDS<br>KGTSSNSKTRAGANSKRRGSQNSSEHRPPASSTSEDEVKASPSS<br>ANKRKNKPLSDMELNSSSEDSKSKRVRTNSMGSA TGPLPGTKV<br>EPTVLDRNCPSVPLIDCPHPNCNKYKHINGLKYHQAHAHTDDD<br>SKPEADGDSEYGEPIHLHADLGSCNG\ASVSQK\GSLSPARSAT<br>PKVRLVEPHSPSPSSKSTKGLCKKLSGEGD TDLGALSNDGSD<br>DGPSVMDETSNDAFDSL ERKCKEKECKKPSLKP EKIPSKSLK<br>SARPI/APLAIPPQIYTFQTATFTAASPGSSSGLTATVAQAMP<br>NSPQLKPIQPKPTVMGEPTVNPALTPAKDKKKKDKKKKESSE<br>LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR<br>LASIKAEADKIYSFTDNAPSPSIGSSRLNTTPTQPLTPLHV<br>TQNGABASSVKTNPSAYS DISDAGEDGEGKVDVSKSKDAEQLVK<br>EGAKTLPFPQPSKDSPPYQGFESYYSPSYAQSSPGALNPSSQ<br>AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSSQPSV<br>IQQRPNMYMSLYYNQYAYVPPYGYSDQSYHTLLSTNTAYRQ<br>YEEQKQRLSEQQQRGVDDKAEMLKEREAAKKEWKQKPSIPP<br>TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDSSSLPGQ<br>APEGLKVKLSDAHLSKEASEAKTGAECGRQAE MPILWYRQEA<br>EPRMWTYVYPAKYSDIKSEDERWKEERDKLKEERSRSKDSVPK |

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|------------|--|--|---|
|            |  |  | EDGKESTSSDCKLPTSEESRLGSKPEPRPSVHVVPSSPLTQHOSY<br>IPYMHGYSYSQSYDPNHPSYRSMPAVMMONYPGSYLPSSYSFSP<br>YGSKVSGGEDADKARASPSVTCKSSSES KALDILQGHASHYKSK<br>SPTISDKTSQERDRGGCGVVGSGGSSVGGASGGERSVDRPRT<br>SPSQRLMSTHHHHHLGYSLPAQYNLPYAAGLSSTAIVASQOG<br>STPSLYPPRR  |
| 6049       | 215  | 1089   | AMTGVFDRRVPSIRSGDFQAPFQTSAMHHSPQESPTLPRESSAT<br>DSJYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGS<br>YPKAYADYSYASSYHQYGGAYNRVPSATNOPEKEVTEPEVRMV<br>NGKPKKVRKPTIYSSFLAALQRRFQKTQYLALEPERAELASL<br>GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNSP<br>QSPAVWEPQGSRSLSLHHPHAPPTSNQSPASSYLENSASWYTS<br>AASSINSHLPPPGSLQHPLALASGTL  |
| 6050       | 566  | 1718   | KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWVL<br>PNTAMKKKVLMLGKSGSGKTSMSRIIFANYIARDTRRLGATILD<br>RIHSLQINSSSLSTYSLVDSVGNTKTFDVEHSHVFLGNLVLNLW<br>DCGGQDTFMENYFTSQORDNIFRNVEVLIYVFDVESRELEKDMHY<br>YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQORDLIFKEREEDLR<br>RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQOLEMNLNR<br>FAEII EADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQ<br>FKLSCSKLAASFQSMVEVRNSNFAAFIDIFTSNTYVMVMSDPSI<br>PSAATLINIRNARKHFEKLERVDGPKQCLLMR   |
| 6051       | 566  | 1718   | KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWVL<br>PNTAMKKKVLMLGKSGSGKTSMSRIIFANYIARDTRRLGATILD<br>RIHSLQINSSSLSTYSLVDSVGNTKTFDVEHSHVFLGNLVLNLW<br>DCGGQDTFMENYFTSQORDNIFRNVEVLIYVFDVESRELEKDMHY<br>YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQORDLIFKEREEDLR<br>RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQOLEMNLNR<br>FAEII EADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQ<br>FKLSCSKLAASFQSMVEVRNSNFAAFIDIFTSNTYVMVMSDPSI<br>PSAATLINIRNARKHFEKLERVDGPKQCLLMR   |
| 6052       | 566  | 1718   | KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWVL<br>PNTAMKKKVLMLGKSGSGKTSMSRIIFANYIARDTRRLGATILD<br>RIHSLQINSSSLSTYSLVDSVGNTKTFDVEHSHVFLGNLVLNLW<br>DCGGQDTFMENYFTSQORDNIFRNVEVLIYVFDVESRELEKDMHY<br>YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQORDLIFKEREEDLR<br>RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQOLEMNLNR<br>FAEII EADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQ<br>FKLSCSKLAASFQSMVEVRNSNFAAFIDIFTSNTYVMVMSDPSI<br>PSAATLINIRNARKHFEKLERVDGPKQCLLMR   |
| 6053       | 201  | 1704   | KGTEMNKSRRWQSRRRHGRSHQONPWFLRDSSEDRSDSRAAOPA<br>HDSGHGDDSPSTSSGTAGTSSVPBLPGFYFDPEKKRYFRLLPG<br>HNNCNPLTKESIRQKEMESKRLRLQEDRRKKIARMGFNASSM<br>LRKSQGLFLNVTNYCHLAHELRLSCMERKKVQIRSMDSALASD<br>RPNLILADTNSDRIFTVNDVTVGSKYGIINLQSLKPTTLKVFM<br>HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL<br>PASLFVNHPAGIDRPG\MLCSFRIPGAWSCAWSLIQANNCFS<br>TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLPFGCRS<br>GEIFAIDLRCGNQKGWKATRLFHDSAVTSVRILQDEQYLMASD<br>MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEGILVAVG<br>QDCYTRIWSLHDARLLRTIPSPYPASKADIPSAVAFSSRLGSSRG<br>APGLMAVGQDLYCYSYS |
| 6054       | 1  | 1054   | PFIARLQEFGTSSRRHMANAPSGVHLLVRRGSHRIFSSPLNHYLH<br>KQSSSQRRNFFRRQRDISHSIVLPAAVSSAHPVPKHIIKKPDY<br>VTTGIVPDWGDSEIVKNEQIQGLHQAQCLARHVLLLAGKSLKV<br>DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH<br>GIPDSRPLQDGDIIINIDVTYYNGYHGDTSSETFLVGNVDECGKK<br>LVEVARRCRDEALACRAGAPFSVIGNTISHITHQNGFQVCPHF<br>VGHGIGSYFHGHPEIWHHANDSLPMEEGMAFTIEPIITEGSP<br>FKVLEDAWTVVSLD/TSKVSQAQFHTVLITSRGAQILTKLPHEA   |

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|------------|--|--|---|
| 6055       | 421  | 2364   | PPYFLLSFLAWLYGQSDRTETDISQSAGPPPGTLQCSALHRDP<br>GCANCSRFCRDCSPACQCHTHVFPGNALNGVQPPPELSRTLALI<br>SSREPPRRKKKKSQTETGKERERTSFLTQGGKRFELQHLGAGICM<br>TLLITGDSIVSAEAVWDHVTMANRELAPKAGDVIVKVLDAENKDW<br>WNGQIDDEEGNFPASFVRLWVNHEDEVEEGPSDVQNGHLDPNSD<br>CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDI CEGYLKQC<br>RKRDMFSDQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDPDL<br>SEIGPCFLEHQDGFWYSEYCNHLDACMELSKLMKDSRYQHFF<br>EACRLQQMIDIA\IDGFLLTFOVKICKYPLQLAELLKYTAQDH<br>SDYRYVAAALAVMRNVTTQINERKRRLNIDKIAQWQASVLDWE<br>GEDILDRSSELIYTGEMAWIYQP\YGRNQORVFFLFDHQMVLCK<br>KDLIRRDILYYKGRIDMDKYEVDIEDGRDDDFNVSMKNAPFLH<br>NKETEIHLLFFAKKLEEKIRWLRFAFREERKMVQDEKIGFEISE<br>NQKROAMTVRKVPKQKGVNSARSVPSPYPPQDPLNKGQYLVP<br>\DGLAQSQVFETPEPKRSQSPFWQNFSLTFFKK   |
| 6056       | 43   | 3358   | SGGRGPFVRVRSEQLSPSAEQVQSISQISLGRRLSSLPFPPPSRA<br>LAPTRAPDTALTMEVAEVESPLNPCKIMTFRPSMEEFREFNK<br>YLAYMESKGAHRAGLAKVIPPEWKPRQCYDDIDNLLIPAPIQQ<br>MVTGQSGFLTQYNIQKAMTVKEFRQLANSKGYCTPRYLDYEDL<br>ERKYWKNTLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE<br>EECGISIEGVNTPYLYFGMNKTTFAWHTEDMDLysinLHFGEP<br>KSWYAI>PEHGKRLERLAQGFPPSSSQGDAFLRHKMTLISPSV<br>LKKYGI>PDKITQEAQEFMITFPYGYHAGFNHGFNCAESTNPFAT<br>VRWIDYGVAKLCTCRKDMVKISMDIFVRKFQPDYQLWKQKGD<br>IYIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP<br>KADDEEVSDVDGADEVNPDSDVTDLLKVSEKSEAAVKLRNTEA<br>SSEESSASRMQVEQNLSDHILKSGNSCLSTSVTEDIKTEDDKA<br>YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSLSWPKSPESCS<br>SVAESNGVLTGEESDVESHGNGLEBPGEIPAVPSGERNSPKVPS<br>IAEGENKTSKSWRHPLSRPPARSPMTLVKQAPSDDELPEVLISI<br>EEVEETESWAKPLIHLWQTKPPNFAAEQYENATVARMKPHCAI<br>CTLLMPYHKPDSSNEENDARWETKLEDEVVTSEKTKPLIPEMCF<br>IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPIH<br>EICDGLWCARCKRANWTAECCLCNLRGGALKQTKNNKWAHVMA<br>VAVPEVRFTNVPERTQIDVGRIPLQRLKLCIFCRHRVKRVSGA<br>CIQCSYGRCPASFHVTCABAAGVLMEPDDWYVNVNITCPRHKV<br>NPNVKSACEKVISVGQTVITKHNRTRYSCRVMVTSQTFFYEV<br>MFDDGSFSRDTFFPEDIVSRLCLKLGPPAEGEVVQVWPDKLYG<br>AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF<br>VSAGRCHLGTQVNSLSPPHVSQAQQETYLGFWINSKSQCNIF<br>LSGTY |
| 6057       | 1  | 853  | FVARLKEQEGEGGLGPRKEKGRARGRRRRKMQLTRCCFVFLVQ<br>GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS<br>RPMANSTLLGLLAPPGAWGILGQPPNRPNHSPPPSAKVKIFG<br>WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS<br>ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMWEKVE\RGRR<br>TSLFTHDPAKICSRDHAQSSATWSCSQPPKVVCVYIAPYSTDYR<br>LVQKVC PDYNYHSDTPYPSG   |
| 6058       | 1  | 986  | HPLPSASLGLPSVSLGVSLCVRSALEAVVPMLEKRRRARVGSF<br>SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR<br>VLDACSSEATHVMEETSAAEAVSWQERRMAAAPGCTPPALLD<br>ISWLTESLGAGQPVVPECRHRELVAGPSKGLSPAMMPAYACQR<br>PTPLTHNTGLSEALEILAEAGFEGSEGRLLTFCRAASVLRAL<br>PSPVTTLSQLQGLPHFGEHSSRVQELLEHGVCCEEVERVRRSE/<br>RLFTQIFGVGVKTADRWRREGLRTLDDLREQPQKLTOQQKAGEP<br>SRBAGPWASLNCITLDPASATP  |
| 6059       | 2  | 3650   | QQDFESLADLTDRHARHRCPGDGGDDPQLSWVASSPSSKDVASPT<br>QNIGDGCGLGLGEEEGGTGLPYPCQCDKSFIRLSYLKRHEQIH<br>SDKLFPKCTYCSRLFKHKRSRDRHIKLTGDKKYHCECEAFS<br>RSDHLKIHLKTHSSSKPPFKCTVCKRGFSSTSSLSQSHMQAHKKNK<br>EHLAKSEKRAKDDFMCDYCEDTFSQTELEKHLVLRHPQLSEK   |

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|------------|--|--|--|
|            |  |  | ADLQCIHCPEVFVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV<br>\EGVYCHLDSDHQPDSNNHSVSPDPVLGVSAMSSATPDSSASV<br>ERGSTPDSTLKPLRGQKKMRDDGGQGWTKVVYSCPYCSKRDFNSL<br>AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHN<br>HAYPVMQFGNISAFHCNYCPMFADINSLQEHIRVSHCGPNANP<br>SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESVP<br>VQPTQSPMEVYSCPYCTNSPIFGSILKLTKEHNHKNIPLAHS<br>KKSAAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK<br>FSNFESQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLT<br>YMTTSTHYVCESCDKQFSSVDD\LOKH\LLDMPHPLCCTHCTV<br>CQEVFDS\KVIS\QVHLAVKHSNEKKMYRCTACNWDFRKEADLO<br>VHVKSHLGNPAKAKHCIFCGETFTSEVELQCHITTHSKKYNCK<br>FCSKAFHAIILLEKHLREKHCVFDAATENGTAANGVPPMATKKA<br>PADLQGMILLKNPEAPNSHEASEDDVDASEPNYGCDCGAAYTME<br>VLLQNHRLRDHNRPGEDDGSRKAEFIKGSKCNVCSRTFFSE<br>NGLREHLQTHRGPAKHYMCPIGGERFPSLLTTEHKVTHSKSLD<br>TGTCRICMPLQSEEEFIHCQMHDPDLRNSLTGFRVCMQTVT<br>STLELKINGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR<br>SKQDLVKLDVNGLPYGLCAGCMARSANGQVGLAPPEPADRPCA<br>GLRCPECSVKFESAEDLESHMQVDHRLDTPETSGPRKGTQTSVP<br>PRKTTYQCIKCQMTFENEREIQIHVANHMBEGINHECKLCNQM<br>FDSPAKLLCHLIEHSFEGMGFTKPCPVCTVVFQANKLQQHIFA<br>VHGQEDKIYDCSQCPKFFQTELQNHMTMSQHAQ |
| 6060       | 2145   | 202  | SYETVGKKNLEVNHSQKALCKCSLPSRLPLGENLPLDRGFR<br>KEPRSRGSRERDNLMLHHSCLCFRSLWLPAMLAVALLSLAPSASS<br>DISASRPNILLMADDLGIGDIGCYGNMTMPTNIDRLAEDGVK<br>LTQHISAASLCTPSRAAFLTGYPVRSQGMVSSIGYRVLQWTGAS<br>GGLPTNETTFAKILEEKGYATGLIGKWHGLNCESASDHCHHPL<br>HHGDFHFGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLA<br>ALTLVAGKLTILIPVSWMPVINSAVLLASSYFVGALIVHA<br>DCFLMRNHTITEQPMCFQRTTPLLQEVASFLLKRNKHGPFLLFV<br>SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDMVMVGRILDTLDV<br>EGLSNSTLIYFTSDHGGSLNQLGNTQYGGWNGIYKGGKGMG<br>EGGIRVPGIFRWPGLPAGRVIGEPTSLMDVFTVVRLAGSEVP<br>QDRVIDGQDLLPLLLGTAQHSDFELMHYCFERFLHAARWHQRDR<br>GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVHHDPLDFD<br>LSRDPSETHILTPASEPVFYQVMER\VOQAVWBHQRTLSPVPLQ<br>LDRLGNIWRPWLQCCGPFPLCWCLEDDDPQ   |
| 6061       | 110  | 1330   | MNIHMKRRTIKNTFENRMLMLDGMFAVRVKTELLESEQGS<br>VHNYPDMEAVPLLLNNVKEPPEPDSLSVDHFQTEPVDLSINK<br>ARTSPTAVSSSPVSMASASSPSTSTSSSSSSRLASSPTVITS<br>VSSASSSTVLTGQPLVASAGVGGQQLHIIHPVPPSPMNLQ<br>SNKLSHVHRIPVVVQSVVVYTAVRSPGNVNTIIVPLLEDGRG<br>HGKAQMDPRGLSPRQSKSDSDDDDLFNVTLDSVNETGSTALSIA<br>RAVQEVHPSVPSVRVGRNMNQKFPCSI SPFSIESTRRQRTVLN<br>PPDSRKTAYSTDCDF\EGLQKLYTKSSSPGRVHRRTHTEKPY<br>KCTWEGCTWKFARSDELTRHYRKHTGVKPFKACDCDRSFSRSDH<br>LALHRRRHHMLV   |
| 6062       | 71   | 1079   | ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT<br>LIVLFWGSKHFWPEVPKAYDMEHTFYNGEKKKIYMEIDPVTR<br>TEIFRSGNGTDEILEVHDFKNGYTGIIYFVGLQKCFIKTOIKVIP<br>EFSEPEEIDENEIITTTFFEQSVIWPVPAEKPIENRDFLKNKI<br>LEICDNVTMYW\INPTL\ISGTFAKQLHNFAPFIILVSELQDFE<br>EGEDLHFPANEEKGIEQNEQWVVPQVVEKTRHARQASEEELP<br>INDYTENGIEFDPMLDERGYCCICYCRRGNRYCRRVCEPLGYYP<br>YFYCYQGGRCVIRVIMPCNNWVARMGRV   |
| 6063       | 71   | 1079   | ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT<br>LIVLFWGSKHFWPEVPKAYDMEHTFYNGEKKKIYMEIDPVTR<br>TEIFRSGNGTDEILEVHDFKNGYTGIIYFVGLQKCFIKTOIKVIP<br>EFSEPEEIDENEIITTTFFEQSVIWPVPAEKPIENRDFLKNKI<br>LEICDNVTMYW\INPTL\ISGTFAKQLHNFAPFIILVSELQDFE   |

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|------------|--|--|--|
|            |  |  | EEGEDLHFFANERKKGIEQNEQWVVPQVKVEKTRHARQASEEELP<br>INDYTENGIEFDPMLEDERGYCCICRRGNRYCRRVCKPLLGYY<br>YPYCYQGGRVICRVIMPCNWWARMGRV  |
| 6064       | 913  | 311  | NLPQSLPRPTEHSPPPYSLEKMTDLVAVWDVALSDGVHKIEFEHG<br>TTSGRKVVYVDGKEEIRKEWMFKLVGKBTFFYVGAATKATINID<br>AISGFAYEYTLLEINGKSLKKYMEDRSKTTNTNVLHMDGENFRIV<br>LEKQAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACIYKAV\<br>SSG\KRKEGIHTLIVDNREIPEIAS  |
| 6065       | 1153   | 641  | MSVRVARVAVRGLGASYRRGASSFPVPPGAGQVALLRDATG<br>AEEAPWAATERMPGQCSVLLFPGQGSQVVMGRGLLNYPVRV<br>ELYAAARRVLGYDLLELSLHGPQRTLDRTVHCQPAIFVASLA<br>EKLHHLQPSVIENCVAAGFSVGEFAALVFAGAMEFAEG   |
| 6066       | 68   | 3470   | VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW<br>BDLDDDDPKFINVGEKAYSCALKSGKLVAVSNNTIQVHTFPEG<br>VPDGLITRFTTNANHVFNNGDGTIAAGSSD\FLVKIVDVMDS<br>QQKTFRGHDAPVLSLSPDKDIFLASASCDGSRVWQISDQTC<br>ISWPLQKCNVDINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR<br>ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVWNV<br>ETKDCMERVKHEKGYAICGLAWHTCGRISYTDAGNGLGLENV<br>CDPSGKTSSSKVSSRVKDYNDLFDGDDMSNAGDFLNDNAVEIP<br>SFSKGIINDEDEDELMMASGRPRQRSHILEDDENSVDISMLKT<br>GSSLLKEEEDGQEGSIHNLPLVTSQRFFYDGPMPPTPRQKPFQS<br>GSTPLHLTHRFMVWNSIGIRCYNDEQDNAIDVEPHDTSIHHA<br>HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSWDSK<br>EWIIDLQONEDIEAICLGQGWAAATSAALLRLPTIGGVQKEVF<br>SLAGPVVSMAGHGEQLFIVYHRGTGFGDQCLGVQLLELGKKK<br>QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG<br>NIWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP<br>TLRPPAVAILSFKLPYQCIIATEKGQMEEQFWSVIFHNHLDYLA<br>KNGYEYEESTKNQATKEQQELLKMLALSKLREFRCEVLA<br>MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEE<br>EEEEFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE<br>KPEIHKPGONSFSKSTNSDVSAGKAVTFSSQGRVNPFKVAS<br>SKEPAMSMNSARSTNILDNMGKSSKSTALSRTTNNEKSPIIKP<br>LIPKPKPKQASAAASYFQKRNSQTNKTEEVKEENLKNVLP<br>CPQNTENQRPKTCFQMWLEENRSNLSNDNPDSEADIIKEGM<br>IRFRVLSTEERKVVANKAGETASEGTEAKKRVRVDESDETEN<br>QEEKAKENLNLSSKQKPLDFTSNQKLSAFAFKQE |
| 6067       | 858  | 321  | LPWQRLGVLLSRGKMAVTGWLESRLTAQKTALLQDGRKRVHYLF<br>PDGKEMAEYDEKTESELLVRKVRKVSALGAMGQWLEVGDPAPL<br>GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYKDVYSV<br>SVDQKERCIIVRTNKKYKKFSIPDLDRHQLPLDDALLSFA\T<br>PTAP   |
| 6068       | 13   | 1730   | GSKMADLANEEKPAIAPPVVFQKDKGQKSPAEQKNLSDSGEEP<br>RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL<br>PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRETTSSLTQ<br>FPPSQSEERSGFRLLKPPTLIHQAPSAGLPSQKPKKEQQRSLR<br>PAVLQAPQPKALSQTVPSSTNGVSLPADCTGAVPAASPDAAW<br>RSPSEAADEVCALEEKPEQKNESNASEEACEKKDPATQQA<br>FGQNLDRVRKLINEVDEADMENAGHPSADTPTATNYFLOYISS<br>SLENSTNSADASSNKFVFGQNMSESVLSPPKLNEVSSDANRENA<br>AAESGSESSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT<br>GEEAESNVLMQCKLFVFDKTSQSWVERGRLRLNDMASTDDG<br>TLQSRSLDAGPRGSLR\LLNLTKLWQMIDKASEK\SIRITAM<br>DNEDQGVKVFLLISASSKDTGVYAALHHRILALRSRVEQEQA<br>MPAPEPGAAPSNEEDSDDDDLAPSGATAAGAGDEGDGQTGTS<br>T   |
| 6069       | 583  | 27   | PTRPGQAGSSSAMAQRLGKRVLSKLQSPSRARGPGGSPGGLOK<br>RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN<br>IDELLELESEERSRKIQGLLSCGKPVDFIQELLAKLQGLHR   |



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|------------|--|--|---|
|            |  |  | Q\PGLRQSPSP\DGQPSAPFQGGARTASPLTLLALFPGPPEP RPALLCVLSCI  |
| 6070       | 478  | 858  | IRVTVDGEFLHYIFPLQFLDSPW/RFTETHRGHF\QVTLTAE TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND RVYIGKRYEYDIRLNFYQOMSTPEIRRSPLTQHFNQNSRRYW  |
| 6071       | 2  | 1654   | HEARTKGNMALARP\VRLFSLVTRLLAPRGLTVRSPEFLPV VRI PVALQRLQEQRRRRNLPRPVLVRPGPLLVSARRPELNQP ARLLTGRWERAPLASQGWKSRARRRDHFSIERAQGEAPAVRKLS SKGSFADLCAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR GRHVVCAAETGSGKTL SYLLPLQLRLG\HPSLDLPIAPRGL VLVPSRELAQQVRAVAQPLGRSLGLLVRDLGEGHGMRRIRLQLS ROPSADVLVATPGALWKALKSRLTSLQLSFLVLDEADTLDES FLBLVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPFEGVGQ LLNKVASPDVATTITSSKLHCIMPHVKQTFLLKLGADKVAELVH ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL QGQMPALMRVGI FQSFQKSSRDILLCTDIASRGLDSTGVELVNN YDFPPTLQDYIHRAGRVGRVGEVPGTVISFVTHPNDVSLVQKI ELAARRRRSLPGLASSVKEPLQAT |
| 6072       | 1  | 742  | KMERTEMMPTINSQLEFKSKPFLVSSSRNLVKRGELTAYVEDT VLSRRTSKQVYFPLPNDVLIITKKKSESYNVNDYSLRDQLL VESCDNEELNSSPGKNSSTMLYSRQSSASHLPTLVLSNHANEK VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT AKQPDLSLQVADVLI\YQRVSDGWYEGE\LRDGERGWFPME CAKEITCQATIDKNVERMORLLGLETNV   |
| 6073       | 620  | 860  | PCRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT LVEAIKKVKDHRGII PNNGFLRQLLALDRRLRQGLEA  |
| 6074       | 168  | 1110   | PGARCMATELQCPDSMPCHNQVNSASTPSPEQLRPGDLILDHA GGNRASRAKVILLTGIAHSSLPALDSCAGCGSSLNSEGNSSGSG DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTPTGYKYE GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET QRAKVYAKFPDIIYRRKVLLMYPILQTNVIEAVKVLIEHG VQPSVIIILSLFSTPHGAKSI IQEFPETITLTEVHPVAPTHFG QKYFGTD  |
| 6075       | 320  | 1091   | PPTCQPOQVEVHH\YGYVPILGNKTLPSRCHQCQVIVSSSHLGT KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTPTETVFIWFGPPSKMKQKQGSLSVRVIRAGLVFP NMEAYAVSPGRMRQFDDLFERGETGKDREKSHSWLSTGWFTMVIA VELCDHVHYGMVPPNYCSQRPLQRMPIHYIEPKGPDECVTYI QNEHSRKGNHHRFITEKRVFSSNAQLYGITFSHPST   |
| 6076       | 1721   | 107  | HPSPTAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV KKPASVVKVCKVSGYTLTSLSMHWVRQAPGKLEWMAFDPEBD GETIYAQKFQGRVMTEDTSTDTAYMELSSLSRSEDVAVYCATD HGDYAFDIWGGTMTVTVSSAPTAPDVFPPIISGCRHFKDNSPVV LACLITGYHPTSV\TVTWYMGTSQA\QRTFPEIQRRDSYMTS SOLSTPLQQRQGEYKCVVQHTASKSKEIFRWPESPKAQASSV PTAQPAEGSLAKATTAPATTNTGRGGEKKKEKEKEEQEERE TKTPECPSTQPLGVYLLTPAVQDLWRDKAFTTCFVVGSDLDK AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQRSLTLPRLSLWNA GTSVTCTLNHPSLPPQRLMALREPAQAQPVKLSLNLASSDRPE A\ASWLLCEVSGFSPPNILLMWLEHDHGEVNTSGFAPARPLPKP\ RSTTFWA\WSVLVPAFPSPQPATYTCVVSHEDSRTLLNASRSL BVSIVTDHGPMK                    |
| 6077       | 3687   | 1268   | LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGMPTARCDLEALKKKGCPDDIENPR GSKDIKKNKNTNRSKGTAEKLPEDITIQIQQQLVLRLSGEP QTFTLKFKRAEDYPIDLYLM\DLSSYMKDDLENVKSGLTDLNM EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGVEFNELVGKQRI SGNLDSPEGGFDAIMQVA VCGSLIGWRNVTRLLVFSTDAFGHAGDKLGGIVLPNDGQCHL  |

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|------------|--|--|--|
|            |  |  | ENNMYTMSHYDYDPSIAHLVQKLSENNIIQTIFAVTEEFQPVYKE<br>LKNLIPKSAVGTLSANSSNVLIIDAYNSLSSEVILENGKLSE<br>GVTISYQSY\CKNGVNGTGENGKRCNSNISIGDEVQFESITSNK<br>CPKXSDSDFKIRPLGFTEVEVILQYICECECQSEGIPESPKCH<br>EGNGTFECGACRCNEGRVGRHCECSTDEVNSDIGCFARKENQ<br>FQKSASNHGRVPSAGQCVCRRKRDNTNEIYSGKFCECNFNCDRS<br>NGLICSGNGVCKCRVCECNPNYTGSAACDCLDTSTCEASNGQIC<br>NGRGICECGVCKCTDPKFGQGTCEMQQTCLGVCAEHKECVQCR<br>FNKGEKKDCTQECSEYFNITKVESRDKLQPVQPDVSHCKEKD<br>VDDCWFFYFTYSVNGNNEVMHVVENPECPGPDIIPIVAGVVAG<br>IVLIGLALLLIWKLMIIDHRRFAKFEKEMNAKWDTGENPIY<br>KSAVTTVNPVKYEGK |
| 6078       | 1426   | 180  | ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCCKLEGILE<br>GSVRNSLWRPVFKCPTCRKKTFSYWELIPLQVNSLKGIVEKY<br>NKIKISPKMPVCKGH\LGQPLNIP\CL\TDMQLDL\CGIC\ATR<br>GEHTKHVFCSEIDAYAQERDAFESLFQSFETWRRGDALSRLDTL<br>ETSKRKSLLQTLTQSDKVKEFFEKLQHTLDQKNEILSDPETMK<br>LAVMQAYDPEINKLNTILQEQRMFAPIABAFKDVSEPIVFLQOM<br>QEFREKIKVIKSTPLPPSNLPASPLMKNFDTSQWEDIKLVVDVK<br>LSLPQDTGTTFISKIPWSFYKFLLLILLGLVIVFGPTMFLEWSL<br>FDDLATWKGCLSNFSSYLTKTADFIEQSVFYNEQVTDGFFIFNE<br>RFKNFTLVVLNNVAEFVCKYKLL  |
| 6079       | 1586   | 141  | ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLLGGLSP<br>GVLDRLYGHPATCLAVFRELEPSLAKNWMRMLFLEQPLPQAAVA<br>LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ<br>NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVUL<br>HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPCCITSAGFQFL<br>LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSFTSLGKD<br>YSVEGMSDSSLNLFQLHREFGLVFQRRKRSRYPT/RALAINL<br>SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIFSE<br>MLYFPF\NMVV\ARVTR\ESVQQAIASGITAQOIIFHLRTRAHP<br>VMLKQT\VLPPITITDQIRLWELERDLRFTEGVLYNQFLSQVDF<br>ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHSVVKRFRWKQK<br>HSS     |
| 6080       | 1  | 1199   | IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLQDQFK<br>TLRQCLDSGLVFKDPEFPACPSALGYKDLGPGSPQTQGIWK<br>PTELCPSPQFIVGGATRTDICQGLGDCWLLAAIASLTNEELL<br>YRVVPRDQDFQENYAGIFHQPPLCPPSP\FWQYGEWVEVVIDDR<br>LPTKNGQLLFLHSEQGNFWSALLEKAYAKLNGCYEALAGGSTV<br>EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY<br>SAAEAIAITSQLVKSHAYSVTGVEEVNFQGHPEKLIIRLNPWG<br>EVEKSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSSDFVR<br>QFSRLEICNLSPPDSLSEEVHKWNLVLFNGHWTRGSTAGGCQNY<br>PGSS   |
| 6081       | 3  | 865  | EMLPLLLPLPLWA/GALAQDARFLEMPESVTVQEGLCIFVHC<br>SVFYLEYGWKDSTPAYGHWFREGVSDQETPVATNNSQKVQKE<br>TOGRPHLLGDPNRNCSLSIRDARRRDNYSYFFWVARGRTKFSY<br>KYSPLSVYVTALTRPDILIPFELKSGHPSNLTCSPVWVCEQGT<br>PPIFSWMSAAPTSLGPRTLHSSVLTIIIPRQDGHNTLICQVTFP<br>GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLCLCLI<br>ILSFHKKKAVRAVEEENVYAVMG   |
| 6082       | 283  | 1288   | EARSPTQTQTRTAPGLAAGLAQPAALRLLSRPFSAMDGDD<br>PESVGQPEEASPEEQPEEASAEERPEDQEEEEAAAAA\Y\LDE<br>LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL<br>LKCOQEGVLPEGGVEEERDHWQGFYFLSKRRRNLLRNPCGEEDL<br>EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR<br>KAQVIDLQAGYWEELDDTTPAIVVKDWYSGRSDAGCLYELTV<br>KLLSEHENVLAEFSSGQVAVPQSDGGGWMEISHTFTDYGPGVR<br>FVRFEHGGQDSVYKGWFGARVTNSSVWVEP   |
| 6083       | 1865   | 309  | KQWCAERRGLGMSLADELLADLEAAAEHEEGGSYGEEEEEPAIE   |

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|------------|--|--|---|
|            |  |  | DVQEEETQLDLSGDSVKTIAKLWDSKMFABEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKPIRDKYSKR FPELESLVPNALDYIRTVKELGNSLDCKNNENLQQLTNTATIM VVSVTASTTQGGQLSEEELEERLEECADMALNASKHRIEYVE SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG AQRKTLGSPSSTSVLPHTGYIYHSDIVQSLPPIPPPFVAP\DL RRKAARLVAAKCTLAARVDSFHSTEGKVGYELKDEIERKFDKW QEPVPVKQVKPLPAPLDGQRRKRGRRYRKMKERLGLTEIR\KQ ANRMSFGEIEEDAYQEDLGFSGLHGLKSGSGRVRQTQVNEATKA RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI VNPQAAEKRAEANKYFSSMAEFLKVKGEKSGLMST   |
| 6084       | 1865   | 309  | KQWCAERRGLGMSLADLADLBEAEEEEEGSYGEEEEEPATE DVQEEETQLDLSGDSVKTIAKLWDSKMFABEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKPIRDKYSKR FPELESLVPNALDYIRTVKELGNSLDCKNNENLQQLTNTATIM VVSVTASTTQGGQLSEEELEERLEECADMALNASKHRIEYVE SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG AQRKTLGSPSSTSVLPHTGYIYHSDIVQSLPPIPPPFVAP\DL RRKAARLVAAKCTLAARVDSFHSTEGKVGYELKDEIERKFDKW QEPVPVKQVKPLPAPLDGQRRKRGRRYRKMKERLGLTEIR\KQ ANRMSFGEIEEDAYQEDLGFSGLHGLKSGSGRVRQTQVNEATKA RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI VNPQAAEKRAEANKYFSSMAEFLKVKGEKSGLMST |
| 6085       | 2  | 1456   | SGPFSFQGNRAVGRISLGGKRNPEVTLPGVSSERVRWRARRV GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTLP\LTLYLCAGT QAESAQSNRLMMLRMHNLHGTPPPSEGSDEEEDEDEDEER KPQLELAMVPHYGGINRVRVSWLGEFPVAGVWSEKGVFVAFAL RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR VTGRLLTGDCQKNHILWTPTDGGSWHVDQRPFFVGHTRSVEDLQW SPTENTVFASCSADASIIRWDIRAAPSKACMLTATATHDGDNV ISWSRREPFLSGDDGALKINDLRQFKSGSPVATFKQHVAPVT SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPEAGDVEADPG LADLPQQLLFVHQGETELKELHWHWPQCPGLLVSTALSGFTIFRT ISV                                  |
| 6086       | 2419   | 1357   | GAATQHGGMNLLPCNPHNGNLLYAGFNQDHGCFACGMENGFVRV YNTDPLKEKEKEFELEGGVGHVEMLFRCNYLALVGGGKKPKYPP NKVMIWDDLKKKTVEIEFSTEVKAVKLRR\DKIVVVLDSMIKV FTETHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGTHTG HVQLVDLASTEKPPVDIPAHEGVLSIALNLQGTRIATASEKGT LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLIVCSSDHG TVHIFAAEDPKRNKQSSSLASASFLPKYFSSKWSFKQVPSGSP CICAFTGTEPNAVIAICADGSYKFLFNPKGECIRDVYAQFLEMT DDKL   |
| 6087       | 476  | 1877   | QNSQRTGLPITIFSRSPLLTGSDLCBNMPCTCTWRNWRQWIRP LVAVIYLVSIIVAVPLCVWELQKLEVGINTKAWFIAGIFLLLT I PISLWVILQHLVHYTQPELQKPIIRILMMVPIYSLDSWIALKYP GIAIYVDTCRECYEAYVIYNFMGFLTNLYLTNRYPNLVILEAKD QQKHFPPLCCCPWAMGEVLLFRCKLGLVLYTVVRPFTTIVALI CELGIIYDEGNFSPSNAWYLVIIINMSQLFAMYCLLLFYKVLK EELSPIQPVGKFLCVKLVVVFVFWQAVVIALLVKVGVISEKHTW EWQTVFAVATGLQDFIICIEMLAAIA\HHYTFYKPYVQEAEE GSCFDSPLAMWDVSDIRDDISEQVRHVGRTRVGRHPRKLFPEDDQ DQNEHTSLSSSSQDAISIASMPPSPMGHYQGFHGTVPQTTP TTAKISDEILSDTIGEKKEPSDKSVDS   |
| 6088       | 1684   | 689  | GASGLVRLLOQGHRCLLAPVAPKLVPPVVRGVKKGFRAPFRQKE LERQRLRCPPPPVRSEKPNWDYHAEIQAFGHRQLQENFSLDLL KTAFFVNSCYIKSEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYDMPTEGINKLVDFLTGEEVVCHVARNLAVE QLTLSSEFPVPPAVLQQTFFAVIGALLQSSGPRTALFIRDFLI TQMTGKELFEMWKIINPMGLLVEELKKNVSAPE SRLTRQSG\A  |

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|------------|--|--|---|
|            |  |  | PTALPLVYFVGLYCDKKLIAEGPGETVLVAEEAARVALRKLYGF<br>TENRRPWNYSKPKEITLRAEKSITAS  |
| 6089       | 3  | 3054   | TRLGIPGSTISSRRLCALAEGHFLGHSWTGSRAGAHTGAPAW<br>PSRRLRLDPAGGMWRLRRAVACEVCQSLVKHSSGIGKSLPLQK<br>LHLVSRSIYHSHPTLKLQRPQLRTSFOQFSSLTNLPLRKLKFS<br>PIKYGYQPRRNFWPALATRLKLRLYLILGSVGGGYTAKTTFD<br>QWKDMIPDLSEYKWIIVPDIVWEIDEYIDFEKIRKALPSSSEDLVK<br>LAPDFDKIVESLSLLKDFFTSGSPPEETAFRATDRGSESDKHFRK<br>VSDKEKIDQLQEELLTQLKYQRILERLEKENKELRKLVLQKDD<br>KGIPFIESLRKSLIDMYSEVLDVLSYDASYNTQDHLPRVVVV<br>DQSAGKTSVLEMAIQAARIFPRGSGEMMTRSPVKVTLSEGP HHVA<br>LFKSSSREFDLTKEEDLAALRHEIELMRKKNVKEGCTVSPETIS<br>LNVKGPGLQRMVLVDLPVINTVTSGMAPDTKETIPSISKAYMQ<br>DPNAILLCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL<br>AEKNVASPSRIQIIEGKLFEMKALGYFAVVTGKGNSSIESIAI<br>REYEEFPQNSKLLKTSMLKAHQVTRNLSLAVSDCFWKMVRES<br>VEQQADSFKATRFNLETEWKNKYPRLRELDRLNEFEKAKNEILD<br>EVISLSQVTPKHWEELQOQLWBRVSTHVIENIYLPAAQTMNSG<br>TFNTTVDIKLKOWTDKQLPNKAVEVAVETLQEEFSRFMTPEKKG<br>EHDDIFDKLKEAVKERSIKRHKWDFAEDSLRLVIOHNALEDRSI<br>SDKQQWDAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW<br>KNRTQEQCVHNETKNELEKMLKCNNEHPAYLASDEITTVRKNLE<br>SRGVEVDPSLIKOTWHQVYRRHFLKLTALNHCNLCRRGFYYYQRH<br>FVDSLEECNDVVLFWRIQRMLAITANTLRQQLTNTVEVRLKKNV<br>KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE<br>ALHQEK |
| 6090       | 194  | 1560   | PVFVPAGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASTL<br>FELQLFFCOLIALFVHYINIKTVWVYPPSHPPSHTSLNFHLID<br>FNLMTTIVLGRRFISIVKEASQGRKVSLEPSILLFLTRFTV<br>LTATGWSLCRSLIHLERTYSFLNLL/FPLLSVWDVHSPAAELR<br>P\RKTSLEFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS<br>CMARTPCP/PHACCLSPSLIRSEVEFLKMDENWRMKEVLVSSML<br>SAYYVAFVPVWFVKITHYDKRWSCEFLVLSISTSVILMOHLL<br>PASVCDLLHKAHAHLGCWQKVDPALCSNVLQHPWTEECMWPGQV<br>LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRIILNILL<br>LEGAVIVYQYLSLMSSEKWHQITISLALILFSNYYAFFKLLRDL<br>VLGKAYSYSASQPRDLDRFS   |
| 6091       | 3279   | 412  | SSRTREMEKEILRRQIRLLQGLIDDYKTLHGNAAPGTPAASG<br>WQPPTYHSGRAFSARYPRPSRRGYSSHGSPWRKKYSLVNRFP<br>PSDFPADHAVRPLHGARGGQPPVPOQHVLEROVLSQGNVVIK<br>VKPPSKSGSASASGAQGSLEEFEDTPWSDQRPREGEGEPGRQ<br>LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKS VGSVGDSPRE<br>PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ<br>LLGDRRVDAGHTDQPVPSGSGVGGPARPASGPRQAREASLVVTCR<br>TNKFRKNKYKWAASSKSPRVARRALSPRVAENVCKASAGMAN<br>KVEKPLIADPEPKPRKPATSSXPGSAPS KYKWKASSPSASSSS<br>SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPVGHSGLKPLSGE<br>TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR<br>RROALRGKSSPVLKKT PNKGLVQVTHRLCRLPPSRAHLPTKEA<br>SSLHAVRTAPT SKVIKTRYRIVKKT PASPLSAPPPPLSLPSWRA<br>RRLSLRSRLVNLRLRPVASGGGKAQPGSPWWSKGYRCIGGVLY<br>KVSANKLSKTSQPSDAGSRPLLRTRGLDPAGSCSRSLASRAVQ<br>RSLAIRQARQRREKRKEYCMYNNRFGRCNRGERCPYIHDPEKV<br>AVCTRFVRGTCKKTDGTCPFSHHVSKEMKPVCSYFLKGICNSN<br>CPYSHVYVSRKAEVCSDFLKG YCPLGAKCKKHTLLCPDFARRG<br>ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSVASHG<br>PRKPSASQRPTRQTPSSAALTAATAVAAPPHCPGGSASPSSSKAS<br>SSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS<br>SPSPGAQPRVRAPRAPLT KD SGKPLHIKPL  |
| 6092       | 143  | 3190   | AKAPPTGESSEPEAKVLHTKRLYRAVVEAVIRLDLILCNKTAQ<br>EVFKPENISLRNKLREL CVKLMFLHPVDYGRKAEELLWRKVYYE  |

| SEQ<br>ID<br>NO: | Predicted<br>beginning<br>nucleotide<br>location<br>corresponding<br>to first<br>amino acid<br>residue of<br>amino acid<br>sequence | Predicted end<br>nucleotide<br>location<br>corresponding<br>to first<br>amino acid<br>residue of<br>amino acid<br>sequence | Amino acid segment containing signal peptide<br>(A=Alanine, C=Cysteine, D=Aspartic Acid, E=<br>Glutamic Acid, F=Phenylalanine, G=Glycine,<br>H=Histidine, I=Isoleucine, K=Lysine,<br>L=Leucine, M=Methionine, N=Asparagine,<br>P=Proline, Q=Glutamine, R=Arginine,<br>S=Serine, T=Threonine, V=Valine,<br>W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop<br>Codon, /=possible nucleotide deletion,<br>\=possible nucleotide insertion)   |
|------------------|---|--|---|
|                  |   |  | <p>VIQLIKTNKKHIHSRSTLECAVRTHLVAGIGFYQHLLLYIQSHY<br/> QLELQCCIDWTHVTDPLIGCKKPVASGKEMDWAQMACHRCVY<br/> LGLDSRYQNELAGVDTELLAERFYQALSVAPOIGMPFNQIGTL<br/> AGSKYYNVEAMCYLRICIQSEVSFEGAYGNLKRLYDKAAKMYHQ<br/> LKKCETRLSPGKKRCKDIKRLVNFMYLQSLQLPKSSSVDSSEL<br/> TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFPLDL<br/> LIFQMVIICLMCVHSLERAGSKQYSAIAFTLALFSLVNHVNI<br/> RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEPPDPEPPVPT<br/> PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD<br/> SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME<br/> EEEGTRSPLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ<br/> MFQTKRCFR LAPTF SNLLQLPTNPHTSASHRPCVNGDVKPSE<br/> PASEEGSESESGESSGRSCRNERSIQEKLQVLMAGLLPAVKVF<br/> LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA<br/> LCPEVQDLLEGCELDPDLPSSLLLPEDMALRNLPLRAAHRRFNF<br/> DTRPPLLSTLEESVVRICIRSFHFIARLQGSILQFNPEVGIF<br/> VSI AQSESESLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV<br/> SOLEGSLQPKAQASAMPYLVPDTQALCHLPVIRQLATSGRFI<br/> VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE<br/> VGKSFERHKLKRDADAWTLTKILDSCKQLT\LAQGAGEDPSG<br/> MVTIITGLPLDNPSLLSGPMQAALQAAHASVDIKNVLDIFYKQW<br/> KEIG</p> |
| 6093             | 76  | 1002   | <p>ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL<br/> PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\<br/> PAAGAGAAAAPGGQWGPASTPSLYENPWITPNNLSMTRIGLAP<br/> VLGYLIIIEEDFNIALGVFALAGLTDLDDGFIARNWANQRSALGS<br/> ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDMVLI AAVF<br/> YVRVYRTLPTRTLAKYFNPCYATARKPTFISKVNTAVQLILVA<br/> ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV<br/> IKD</p>  |
| 6094             | 23  | 1010   | <p>PFLRCLRGDQKAKMSERKVLNKYPPDFDPSKIPKLLPKDRQY<br/> VVRLMAPFNMRCCTCGEYIYKGGKFNARKETVQNEVYLGPIFR<br/> FYIKCTRCLAEITFKTDPENTDYTMHGA TRNFQAEKLEEEEEK<br/> RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR<br/> QAHVDFEAMLRQHRLSEERRRQQQBEDEQETAALLEEARKRRL<br/> LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKEVVEQSV<br/> GSLGSRPPLSRLVVVKKAKADPDSCSNGQPQA/APHPRSPAEBQEG<br/> GQPYTPDAWRVLPEPTGCI PGQ</p>   |
| 6095             | 1   | 1599   | <p>TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES<br/> GSRSGNMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMMNQTCPPQ<br/> YTIRCRPLQFQPSKSHKKVLKMLKFLAKGEVPKGSCE\DEPMD<br/> STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGNSSKKE<br/> BPQELLQSQDFVGEKLGSGEP SHS</p>  |

TRADOC5:1416257.1(%CSH011.DOC)

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|------------|--|--|--|
|            |  |  | VKVHTVPKPGKADLSKPPCRKAKEIRKERRKRLKLMQONPAGEL<br>EGFOAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR<br>VVRSSPPSSQFKATLLESYQVYKRYQMVHKNPPDPTPTESQFTR<br>PLCSSPLEAETPPNGPDCGYGSFHQQYWLGDGKIIAVGVIDILPN<br>CVSSVYLYDDPDYSFLSLGVYSALREIAFTRQLHEKTSQLSYYY<br>MGFYIHSCPKMKYKQYRPSDLLCPETYVWVPIEQCLPSLENSK<br>YCRFNQDPEAVDEDRSTEPDRQLQVFHKRAIMPYGVYKQKQKDP<br>BEAAVLQYASLVGQKCSERMLLFRN  |
| 6096       | 2277   | 575  | QVRRAALLSSAMEDSEALGFEHMGDLPRLLQAVTDLGWSRPTLI<br>QEKAIPLALEGKDLARARTGSGKTAAYAI PMLQLLLHRKATGP<br>VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAR<br>EDSVSQRAVLMKPDVVVGTSPSRILSHLQDQSLKLRDSLELLVV<br>DEADLLFSFGFEELKSLCHLPRIYQAFLMSATFNEDVQALKE<br>LILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK<br>LSLIRGKSLLFVNTLERSYRLRLEFQFSIPTCVLNGELPLRSR<br>CHIIISQPNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDASDP<br>EAGVARGIDFHHVSAVLNFDLPETPEAYIHRAGRTARANNPGIV<br>LTFVLPTEQFHLKIEELLSGENRGPILLPYQFRMEEIEGFRYR<br>CRDAMRSVTQAIAREARKETKEELLHSEKLKTYFEDNPR\DLQ<br>LLRHDLPLHFAVVKPHLGHVDPDYLVPALRGLVRPHKK\GRSCL<br>PLVGRPREQSPRTHCAASSTKERNSDPQSPPEVVGPLWS |
| 6097       | 1673   | 192  | APGTMSSGGKKSSFOITSVTTDYEGPGSGASDPTTPOPTGFP<br>PRLPNGEPSDPGGKGTFRNGSPPPGAPSSRFVVKLPFHGLGEP<br>YRRGRWTCVDVYERDLEPHSPGGLLEGIRGASGGAGGRSLDSRL<br>ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLGQ<br>LVVPSKAKAEKPLSASSPQQRPPPETGESAGTSRAATPLPSL<br>RVEAEGAGSGARTPPLSRRKAVDMRLRMLGAPPEMGOVPLDS<br>RPSSPALYPTHASLVHKSPPDFGAVAAQKFSLAHSMIAISGHL<br>DSDDSGSGSLVGIDNKIEQAMDVLKSHLMFAVREEVEVLKEQI<br>RELAERNAALEQENGLRALA\SPEQLGSAGPPRGVPR\LGPPA<br>PNGPFVLSLPSLTIVPLGLPLASAAWPLPMALIVPVFPVGV<br>VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTRGQQGAPFGEET<br>QPPPSLPGTPOQ  |
| 6098       | 168  | 1074   | NYCLRHRSPLERDSSPGSSSTSLIKKQRETSPTIMRALKELD<br>EGKIFKNWGTQTEKEDTSNINPROTETS VNASRSPEKCAQQRQK<br>RLNSASQRSSSLPPSNRKSSTPTKREIMLTPTVAYSPKRSPE<br>NLSPGFSHLLSKNESSPIREFDILLDDLDTPVSTLQRTNPRKQL<br>\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCEPVPNGVKVSVR<br>TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D<br>ELTKEKDQIEAALSMPSPGGRITLQTRLNQEAFGRSFGKD  |
| 6099       | 168  | 1074   | NYCLRHRSPLERDSSPGSSSTSLIKKQRETSPTIMRALKELD<br>EGKIFKNWGTQTEKEDTSNINPROTETS VNASRSPEKCAQQRQK<br>RLNSASQRSSSLPPSNRKSSTPTKREIMLTPTVAYSPKRSPE<br>NLSPGFSHLLSKNESSPIREFDILLDDLDTPVSTLQRTNPRKQL<br>\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCEPVPNGVKVSVR<br>TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D<br>ELTKEKDQIEAALSMPSPGGRITLQTRLNQEAFGRSFGKD  |
| 6100       | 2  | 713  | FVEVSGYRSRADPEPRGRDTPMTYAYLFKYIIIGDTGVGKSCLLL<br>QFTDKRFQPVHDLTIGVEFGARMVNDGKQIKLQIWDTAGQESF<br>RSITRSYYRGAAGALLVYDITRRETENHLSWLEDARQHSSNM<br>VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETS AKTACN<br>VEEAFINTAKEIVRKIQQGLFDVHNEANGIKIGPQOSISTSVGP<br>SASQRNSRDIGNSGCC  |
| 6101       | 1  | 1399   | FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSRALSPLLAFR<br>GKMVFPPLSCAVQQYAWGKMGSNSEVARILLASSDPLAQIAEDKPY<br>ABELWMGTHPRGDAKILDNRISQKTL SQWIAENQDSLGSVKVDTF   |

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|------------|--|--|---|
|            |  |  | NGNLPFLFKVLVSVEPLSLIQAHPNKELAEKHLQAPQHYFDANH<br>KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH<br>LKQTMSHDSQAVASSLQSCFSLMKSEKKVVVEQLNLLVKRISQ<br>QAAAGNNMEDIFGELLQLHQQYPGDIGCFIYFLNLLTLKPGE<br>AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE<br>NLSYTPSSSKDRFLPLTRSQEDPYLSIYDPPVPDFTIMKA\EPV<br>G\SVTEYKDLALDSASILMVQGTVIASPTPTTQTPILQRRGVL<br>FIGANESVSLKLTBPKDLLIFRACCLL   |
| 6102       | 70   | 2415   | QTPQATLAANGAEDSRGGEMLPAGSIGASPAAPCCSESGDERKN<br>LEEKSDINVTVLIGSKQVSEGTONGDLPSYVSFAFIEKEVGNLKL<br>SLKKLKLIEQRTVSKMQLEEQVLTISSEIPKRIRSAKNABES<br>KQFLNQFLEQETHLFSAINSHLLTAQFWMDLGTMISSIEIER<br>HLAYLKWISQIEELSDNIQQYLMNTNVPFAASTLVSMALDIKL<br>QESSCTHLLGFMRAVTKFWHKILKDKLTSDFEELAQHLWPFIA<br>PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\<br>HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNRQTNVLS<br>KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSVLNARLEFSRG<br>LMLLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP<br>GTFASCMHILSEETCFQWLTVERKFALQKMSLSSEAAWVSQ<br>YKIDITDVBEMKVPDCAETFMILLVITDRYNLPTASRKLOFLE<br>LQKDLVDDFRIRLTQVMKEETRASLGFYCAILNAVNYISTVLA<br>DWADNVFFLQLOQAALVFAENNTLSKLQGLQASMESSVFDMM<br>INLLERLKHDMLTRQVDHVFEVKDAAKLYKKERWLSLPSQSEQ<br>AVMSLSSSACPLLLTLRDHLIQLLEQLCFSLEKIFWQMLVEKLD<br>VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPNFYF<br>RHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT |
| 6103       | 207  | 2523   | ESNSTMTTYLEFIQQNEERDGVRFSSWNVPSSRLAETRMVVPVA<br>ALFTPLKERPDLPPIQYEPVLCSSRTTCRAVLNPLCQVDYRAKLW<br>ACNFCYQRNQFPSPSYAGISELNQPAELLPPQFSSIEYVLRGPQM<br>PLIFLYVVDTCMEDELQALKESMQMSLSLLPPTALVGLITFGR<br>MVQVHELGCESISKSVVFRGTDLSAKQLQBMGLSKVPVTQAT<br>RGPOVQQPPPSNRFLQPVQKIDMNLTDLLGELQDPWPVPQGR<br>PLRSSGVALSIAVGLECTFPNTGARIMMFIGGPATQGGPMVVG<br>DELKTPIRSWHDIDKDNAYVKKGTKHFEALANRAATTGHVIDI<br>YACALDQTLLEMKCCPNLTGGYVMVGDSEFNTSLFKQTFQRFVT<br>KDMHGQPKMGFGGTLEIKTPR\BIKISGAIGPCVSLNSKGPVS<br>ENEIGTGTGTCQWKICGLSPTTTTLAIYFEVVNQHNAPIQGG\RG<br>A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD<br>QEAAILMARLAIYRAETEGPDVLRWLDRQLIRLCQKFGEYHK<br>DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH<br>FMRQDLTQSLIMIQLIYAYSFSGPPEPVLLDSSSILADRILLM<br>DTFFQILYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE<br>ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES<br>GAPILTDVSLQVFMHLLKLAUSSAA        |
| 6104       | 124  | 732  | KVSEYIILSKDKILFHALAMLVLVVSFWSAARGVLRNYWERLLR<br>KLQSRPFGFPPWGPALAVQ\AQPCLOSQMQIPVEVKRI/RS<br>LDSIFWMAAPKNRRTIEVNRCCRNPQKLIKVNNDIVCECGH<br>LKQKHVLCAICYEKVKETAETIRRGKQEGGPFKAPTITETVVL<br>YTGETPSEQDQGR I IERDRKRPWSFTQN   |
| 6105       | 3  | 989  | PLHGACTSLVLQRFCHRRRPRCAPARPEDMRRPAAVPLLLLLCF<br>GSORAKAATACGRPRMLNRMVGGQDTQEGEPWQVSIQRNGSHF<br>CGSLIAEQVWLTAACHFRNTSETSLYQVLLGARQLVQPGPHAM<br>YARVRQVESNPLYQGTASSADVALVEAPVPFTNYILPVCLPD<br>PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR<br>CNLLYSKDTTEFGYQFKTIKNDMLCAGFEKGKACKGDSAGPLV<br>CLVGQSWLQAGVISWGECCARQNRPGVYIRVTAHHNWIHRIIPK   |

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|------------|--|--|--|
| 6106       | 3  | 1302   | LQVQPSSEVGRPEVTPPGPGAP<br>GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIESRGRPAAS<br>AGLRDRRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPG<br>WSRARHQPGLCLLLLLLCCQFMEDRSAQAGNCNLROAKNGRCQV<br>LYKTELSKEBCCSTGRSTSWTEEDVNDNTLFKMMIFNGGAPNC<br>IPCKETCENVDCGPGKKCRMNKKKPRCVCAPDCSNITWKGPCV<br>GLDGKTYRNECALLKARCKEPELEVQYQGRCKKTCRDVFCPS<br>STCV\VDQTNAYCVTCNRIPEPASSEQYLCGNDGVITYS\SAC<br>HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV<br>GRGRCSLDELCPDSKSDPEVCASDNATYASECAMKEAACSSGV<br>LLEVKHSGSCNSISEDTEEEEDDQDYSPFISSILEW  |
| 6107       | 623  | 168  | SRCSFRPEPGRGRGK/LSPSEHRRKWEVFKACDEDHKGYSRE<br>DFKTAVMMLFGYKPSKIEVDSVMSSINPNTSGILLEGPLNIVRK<br>KKEAQRYRNEVRHIFTAFDTYYRGFLTLEDFKKAQROVAPKLPE<br>RTVLEVFREV\DRDS\DGHVSE   |
| 6108       | 3  | 1348   | GCSLRFSPRPVSCSRVFCVPPGGCGLPSFMSASRPQSPTTPW<br>CLPRRYMKHKRDDGPEKQEDSAVDVTPVMTCVFVVMCCSMLVLL<br>YYFYDLLVYVIGIFCLASATGLYSLAPCVRRLP\SASAGESA<br>LLAPTIPNNSLPYFHKRPQARMLLALLFCVAVSVVWGVFERNEDQ<br>WAWVLQDALGIAFCLYMLKTI RLPTFKACTLLLLVFLYDIFPV<br>FITPFLTKSGSSIMVEVATGPSDSATREKLPMLVKVPRLNSSPL<br>ALCDRPFSLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI<br>AYGVGLLVTFVALALMQRGQFALLYLVPCTLVTS CAVALWRRRL<br>GVFWTSGGFAKVLPPSPWAPADGPPKDSATPLSPQPPSE<br>PATSPWPAEQSPKSRTESEMGAGAPMREPGSPAESSEGRDQAQPS<br>PVTQPGASA   |
| 6109       | 1  | 1381   | CRSRAGAASGGGAILGKTLRRQRVDNTNKLDPVPSALRAAMLY<br>LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNDQLEQRVSEFF<br>MNAKKNKPEWREEQMASIKKDYKALEDADEKVQLANQIYDLV<br>RHLRKLQDELAKFKMELEADNAGITEILERRSLELDTPSQPVNN<br>HHAHSHTPVEKRYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA<br>SKENTLGCRRNNSTASSNNAYNVNSSQPLGSGYNIGSLSSGTGAG<br>GI\TMAAAQAVQATAQMKEGRRTSLLKASYEAPKNNDQGLGKEF<br>SMARETVGYSSSSALMTTLTQNASSSAADSRGKSKNNKSSS<br>QSSSSSSSSSLSSGSSSTVVQEI SQTTVVPESDNSQVDWT<br>YDPNEPRYCICNQVSYGEMVGC DTQDCPIEFHYGCVGLTEAPK<br>GKWCPCQCT\AAMKRGRSRHK   |
| 6110       | 77   | 2464   | ACPSAATMSDQDHSMDTAVVKIEKGVGGNNGGNGGGGAFSQ<br>ARSSSTGSSSTGGGGQESQPSPLAIIAATCSRIESPENSNNS<br>QGPSQGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG<br>SSTNGSNGSESSKNRTVSGGQYVVAAPNLQNVQLTGLPGVMP<br>NIQYQVIPQFQTVDGQQLQFAATGAQVQDQSGQIQIIPGANQQ<br>IITNRGSGGNI IAAMPNLLQQA VPLQGLANNVLSGQTQYVTNP<br>VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS<br>GTTISSASLVSSQASSSSFFTNANSYSTTTTSSNMGIMNFTTSG<br>SSGTSNGGQTPQRVSGLGSDALNIQONQTS GGS LQAGQKEGE<br>Q\NQQTQAAPKSI.SRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA<br>ISQETLQNLQAVPNSGPIIIRTPTVGPNGQVSWQTLQNLQNLQ<br>VONPQAQTTITLAPMQGVSLGQTSSTNTLTPIASAASIPAGTVT<br>VNAAQLSSMPGLQTLNLSALQTSQIQVHP IQGLPLAIAAPGDH<br>GAQLGLHGAGGDIHDDTAGGEEGENSPDAQPAQRRTREACT<br>CPYCKDSEGRSGDPGKKKHICHIOGCGKVYKGTSHLRAHLRW<br>HTGERPFMCTWSYCGKRFTSRDELQRHKRTHTGEKKFACPECPK<br>RPMRSDHLSKHIKTHQNKKGPGVALSVGTLPLDSGAGSESGST<br>ATPSALITNMVAMEAICPEGIARLANSGINVKEGGQFCSPINT<br>SANGF |



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|------------|--|--|---|
| 6111       | 1637   | 797  | RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAGSVEAVARLKRSLKVRFCNTESQKSRAELVGGQLQRLGFDISEQEVTPAPAPACQILKERGLRPYLLIHDGV\ASEFDQIDTS/STPNCVVIADAGESFSYQNMNNAFQVLMLEKPVLLSLGKGRYYKETSGLMLDVGPYMKALEYACGIIKAEVGGKPSPEFFKSALQAIGVEAHQAVMIGDDIVGDVGGAQRCGMRALQVTRTGKPRPSEHHPVEVKADGYVDNLAEAVDLLQHADK  |
| 6112       | 77   | 196  | MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTNKIRHNWK   |
| 6113       | 1779   | 567  | WGRSNAACGVN:QGAWGERSGVRASEAESPGKRAVDSSWSRQLETMVDHLANTEINSQRIAAVESCFGASGQPLALPGRVLLGEGVLTKECRKAKPRIFFLNDILVYGSIVLNKRKYRSQHIIPLEEVTELLPETLOAKNRWMIKTAKKSFVVSASATERQEWISHTIEECVRRQLRATGRPA\STEHAAPNIPDKATDICTMRCTQTRFSALTRRHCRKRCRVVCAECRSQRFLPRLSPKPVVCSLCYRELAAQQRKEAEAEQAGVPRASHLARPICGRPVEMTMTPTRTTRAAGTATGPAAWSSTPRGWGLPSTADPRPAEHLSPQLHCPGPGEGSSRSCPGLRDPPIPWQVQRWGVALSGLPVFPFCNTLCPYGTAGNAFFPRKPQNTHRWS     |
| 6114       | 818  | 246  | PTSRPRPSPGSPAMSWACVSAAPSSSWPSSSWPCGPRRCCTRRRCSPRCGLAAGSMCSCSPSWRCTPVFACWPSPP\PAEQVQCGHLPPHADRRRLRLVAAPARGPGPGHPAGPAGPRPARTPPASP HGPGRPTVPAPPCPLAATEPTPSRPHQRWTRDRMLGRGSQVTRPQWFLRGLVLFSL  |
| 6115       | 324  | 71   | DVCGRVCAHPHYLIHMHICAHAC\IHTHAQLC/ITASHALAHSHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR  |
| 6116       | 595  | 1430   | TGVMPGGRWHA/ISSSGPVFEGARA/LQTVKKBEEDSYTPVQAARPTLNRPGQELFRQLRQRYHBSGPLETSLRLRELCRWNLRPDVLKSAQILELLVLEQFLSILPGELRVVQLHNPESGEE/LNPCWRSRGTLMGHPGGTRALP\EPICALDGYRS/LRSAQIWSLASPLRSSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPREGCPGDQVTPTRSLTAQLQETMTFKDVBVTFSDQEWGLDSQRNLYRDVMLENYRNMA SLGK   |
| 6117       | 1433   | 222  | VGVSPAPPSCSWEVGPGGGWTPGILKEGQGGRRTPLLLLATRTRLGLSLFPAPAMHPAFLPVVVAVLWGAAPTRGLIRATSDHNASMDFADLPALFGATLSQEGQLQGLVEAHPDNACSPIAPPAPVNGSVFIALLRRFDCNFDLKVLAQKAGYGAAVHNVNSNELLNMVNSEBIQQIWIPIPSVFIGERSSEYLRLALFVYEKGARVLLVPDNTFPLGYLLIPFTGIVGLLVLAGAVMIARCIQHRKRLQRNRLTK\EQLKQI\PTHQYQKGDQYDVCAICLDEYEDGDKLRVLPCHAHYHSRCVDPWLTQTRKTCPICKQPVHRGPGDEDEQEEETQCGEEDBGEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPLSPSSSPVILV |
| 6118       | 1044   | 247  | STISCRACSTGATPGAQSHRSARGHAAGGKETAALGMERGKVKKEKEKETQKEKIGKEGKEEKVKEKEVEQKIKQEKQEKQERRKGEKEEKRTQKGKTNKEKEQPKGQEEKGENKDSLTTRTPLEPLEKNKQILVLGLDGACKTSVLHSLASNRVQHSVAPTQGFHAVCINTEDSQMEFLEIGGSKPFRSYWEMYSN/ADSLARSFVSGFKQDSQPI TWKAKKYLHQLIAANPVLPVVFANKQDLEAAYHITDIHEALAI   |
| 6119       | 1217   | 462  | DPRFVIENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATRQELLAKALETLLNGVLTIVLEEDGTAVDSBDFQLEDDTCLMLVQSGQSWSPTRSGVLSYGLGRERPKHSDIARFTFDVYKQNPRLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQGLGHMLLGISSTLRHAVEGAEQWQKQRLHSY   |

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|------------|--|--|--|
| 6120       | 785  | 179  | LERAGGGGLSSRALVSGACLSLVARANGKGLPRGRKEFVRAVR VRYVAFRYRTPRAVCLRLWSCRRVIMSGRGKQGGKVRRAKAKSR SSRAGLQFPVGRVHRLLRKGNVAERVGAGAPVYLAHVLEYLTAE ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGKVTIAQG G\VLPNIQAVLLPKKTESQKDEGANDP   |
| 6121       | 1612   | 107  | FVRAQARGSRQPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN RGNGLRAVTPLRPGELLFRSDPLAYTVCKSGRGVVCDCRLGKE KLMRCSQCRVAKYCSAKCOKKAWPDHKRECKCLKSCKPRYPDS VRLGGRVVKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR QLVMTFQHFMRREIQDASQLPPAFDLFEAFKVICNSFTICNAE MQEVGVGLYPSISLNLHSCDPNCISIVFNGPHLLRAVRDIEVGE ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCOAIISSNSERL PDINIYQLKVLDCAMDACINLGLLEALFYGTRTMEPYRIFFPG SHPVRGVQVMKVGKQLQHQGMFPQAMKNLRLAFDIMRVTHGREH SLIEDLILLE/AMRRQHQSIILERSQREIRRVSLLNALLRSHT LCFVSCVNLSYWKFCSVFV   |
| 6122       | 2  | 2324   | RFRKMDGGAASQDESSAAAAAADSRMNNPSETSKEPSMESGDG NTGTQTNGLDQKQPVVGGAIATAQAQAFGLGHQVLAGTSL QAAQSLNVQSKSNEESGDSQOPSQPSQPSVQAAIPOTQLMLA GGQITGLTLTPAQOQLLQQAQAQALLAAVQQHSASQQHSAA GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQLNLQQFV LVHPTTNLQPA\QFIIISQTPQOQOGLLQA\QNLTLQLPRQS QAN LLOSQPRI\TLTSQPATPTCTIAATPIQTLPSQSSTPKRIDTFS LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND FSPTTIFRFEALNLSFKNMCKLPLEKWLDAENLSSDSSLSS PSALNSPGIEGLSRRRKRRTSIEA\NIRVALEKSFLN\QKPTS BEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP IKAIFPSPTSLVATTPTSLVTSSAATTLTVSPVPLPLTSAAVTNLS VTGTSDDTSSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA SSASETSTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG AAQLPANASLAAMAAAAGLNPSLMAQSQAAGGALLSLNPGTSL GALS PALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA PNIVTAPLFLNPQNLSSLTSNPVSLVSAAAAAGNSAPVASLHA TSTSAESIQNSLFTVASASGAASTTTTASKAQ   |
| 6123       | 3  | 2944   | HLLHRWFQTDQMIFNTTGFQTEACPYLGTSHSESRFGILHL HLQPLEMKRVGVVFTPADYGVKVTSLILIRNNLTVIDMIGVEGFG ARELLKVGGRLPAGGSLRFKVPSTLMDCRRQLKDSKQILSIT KNFKVENIGPLPITVSSLKINGYNCCQGYGFVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHLL PLCADVVPGPSWEESFWRLTVFFVSLSLGLVILIAFQQAQYIIM EFMKTRQRQNASSSSQNNNGPMDVISPHYSKSNCKNFDLTGYS DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSSOKKHKCSVYYSK HKTSTAAASSTSTTEEKQTSPLGSSSLPAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPESRKNNNGNQVPVKNEVDHCENLKKVDTK PSSEKKIKHTSREDMFSEKQDIPFVEQEDPYRKKLQEKREGNL QNLNWSKSRCTCRKNKRGVAPVSRPPEQSDKLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASLPAQAQREAGYQKPEK KCVDFKCSDDSSDCGSSSGSVRASRGWSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTTPVCVTSSLNCTLE NGVPCVQIESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAPP ENMNYANGFPCCPADVQTDFFIDHNSQSTWNTPP\NMPAS\WGNA QFPSSSRPYLKSTPKACLPMGLFGPI\WAP\QSDVYENCCPIN |

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|------------|--|--|--|
|            |  |  | PTTEHSD/THMENQA\VVCKEYYPGF\NFFRAYMNLDIWTTT\ANRANFPLSRDSSYCGNV  |
| 6124       | 1573   | 236  | SDEALRLAGERGMGRVQLFEISLHGRVVYSPGEPLAGTVRVRLGAPLPFRAIRVTCIGSCGVSNKANDTAWVVEGYFNSSLSLADKGSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRFSKDHKCSLVFYILSPLNLNSIPDIEQPNVASATKKFSYKLVKGTGSVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKVSYKAKRWIHDVRTIAEVEGAGVKAWRAQWHEQILVLPALPQSALPGCSLIHIDYLLQVSLKAPEATVTLVPVFIGNIAV/NPCPSEPPARPGAASWGPTPGG\PSAPPQEEAEAAAGGPHFLDPVFLSTKSHSQRPPLLATLSSVPGAPEPCPDGSPASHPLHPLCISTGATVPYFAEGSGGPVPTTSTLILPPEYSSWGYPEAPPSYEQSCGGVEPSLTPE   |
| 6125       | 1  | 904  | KTCPKLTCAFTVSVPDSCCRVCRGDGELSNEHSDGDI FRQPANREARHSYHRSHYDPPPSRQAGGLSRFGARSHRGALMDSQASGTIVQIVINNKKHKGQCVSNKGTYSHGESHWPNLRAFGIVECVLCTCNVTKECKKIHCNRYPCKYPKIDGKCKKVCBG/KKAKEBLPGQSFDNKGYFCGBETMPVYESVFMEDGETTRKIALETERRPPQVEVHVWTIRKIGILQHFHIEKISKRMFEELPHFKLVTRTTLTSLQWKIFTEGEQIQISQMCSSRVCRTELEDLVKVLYLERSEKGC  |
| 6126       | 1224   | 389  | RLLEAPCPRRRRFQMNPEWGAQFVHVAVAGGLCAVAVFTGIFDSVSQVQGYEYAEAPVAGLPAPLAMPFNSI.VNMAYTLGLSWLHRGGAMGLGPRYLKDVFAAMALLYGPVQWLRLWTQWRAAVLDQWLTLPFAFWPAWCLYLDLDRGWRP\WLFSLSECVSLASYGLALLHPQGFVALGAHVVPVAVGQALRT\HRHYG/SATPSATYALGVLSCLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCVLFQHFAPLFLTHFNTHPRFHPSSGGKTR  |
| 6127       | 1335   | 463  | VLPRRCLVFVNTMDSSREPTLGRDLAAGFWQVQWRFDADEKGYIEEKELDAFFLHMLMKLGTDDTMKANLHKVKQFMTTQDASKGRIRMKELAGMFLSEDENFLLFRRENPLDSSVEFMQIWRKYDADSSGFISAAELRNFLRDLFLHKKAISEAKLEEYTGTMKIFDRNKDGRDLNDLARILALQENFLQPKMDACSTEKRGDFEKIFAYYDVSKTGALEGP\EVDGFKVDMMLVQPSISGVLDLDFKFEILLRHCDVNDGKIQKSELALCLGLKINP  |
| 6128       | 2511   | 843  | TCRMSRRQLERWVWSSQVQVQARGNRVAPRLGKIAMGLEMSSKDSFGSLDGRAWEDAQKQPSAWCGGRKTRVYATSSRRAPPSEGTTRGGARPEKTABEGPPAAPGSLRHSGPLGPHACTALPEPQVTSAMSSQVVGIEPLYIKAEFASPDSPKGSSETETEPVALAPG\PAPTRCLPGHKEEDGEGAGPGEQGGKLVLSLPLKRLCLVCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKACQACRFTKCLRVGMLKEGVRLDRVGRGRQKYKRRPEVDPLFPFGPPFAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPDGHLPAVATLCLDFDREIVVTISWAKSIPGFSSLSLSDQMSVLQSVWMEVLVLGVAQRSLTLDLQELAFAYLVLDDEGARFAGLGELG\AALLQLVRRLLQALRLERERYVLLKALALANSDSVHIEDEPRLWSCEKLLHEALLEYACRAGPGGGAERRRAGRLLLTLPLLRQTAKVLAHFGYGVKLEGKVPMMKLFLEMLEAMMD |
| 6129       | 1764   | 771  | ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAKHPCNASMECDKQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMMKSSDCVIKHAGVYSTGLAMVGAICDFCEANVCHGRKCLSTHACAPLTDAC\VEECERGVWDHGGRI FSCS FCHNFLCEDDQFEHQASCOVLEAETFKCVSCNRLGQHSCLRCKACFCDHTRSKVFKQEGKQPPCPKCGHETQETKDLMSSTRSLKFGRTGGEEDGASGYDAYWKNLSSDKYGDTSYHDEEEDYEAEDEDEEEDGRKDSDESSDLFTNLNLGRTYASGYAHYEQEN   |
| 6130       | 3  | 577  | GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCFIEKYDPTIE  |

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|------------|--|--|--|
|            |  |  | DFYRKEIEV\DSPPSVAGISWTQOGTEQF\ASMRDLYIKKGQGC ILVYSLVNQQSFQ\DIKPMRDQIIIRVKVSEKVPVI\LVGN\SVD LESEREVSSSEGRALAEENGCFPMETSAKSKTMVDELFAEIVRQ MNYAAQPKDKDPPCCSACNIQ  |
| 6131       | 3  | 1811   | SSPREKTS DSSHRPSRHGFLFLRLVGLSPFSYLCVPPSRPVPGS PRSLSANRLLPLAPGRLRRGSPRHLPSCPALLLLVLGGCLGVF GVAAGTRRPNVLLLTDDQDEVLGGMTPKKTALIGEMGMTFS SAYVPSALCCPSRASILTGYPHNHVNNNTLEGNCSSKSWQKI QEPNTFPAILRSMCGYQTF\AGKYLNEYGAPDAGGLEHVPLGW SYWYALEKNSKYNYTSLINGKARKHGENYSVDYLTVDLVANVSL DFLDYKSNFEPFFMNTATP\APHSPWTAAPQYQKAFQNVFAPRN KNFNHGTNKHWRIRQAKTPMTNSSIQFLDNAFRKRWQTLTSSVD DLVEKLVRKLEFTGELNNTYIFYTSNGYHTGQFSLPIDKRQLY EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPITLDIAGYDLNK TQMDGMSLLPILRGASNLTRSDVLVEYQGEGRNVTDPCTPSLS PGVSQCFPDVCEDAYNNYACVRTMSALWNLYCEFFDDQEVFV EYVNLTAADPDQITNIAKTIDPELLGKMNYRLMLQSCSGPTCRT PGVFDPGYRFDPRLMFSNRGSRVTRRFRSKHLL   |
| 6132       | 96   | 1241   | AAGLLPPGLVPEDPRTRNLLPFGIQGPPFALSRLPFCVESGW AWEAMEPEFLYDQLPKGVPEPAAEEELSKGGKKKYLPTSRKD PKFEELQKPA\VLMEWINATLLPEHIVVRSLIEDMFDGLILHLL FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRP SGA\WESIFNKDLLSTLHLLVALAKRFOPDLSLPTNVQVEVITI ESTKSGLKSEKLVQEQLTEYSTDKDEPPKDVDFELFKLAPEKVNVA VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLIGOLEGFF LHLKEFYLPFNSPAEMLHNVTALALELL/IGRGAQLPC/LALK/ TIVNKDAKSTLRVLVGLFCKHTQKAHRDRTPHGAPN  |
| 6133       | 2  | 4256   | FVHGSMADTDLFMECEEELEFPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAVPPIAAHASVAGHLSTSTTVSSSGAQNDSSTK KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTPVLR PVQVMQNAHVTSPPVASQPIFITTQGFVVRNVRPVQNAQVQV IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTFVRPG STMPVRPTNTFTTIVIPATLTIRSTVQSQSQQTSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSPFPSPAVSIASFVT VKRPGVTGENSNEVAKLVTNLNTIPSLGQSPGPVVVSNSSAH\ GSQRTSGPSSMKVTSSIPVFDLQDGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSPTIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFFY GRDGGKVAQLTNFPKVATSPRCPHCTKRLKNNIRFMNHMKHVE LDQONGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLOHMKDTHKPGEMPYVQVQCYRSSLYSEVD VFRMIHEDTRHLLCPYCLKVFKNGNFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPQKLEGLKPGTKVTIRA SRGQPRTPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPNHFPTYVHCSLCRYST CCSRAYANHMNNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILFRGLTWIAHSRHGQTRDRVHDR NVKNMYPFPPSPFTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTOEPE LASGGGGSGGVGKKEQLSVKKLRVVLALCCNTEQAAEHFRNPQ RRIRRWLRRPQASQGENLEGKYLSEAEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFLMRHHLTPHARRA VAHTLPKQVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVQKHTACQ RSKGMLVMDCHRTLSEEVLAMLSASSTLPVVPAGCSSKIQPL |

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|------------|--|--|--|
|            |  |  | DVCIKRTVKNFLHKKWKEQAREMADTACDSVLLQLVLVWLGEV<br>LGVIGDCPELVQRSFLVASVLPDGNINSPTNRNADMQEELIAS<br>LEEQLKLSGEHSESTPRPRSSPEETIEPESLHQLFEGESETES<br>FYGFEEADLDLMEI  |
| 6134       | 2  | 4256   | FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT<br>TTVSVSQQPVSAFPIAAHASVAGHLSTSTTVSSSGAQNDSSTK<br>KTLVTLIANNAGNPLVQGGQPLILTQNPAPGLGTMVTPVLR<br>PVQVMQANHVTSPPVASQPIFITTOGFPVRNVRPVQANMNQVG<br>IVLNVQGGQTVRPITLVPAPGTQFVKPTVGVQVFSQMTFVRPG<br>STMPVRPTTNTFTTVPATLTIRSTVPQSQSQTKSTPSTSTTP<br>TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPPPAVSIASFVT<br>VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNSSAH\<br>GSQRTSGPESMKTSSIPVFDLQDGGRIKPCRNAQFRVTEAL<br>RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPKTAAPVAS<br>/THPSSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFY<br>GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNMMKHVE<br>LDQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC<br>KICEWAFSESEPLFLQHMMDTHKPGEMPYVCQVCQYRSSLYSEVD<br>VHFRMIHEDTRHLLCPYCLKVFKNAGAFQHHYMRHQR\NVYH\<br>CNKCRVQFLFAKDIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA<br>SRGQPRTPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS<br>IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFTYVHCCLCRYST<br>CCSRAYANHMNNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT<br>SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHHGQTRDRVHNR<br>NVKNMYPSPSPFNKAATVKSAGATPAEPEELLTLPALPSPPA<br>STATPPTPTHQALALPLATECAECLNVDDQDEGSPVTQPEPE<br>LASGGGGSGGVGKKEQLSVKKLRVVLALCCNTEQAHEFRNPQ<br>RRIRRWLRRFQASQGENLEGKYLSEAEKLAEWVLTQREQLP<br>VNEETLFQKATKIGRSLGGFKISYEWAVRFLRHHTPHARRA<br>VAHTLPKDAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL<br>DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY<br>RGOMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ<br>RSKGMVMDCHRTSLSEVLAMLSASSTLPAVVPAAGCCSKIQPL<br>DVCIKRTVKNFLHKKWKEQAREMADTACDSVLLQLVLVWLGEV<br>LGVIGDCPELVQRSFLVASVLPDGNINSPTNRNADMQEELIAS<br>LEEQLKLSGEHSESTPRPRSSPEETIEPESLHQLFEGESETES<br>FYGFEEADLDLMEI |
| 6135       | 2  | 4256   | FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT<br>TTVSVSQQPVSAFPIAAHASVAGHLSTSTTVSSSGAQNDSSTK<br>KTLVTLIANNAGNPLVQGGQPLILTQNPAPGLGTMVTPVLR<br>PVQVMQANHVTSPPVASQPIFITTOGFPVRNVRPVQANMNQVG<br>IVLNVQGGQTVRPITLVPAPGTQFVKPTVGVQVFSQMTFVRPG<br>STMPVRPTTNTFTTVPATLTIRSTVPQSQSQTKSTPSTSTTP<br>TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPPPAVSIASFVT<br>VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNSSAH\<br>GSQRTSGPESMKTSSIPVFDLQDGGRIKPCRNAQFRVTEAL<br>RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPKTAAPVAS<br>/THPSSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFY<br>GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNMMKHVE<br>LDQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC<br>KICEWAFSESEPLFLQHMMDTHKPGEMPYVCQVCQYRSSLYSEVD<br>VHFRMIHEDTRHLLCPYCLKVFKNAGAFQHHYMRHQR\NVYH\<br>CNKCRVQFLFAKDIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA<br>SRGQPRTPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS<br>IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFTYVHCCLCRYST<br>CCSRAYANHMNNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT   |

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|------------|--|--|--|
|            |  |  | <p>SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR<br/> NVKNMYPSPSPPTNKAATVKSAGATPAEPEELLTPALAPLPSA<br/> STATPPPTPTHQALALPPLATEGAECINVDQDEGSPVTQEP<br/> LASGGGGSGGVGKKEQLSVKLRVLFALCCNTEQAAEHFRNPQ<br/> RRIRRWLRRFQASQGENLEGKYLSEABEKLAEVWLTQREQQLP<br/> VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHTPHARRA<br/> VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL<br/> DTEVLSSDDRKENALQTVGTGEPWCDVLAAILADGTVLPTLVFY<br/> RQMDQPANMPDSILLEAKESGYSDDIEMELWSTRVWQKHTACQ<br/> RSKGMVMDCHRTLSSEVLAMLSASSTLPVAVPAGCSCSKIQPL<br/> DVCIKRTVKNFLHKKWKEQAREMADTACDSVLLQLVLVWLGVEV<br/> LGVIGDCPELVQRSFLVASVLPDPGNINSPTRNADMQEELIAS<br/> LEEQLKLSGEHSESTPRPRSSPEETIEPESHLQLFEGESETES<br/> PYGFEEADLDLMEI</p>  |
| 6136       | 1704   | 539  | <p>PGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEYRLGQVAS<br/> SLFRGEHHSRGGTGRLASLFSLEPOIQPVYVPVK\ESALASA<br/> DLEEEIHQKQGGKRNKNSQPGVKVADRKILDDTETVVSQRKIQ<br/> INQEEERLNERTVFGVNLVPTCNKKLKSFFKEYGQIESVRFR<br/> SLIPAEGTSLSKLAAIKRKIHPDQKNINAYVVFKEESAATQALK<br/> RNGAQIADGFRIKVDLASETSSRDKRSVFVGNLPYKVEESAIEK<br/> HFLDCGSIMAVRIRVDKMTGIGKGFYVLPENTDSVHLALKLNN<br/> SELMGRKLRVMSVNKEKFKQNSNPRLKNVSKPKQGLNFTSKT<br/> AEGHPKSLFIDGEKAVLLKTKKKGQKSGRPKKQRKQK</p>  |
| 6137       | 141  | 2656   | <p>RALRRRCGPGRRGALGSGPGPQRRPGRVPEERPAFPRERKHFG<br/> MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGLAKK<br/> YLWQG\LFQLYLDEAGRGHSFSGHGAALTAPKQGGELMAKALE<br/> LSCPKDMAPSHCAEHKQFLQLSQYRQLKTAEDYQALNKDIEAQ<br/> LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGGAWLRVV<br/> LEKPFQHDHPSAQQLATELGTFFQEEMRYRVDHYLGKQAVQAL<br/> PFRDQNRKALDGLWNRHHVERVEIMKETVDAEGRTSFYEEYGV<br/> IRDVLQNLTEVLTAVAMELPHNVSSAEAVLRHKLQVFOALRGL<br/> RGSAVVGQYQYSYEQVRRELQKPDSEHSLTPTFAGVLVHIDNL<br/> RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAQ<br/> QCLPRQLVFHGHGDLGSPAVLVSRLFRPSPSSWKEMEGP<br/> LRLFGSPLSDYAYSPVRRERDAHSLVLSHIFHGRKNFFITTENL<br/> LASWNFWTPLLSELAHKAPRLYPGAENGRLLDFESSGRLLFFS<br/> QQQPEQLVPGPGPGMPSPDFQLRAKYRESLSVSAWSEELISK<br/> ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN<br/> AHTHLWLVDERCVPVLPSPESNFQGLQAHLLQHVRIPIYNIH\AM<br/> PVHLQORLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH<br/> TASLPQSPGTGLDGEQLVLTSPSPQPHRRMSLSLPLINRAKKV<br/> AVLVMGRMKREITTLVSRVGHGEPKKWPISGVLPHSGQLVWYMDY<br/> DAFLG</p> |
| 6138       | 4587   | 934  | <p>EFSKLTDRWQNAVQGVQRKGDVDGLVRQWDFTTSVENLFRFL<br/> TDTSHLLSAVKQGERFSLYQTRSLIHELKNKEIHFQRRRTICAL<br/> TLEAGBKLLLTDTLKTESVGRRIISQLQDSWKMEPQLAEMIKQ<br/> FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPPELHEDLHNEK<br/> ELIKELEQSLASWTONLKEQTMKADLTRHVLVEDVMVLKEQIE<br/> HLRQWEDLCIRVAIRKQEIEDRLNTWVVFNEKNKELCAWLQVM<br/> ENKVLQADISIEEMIEKLQKDCMEEINLFSENKILQLKQMGDQL<br/> IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI<br/> QQLDKNMSNLRITWLARIESELSKPVVYDVCDDQEIQKRLAEQD<br/> LQDIEQHSAGVESVFNICDVLHSDACANETECDSIQQTTRS<br/> LDRWRNICAMSMERRMKIETWRLWQFLDDYSRFDWLKSAB<br/> RTAACPNSEVLYTSAKEELKRFQFQRIHERLTQLELINKQY<br/> RRLARENRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRRLRHFT</p>  |

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|------------|--|--|---|
|            |  |  | NQREEFEGTRESILVWLTMDLQLTNVEHPSDADDKMRQLNG<br>FQOEITLNTNKIDQLIVFGEQLIQKSEP\LDVAVLIEDELEELHR<br>YQOEVFGRVSRFHRRLTSTCPGLEDSKEASENETDMEDPREIQT<br>DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE<br>WDHTGRRRGGPSSSH\EEDEEAQYY\SALSGKSISDGHSHWVPDS<br>PSCPBBHYKQMEGDRNVPPVPASSTPYKPPYKLLLPPTDGG<br>KEGPRVLNGNPQOEDGGLAGITEQQSGAFDRWEMIQAEQEL\HNK<br>LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIOEIE<br>LRVKRLQEILKAFDITYKALVSVSVNVSSKEFLQTESPESTELQSR<br>LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLEWLA<br>SAKNRRQKAHVTPKADPRALLECRRELMLQLEKELVERQPPQVDM<br>LQEISNSLLIKGHGEDCIEAEKVVHVI\EKKLKQLEQVSDQDM<br>ALQGTQNPASPLPSFDEVDSDGQPPATSVAPRAKQFRAVRTE<br>GEEETESRVPGSTRPQRSFLSRVVRALPLQLLLLLLLACLL<br>PSSEEDYSCTQANNF\ARSFYPMRLRYTNGPPPT              |
| 6139       | 52   | 1131   | LGDNVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE<br>TERRPWEASSWKT/LAGWIGGAASVIVGHPLDTVKTRLQAGVG<br>YGNLTSCIRVVYRRESMFGFFKGMSPFLASIAVYNSVVFVFSN<br>TQRFSLQHRCEPEASPPRTLSDLLASMVAGVSVGLGPGVDL<br>IKIRLQMOTPPVSGRQPRFEVQSGSCG\EPAYQGPVHCITTI<br>RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG<br>PSPCAVWLAGGMAGAI SWGTATPMDVVKSRLOADGVYLNKYKGV<br>LDCISQSYQKEGLKVFFRGITVNAVVRGFPMSAAMFLGYELSLQA<br>IRGDHAVTSP   |
| 6140       | 694  | 136  | RPELELWRLRSRWRPLGVPRRCHRRNWKPEVRAQPLSVTVWAP<br>RCQRP/QPPAPEPSSPNAAPPEAIPTPRAAASAALEPLGPAPV<br>SVAPQAEAEARSTFGPAGSRGPGTFRQRFQRYQDAAGPREA<br>FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR<br>ARRIRRRTDVIRITG  |
| 6141       | 2  | 984  | AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS<br>ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS<br>PSEILYCTLNTPKIDMERLLGGQLGLEDFFIAHVKGIEKEVNVY<br>KSEDSLGLTITDNGVGYAFIKRIKDGVIDSVKTCVGDHIESI<br>NGENIVGWRHYDVAKKLKELKEELFTMKLIEPKKAFEIELRSK<br>AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD<br>VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLDGFAFP<br>DEFVFDVWVGIGDAKRRGL  |
| 6142       | 116  | 602  | EAEGEQVCGAKCCGDAPHVENREBETARIGPGVMESKEERALNN<br>LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR<br>FRVRQPIQYRWDIMHRLGEPQARMREENMERIGSEVRQLMEKL<br>REKQLSHSLRAVSTDPFHHDHDEFCLMP   |
| 6143       | 2802   | 270  | FRMRIFLHCPWNQOMWKIWNLLTSLESCAHLSTQKLLKER\Q<br>\QLPVFKHRDSIVETLKRHRVVVAGET\GSGKSTQVPHFLLED<br>LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN<br>SLCGYQIRMESRACESTRLLYCTIGVLLRKLQEDGLLSNVS/HM<br>FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE<br>KFSTYFTTHCPILRISGRSYPVEVFHLEDIEBETGFVLEKDSEYC<br>QKFLEEEEEEVTINVTSKAGGIKKYQEIYIPVQTGAHADLNPPYQK<br>YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI<br>FLPLGLAHIQQLYDLSNDRRFYSERYKVIALHSILSTQDQAAAF<br>TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHES<br>QMSLVETVFSKASALQROGRAGRVRDGFCFRMYTRERFEGFMD<br>YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN<br>AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAI<br>GCLDPVATLAAVMTSEKSPFTTPIGRKDEADLAKSALAMADSDHL<br>TIYNAYLGWKKARQEGGYRSEITYCRNRLNRTSLLTLEDVQOE |

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|------------|--|--|--|
|            |  |  | LIKLVKAAGFSSSTTSTSWEGNRSQTLSFQETALLKAVLVAGL YDNVVGKIIYTKSVDTVTEKLACIVETAQGGKAQVHPSSVNRDLQTH GNLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERLLS IDGWIYFQAPVKIIVIFKQLRLVIDSVLRKKLENPKMSLENDKI LQIITELIKTENN  |
| 6144       | 1289   | 568  | SGPGSMGQQRVDVKKVVMGLKEYVGKTSLVERYVHDFLVGPYQN VSASGGARHGGRSGGVPVICTYGPDLFPLVA\TIGAAFVAKVMS VGDRTVTLGWDTAGSERYEAMSRYYRGAKAIVCYDLTDSSS FERAKFWKELRSLEEGCQIYLCGTKSDLLLEDRRRRRVDFHDV QDYADNIKAQLFETSSKTGQSVDELQKVAEDYVSVAAPQVMTB DKGVDLGQKPNPYFYSCCH  |
| 6145       | 1109   | 196  | GMMDLSBLERDNTGRCRLSSPVPVAVCRKEPCVLGVDEAGRGFVL GPMVYAIICYPLPRLADLEALKVADSKTLESERERLFAKMEDT DFGWALDVLSPNLISTSMGLRVKYNLNSLSDHDTATGLIQYALD QGVNVTQVFDVTGMPETYQARLQGSFPGIEVTVKAKADALYPV \VSAASICAKVARDAQVKKWQFVEKLQDLDTDYG\SGYPNDPQD /TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS L  |
| 6146       | 428  | 781  | LKKKGKKEAEAQVEALFGPSLDQWHRSAAGEEDGVPVLTDEQKS R/YPGHEANDQGG\WDAROSIIRKVVDPETGRTRLIKGDEGVLE EIVTKERHREINKQATRGRDCLAFQMRAGLLP   |
| 6147       | 1  | 2304   | CTRQLPPPSPGSGPGDSPEGPEGEAPERERRKAHGMKLKLYYGLSE GEAAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS ETDMMVRQIRALDSMQTLVYENYNKFISATDTIRKMKNDFRKME DEMDRLATNMVITDPSARISATLQDRHERITKLAGVHALLRKL QFLFELPSRLTKCYELGAYGQAVRYQGRAQAVLQOYQHLPSFRA IQDDCQVITARLAQQLRQRFREGGSGAPEQAECEVELLLALGEP A EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTHDG\S SGFVGGCLCQVAAAYQELFAAQGPAGAEKLAFAARQLGSRYFALV ERRLAQEQGGGDNLSLLVRALDRFHRRRLRAPGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFLGCLTDVROALAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYPGRGF CSQGVREGLIVGFVHSMCQTAQSFCDSPGEGGATPPALLLLLS RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLTHYVKVQGLVISQMLRKSVETRDNLSTLEPRNVRAVMKRV VEDTTAIDVQVLPRLAGVALTQAGGTVP SRGAGAAEDHWQSLPG GDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS CSFSAQDYDIFAPILPVEKQRLRVTEVRAGLVVLKIRPQTNS CILPLPHSTGSINS DHVPTK |
| 6148       | 3056   | 353  | VPAVGCTFADGAMGEAEKFHYIYSCDLIDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSLDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLVPKYPDLPNAQVALTIWDVYGP GKAV PVGGTTVSLFGKYGMFRQGMHDLKVPNCRSQMDQKPTKTPGRT SSTLSEDDMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYEEKDGEDESSPILTSFE LVKVPDPQMSLENLVESKHNLPRSLRSGPSDHDLPYPSPRDQ LKNIVSPYPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAQALALLGKWKPMDEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVNSNGINSAEIDSSQIIT/SAPFPPSVSSPPP\ASKTKEVPDQ ENLEQDLCTFLISRASKNSTLANLYWYVIVECEDQDTQQRDPK THEMVLNVMRFSQALLKGDKSVRVMRSLAAQQTFVDRVLVLM KAVQRESGNRKKKNERLQALLGDNEKKNLSDELIPLEPQVK IRGII PETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDL RQD QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV   |



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|------------|--|--|--|
|            |  |  | PVAEVLDTGEGSIONFFRKYAPSENGPNGISAEVMDTYVKSCAGY CVITYILGVGDRHLNLLLTKTGKLFHIDFGYILGRDPKPLPPP MKLNKEMVEGMMGTQSEYQEQEFKQCYTAFHLRRYSNLILNLF SLWVDANIIPDIALEPDKTVKKVQDKFRLDLSDEBAVHYMQSLID ESHALFAAVVEQIHKFAQYWRK   |
| 6149       | 1  | 1413   | RVDPVRRENGTANPIKNGKTS PASKDQRTGKKT SVQGVQKQKND ESESDFESDPPSPKSS EEEEDDEVLQGEQGFNDDDTEPENL GHRPLLMDSDEEEEEKHSSDS DYEQA KAKYSDMSSVYRDRSGS GPTODLNTIL TSAQLSSDVAVETPKQEFDFVGAVPFFAVRAQQ PQQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKNVQECVA VGPEAHTIPGYPKSVDVFGSTPFQPF LTSTSKSESNEDLFGLVP FDEITGSQQQXVKQRS LQKLSSRRRTKQDMKSNKGRHHGTPT STKTKLTPTTPTPERARRHKKVGRDSSQSSNEFLTISDSKENIS VALTDGKDRGNVLPFEESLLDPFGAKPFHSPD\LSWHPP\HQGL S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F LTELVSQSI THQSQSQSPV\ELDPFGAAPPSPSQ  |
| 6150       | 372  | 37   | MSNIKKYIIDYDWKASIEIEIDHDVMTERRLHQINNFWSDSEYR LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVCFDWNNGNG QEGWPPMDGSEGIRITDIDTSGIF   |
| 6151       | 1555   | 521  | DSNQSVSGTAASTLLHSFKATIIYQGTGHVQOQFYGVTSFYSQT TPIVQSYAQPSLQYIQGQIIFTAHPQGVVQPAAVTIIYVAPG QPQPLQPSMVVNNLLDLPSPPKPKTI VLPNWK TARDPEG KIYYHVITRQTQWDPTTWPESPGDDASLEHEAEMDLGTPTYDEN PMK\ASKKPKTAEADTSS ELAKSKSEVFRKEMSQFIVQCLNPNYR KPDCKVG\RITTTEDFKHLARKLTHGVMNKELKYCKNPE\DL E C NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPWEDGWS GKTD SRRERKSCGPF CSTPVSTVLLMIHHPGFNPADVN  |
| 6152       | 1366   | 648  | NRTWSTPSTWGMVALPPLCSTGPFVTRQITARTTCGAVPAKCP PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHPGQCQRPC KCEHHCPDCKTGNCSSVRVKQCLQPPPEATLRAGELSFFTRTAW LALTALAFLLLI STAANLSLLLSRAERNRRLHGDVAYHPLQEM NGEPLAAEKEQPGGAHNPFD   |
| 6153       | 2  | 3368   | GRVGARSPGRAYALLLLICFNVGSGHLQLVLSRNNKLLPKH PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAERGLKI TYKYTGKGITEPPFGIFVFNKDTGELNVTSLDREETPPFLLTG YALDARGNNVEKPLELRIVLDINDNEPVFTQDVFVGSVEELSA AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT GEIYTTSVTL DREEHSSYTLTVEARDGNGEVTDKPVKQAVQIR ILDVNDNIPVVENKVL EGMVEENQVNVETRIKVFDADEIGSDN WLNFTFASGNEG GYFHIETDAQTN EGI VTLIKEVDYEEEMKNLD FSVIVANKAAFHKS IRSKYKPTPIPIKVKNVKEGIFKSSVI SIYVSESMDRSSKQIIGNFQAFDEDTOLPAHARYVKLEDRDNW ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDIYPRKTI TGTVLINVEDINDNCPTLIEPVQTI CHDAEYVNVTAEDLDGHPN SGPFSSVIDKPPGMAEKWKIARQESTSVLLQQSEKLG RSEIQ FLISDNQGFSCPEKQVLT LTVCEVLHGS\GCREAQHDSYVGLP AATLALMILAFLLLLVPLLLLMCHCGKAGFTPIPGTIEMLHP WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE TTITARATGASRDVAGAAVAALNEEFKNYFTDKAASYTEED ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL KFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM VNSENTYSSGSSFPVPKSLQEANA EKV TQEI VTERS SVSRQAQK VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPSQLIV TERVYAPASTLVDPYANEGTVVTVTERVIQPHGGSSNPLEGTQH |

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|------------|--|--|--|
|            |  |  | LQDVPPYVMVRERESFLAPSSGVQPTLAMPNIYVGVQNVTVTERVL<br>APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH<br>SNSITITSSSTRVTKHSTVQHSYS   |
| 6154       | 3660   | 2146   | KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN<br>SDTAHIKSIBITISILNQLQASESSAEDSEQBDEGAQDMDNNGK<br>EESKIDHLTNNRNDLISKEBQNSSSLLEENKVHADLVISKPVSK<br>SPERLRKDIEVLSEDTDYEBDEVTKKRKDVKKDITDKSSKPKIK<br>RGKRRYCNTECLKTGSPGKKEBKAKNKESLCMENSNSSSSDED<br>EBETKAKMTPTKKYNGLKEKRKSLRTTGFGYSGFSEVAEKRIKL<br>NNSDERLQNSRAKDRKDVWSSIQGWPKKTLKELFSDSDTEAAA<br>SPPHPAPEEGVAEESLQTVAAEESCSPSVELEKPPPVNVDSKPI<br>EBKTEVENDRKAEPSSSGSNFSA*IPLPYLHLNRLHQS*QKGS<br>RQSSSVTVSEPLAPNQEEVRSIKSETDSTIBVDSVAGELQDLQS<br>ERE*LASRF*QCELEQ**SARTRTS*KSLYRSEKSERCSGRRK<br>FIKKAKEKP*NSGKQKQEGK   |
| 6155       | 869  | 121  | HLFPELRGKSWITMKYVYFLGVLGTFFFADSSVQKEDPAPYLV<br>YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMGNFKSRVRDG<br>TEQTINPIQIVRYWNYSHSAPQDDMLIKLAKPAMLNPKVQALN<br>P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLAPVMSDRE<br>CQKTEGGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLOGIE<br>VGHFMGGDVGITYNVYKYVSWIENTAKDK  |
| 6156       | 5725   | 3984   | GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV<br>VMKSETYAPLFCPLSPFHKFCCKGLLADTLVEDVNICLQACSSHL<br>ALSSSLPDDLQRCVDVCRVQLVHRGTCTIRQAFGKLLKSIPLGV<br>FLSNNNHTEIQEISLALRSHMSKAPSNTFFHPQDFSD/VISFILI<br>GNSHRTGKDKWLERLFYSCQRLDKRDQSTIPRNLKTDVFLWQW<br>AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPQD<br>DVSQWTTADNDEGHGNNQLRLVLLQLYLENLEKLMYNAYEGCAN<br>ALTSPPKVIRTFLYTNRTQCDWLTRIRLSIMRVGLLAGQPAVT<br>VRHGFDDLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEATQG<br>IAVSSSSIVGKHLWINSVAQQAEGRFKASVEYQOHLCAMTGV<br>DCCISSFDKSVLTASAGCKSASLKHCLNGESRKSIVLSKPTDSS<br>PEVINYLGNKACECYISTADWAAVQEWQNAIHDLLKSTSTSLN<br>LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK<br>IDMKLLRNM |
| 6157       | 946  | 329  | MANRGFSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH<br>PPGGRAHFQKWLMDGTVLCKLINSLYPPGQEPPIPKISESKMAFK<br>QMEQISQFLKAAETYGVRTTDFITQTVDLWEGKDMAAVQRTLMAL<br>GSVAVTKDDGCRYGEPSPWFHRKAQONRRGFSEQLRQGNVIGL<br>QMGSNKGASQAGMTGYGMPRQIM*DAASCP  |
| 6158       | 441  | 1482   | LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPTLAQNPGLAQN<br>PILEGKDNQNTGVDPIIDHVQDRKTD/SRSKSPHKRSKSRER<br>RKSRSRSHSRDKRDKDTREKIKEKERVKEKDREKEREKEREKE<br>KERGKNKDRDKEREKDRDKDKEREKEREKEREKEREKEREKE<br>QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSR<br>RRRRSRSSSRSPRTSKTIKRKSSRSPSPRSRNKDKKREKERD<br>HISERRERERSTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD<br>SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV   |
| 6159       | 53   | 84   | AVIAPLHISLGDRAAPYLKNTKSSSTTCRRRNQSPFPVMSLTH<br>RLHLCKYNGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV<br>IITGTPILTFVKDPQLEVNFYTGMDSDIAFQFRLHFGHPAIM<br>NSCVFGIWRYEKCYLLPFEDGKPFELCIYVRHKEYKVMVNGQR<br>IYNFAHRFPASVKMLQVFRDISLTVLISD*GRCVRITAVQEF<br>DVSVSCDCTTAYQPG  |
| 6160       | 1626   | 1790   | AGAKFPF*F*KVADAQPTSESEKIYNQVNVVLKDAEGILEDLQS<br>YRGAGHEIREAIQHPADEKLEKAWGAVVPLVGKLLKFFYEFQR  |

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|------------|--|--|--|
|            |  |  | LEAALRGLLGALTSTPYSPTOHLEREQALAKQFAEILHFTLRFD<br>ELKMTNPAIQNDFSYYRRTLSRMRINNPAEGENEVNNELANRM<br>SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLTSMASVC<br>RVMLETPEYRSRFTNEETVSFCLRVVMGVIIILYDEVHPVGAFAK<br>TSKIDMKGCICKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI<br>KSMQ*QLLTLVNGK  |
| 6161       | 455  | 1569   | PVSGSESSLRRASWASILRLMLGPRVAVSILCEDGISH*LLEKH*<br>KSHVLEPLSSLALEEQCLALSLDWSTGKTGRAGDQPLKIISDS<br>TQQLHLLMVNETRRLQKVASWQAHQFEAWIAAFNYWHPEIVYS<br>GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT<br>GSYDEHILLWDTNRNMKQPLADTPVQGGVWRIKWHPFHHLLLAA<br>CMHSGFKILNCQKAMEERQEATVLTSHTLPSLVYGADWSWLLF<br>RSLQRAPSWSFPSNLGTXADLKGASELPTPCHECREDNDEGEH<br>ARPSQGMKPLTEGMRKNGTWLQATAATTRDCGVNPEADSAFSL<br>LATCSFYDHALHLWEWEGN  |
| 6162       | 1  | 586  | RTIHATGRAGASPMHRLIVWRLAEANKQHVRCQKCLEFGHWTYE<br>CTGKRKYLHRPSRTABLKALKKEKENRLLQQSIGETNVERKAK<br>KKRSKSVTSSSSSSSDSSASDSSSEETSTSSSESDDTDESS<br>SSSSSSASSTTSSSSSDSDSSSSSKQ*HQHR*QL*R*TTKEE<br>EKEIELLHYSYWDGLKTL   |
| 6163       | 1081   | 785  | RIRSTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAFTYKFFL<br>TPVVFVFFFFFFHRKE*VMQKNPMKSRDEWMEKLNHLHVQRAD<br>MNRLLIMNYLVTEGFKEAAEKFRMESGIBPSVDLETDERIKIRE<br>MILKGQIQEAIALINSLHPELDDTNRYLYFHLQOQHILIELIRQ<br>ETRAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPESP<br>GDLHTMQRKQVNSEVNQAVLDYENRESTPKLAKLLKLLLWQON<br>ELDQKKVKYPRKMTDLSKGVIEEPK   |
| 6164       | 90   | 406  | PCQSPGRSRMRQDKLTGSLRRGGRCCLKRQGGGVGTILSNVLKKR<br>SCISRTAPRLCTLEPGVDTKLKFTLEPSLGQNGFQOQWDALKA<br>VARLSTGIPKEWRRKVWLTADHYLHSAIDWDKTMRTFNERS<br>NPDDDSMGIQIVKDLHRTGCSYCGQAEQDRVVLKRVLLAYAR<br>WNKTVGYCQGFNLAALILEVMEGNEGDALKIMYILIDKVLPE<br>YFVNNLRALSVDMAVFRDLLRMKLPESLQHLDTLQRTANKESGG<br>GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL<br>RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSH<br>LMQTVYSMAFPFPQLAELREKYTYNITPPFATVKPTSVSGRHS<br>KARDSDEENDPDEDAVVNAVGLGPFSGFLAPELQKYQKQIKE<br>PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNMMMERMTDIN<br>ALKRQYSRIKKKQOQVHOVYIRADKGPVTSILPSQVNSSPVIN<br>HLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVYEDLKTCLNS<br>PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA<br>EAFPSGCTATAGREGSSPEGSTRRTIEGQSPPEPVFGDADVDVA<br>VQAKLGALNELNQDAAETELRVHPPCQRHCPEPPSAPENKAT<br>SKAPQGSNSKTPIFSPFSPVKPLRKSATARNLGLYGPTEPTPTV<br>HFPQMSRSFSKPGGNSGP*KMVFSSGTMLSRQLPGYPQEQYQRN<br>GGERFG |
| 6165       | 90   | 406  | PCQSPGRSRMRQDKLTGSLRRGGRCCLKRQGGGVGTILSNVLKKR<br>SCISRTAPRLCTLEPGVDTKLKFTLEPSLGQNGFQOQWDALKA<br>VARLSTGIPKEWRRKVWLTADHYLHSAIDWDKTMRTFNERS<br>NPDDDSMGIQIVKDLHRTGCSYCGQAEQDRVVLKRVLLAYAR<br>WNKTVGYCQGFNLAALILEVMEGNEGDALKIMYILIDKVLPE<br>YFVNNLRALSVDMAVFRDLLRMKLPESLQHLDTLQRTANKESGG<br>GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL<br>RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSH<br>LMQTVYSMAFPFPQLAELREKYTYNITPPFATVKPTSVSGRHS<br>KARDSDEENDPDEDAVVNAVGLGPFSGFLAPELQKYQKQIKE  |

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|------------|--|--|--|
|            |  |  | PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTIDIN<br>ALKRQYSRIKKKQQQVHVQVYIRADKGPVTSILPSQVNSSPVIN<br>HLLLGKKMKMTNRAAKNAVIHPIGHTGGKISPVYEDLTKLNS<br>PWRTHIRVHKKNMPRTKSHPGCGDVTGLIDEQNEASKTNGLGAA<br>EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA<br>VQAKLGALELNQRDAAETELRVHPPCQRHCPPEPPSAPBENKAT<br>SKAPQGSNSKTPIFSPFPSPVKPLRKSATARNLGLYGPRTERTPTV<br>HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRLPGYPQEQYQRN<br>GGERFG  |
| 6166       | 2  | 1206   | HKLWRTVAMAGAENKSLSECKLEKHLPLDLOEVKRVLYGKELRK<br>LDLPREAFEAASREDFELQGYAFBAEEQLRRPRIHVGLVQNR<br>IPLPANAPVAEQVSALHRRRIKAIVEVAAMCGVNIICFQEAWTMP<br>FAFCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMMVVSPILE<br>RDSEHGDVLWNTAVVISNSGAVLGKTRKNHI PRVGDFNESTYYM<br>EGNLGHPVFOTQFGRIAVNICYGRHHPNLNLMYSINGAEIIFNP<br>SATIGALSESLLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS<br>GDGKKAHQDFGYFYGSSYVAAPDSSRTPLGSRSRDGLLVAKLDL<br>NLCQQVNDVWNFMKTGRYEMYARELAEAVKSNYSPTIVKE*PAS<br>VPALG                       |
| 6167       | 1220   | 1844   | YGI VTG PSLCAGDKQPKKQKEKNFVLVSPEFVDEALCACEEYLSN<br>LAHMDIDKDLEAPLYLTPEGWSLFLQRYQVVEGAELRHLDTQ<br>VORCEDILQQLQAVVPQIDMEGDRNIWIKPGA KSRGRGIMCMD<br>HLEEMKLKLVNGNPVVMKDGKVVQKYIERPLLI FGTKFDLRQWF<br>LVTOWNPLTVWFYRDSYIRFSTQPPSLKNLDK*APLYLTPEGWS<br>LFLQRYQVVEGAELRHLDTQVORCEDILQQLQAVVPQIDMEG<br>DRNIWIKPGA KSRGRGIMCMDHLEEMKLKLVNGNPVVMKDGKVV<br>VQKYIERPLLI FGTKFDLRQWFLVTOWNPLTVWFYRDSYIRFST<br>QPPSLKNLDK   |
| 6168       | 84   | 1392   | VWVPSVSAMPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNNK<br>GAKQKQFIKAVTHQVKFGQONPRQVAQSEAEKKLKKDDKKELQ<br>ELNBLFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH<br>DLTLERKCEKRSVYIDARDEELEKDTMDNWDKLEEVNKKHG<br>EAEKKKPKTQIVCKHFLEAIENNKYGFWVCPGGGIDICMYRHAI<br>PPGFVLKKKKKKKKKEDISL*DLIERERSALGNVTKITLESF<br>LANKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEBRP<br>ELVNDDEEADDDTRYTQGTGGDEVDDSVSVNDIDLSLYIPRVD<br>ETGITVASLERFSTYTSKDKENKLSASGGRAENGERSDLEEDN<br>EREGTENGAI DAVPDENLFTGEDLDELEELNLTDLLE |
| 6169       | 112  | 662  | APAAAMAERPEDLNLNPNVITRIKEALPDGVNISKEARSATSR<br>AASVFLYATSCANNFAMKGKRTLNASDVLSAMEEMEFQRFVT<br>PLKEALEAYRREQKGKKEASEQKKKD KKKTDSEEQDKSRDEBN<br>DEDEERLEEEEQNEEEVDN*KGRET VAPWKVPLEMRRATCFCE<br>AFPCWAE   |
| 6170       | 62   | 667  | STKVMLPNTGRLAGCTVFITGASRGIGKAIKAAKDGANIVIA<br>AKTAQPHPKLLGTIYTAABEIEAVGGKALPCIVDVRDEQISAA<br>VEKAIKKFGGIDILVNNASAI SLTNLDTPTKRLDLMMNVNTRG<br>TYLASKACIPYLKKSVAHI PNISPLNLNPNVWFKQHCGRW*VV<br>G*GDGLCLICFELNLCMSDVITICT   |
| 6171       | 382  | 941  | HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST<br>MAEAFSKTTSEEDQSIQEPKEANSMTAQKQK*GLRGSRRRHAN<br>SGGDI FGDSFAAYFPVLKQVHQALSLSQEA VSMVMDSMVRDILD<br>RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT<br>NATLRYTKSK  |
| 6172       | 651  | 54   | GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR<br>SAQERKERLRRALEENRLIPTELRREALAQGSLEFDDAGGEGV<br>TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMF AKELKLVFPGA   |

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|------------|--|--|--|
|            |  |  | QRMNRRHEVGALVRACKANGVTDLLVVEHRTGTPVGLIVSHLP<br>FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV<br>SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDRHNV<br>LTEVGPRFELKLYMIRLGLTLEQATADVEWRWHPYNTTARKRVF<br>LSTE*AAPRPLGQLL  |
| 6173       | 3  | 288  | SVDRHEVQVLSQSMPLTPHQAVALRGERPYMCVECGKCFGRSSHL<br>LQHQRIHTGEKPYVCSVCGKAFSSQSVLSKHRTIHTGEKPYECN<br>ECGKAFRVSSDLAQHHKIHTGEKPHCELECKRAFTQLSHLIQHQ<br>RIHTGERPYVCPCLCGKAFNHSTVLRSHQVRHTGEKPHRCNECGK<br>TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLQHHNVHT<br>GEKPYECSECGKTFSHRSTLMNHERIHTTEKPYACYECGKAFVQ<br>HSHLIQHQKVRKL*PTCVLSVGSALAGVPTSFISVSTLERSP<br>MCAVYVGRPSARAQSLVNTGQFTQVRSFMSVMSVEKPLE   |
| 6174       | 1060   | 959  | PRPPGKRWVAGLGNPGLPGTRHSVGMVGLQARRLGVAESWT<br>RDRHCAADLALAPLGDALVLLRPRLMNANGRSVARAAELFGL<br>TAEVYLVDDELKPLGLRLALKLGSARGHNGVRSCLNSNA<br>MRLRVGIGRPAHPEAVQAHVLCFSPARQELLPLLLDRATDLI<br>LDHIRERSQGPSLGP*H*WFSKKA   |
| 6175       | 2204   | 334  | RYFRADPRSRSGQPRAEGLGAFAGPLRAMAAPVKGNRKQSTEG<br>DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEQEREEQ<br>AFLVSLYKFMKERHTPIERVPHLGFQKINLWKIYKAVEKLGAYE<br>LVTGRRLWKNVYNELGSGSPGSTSGATCTRRHY*RLVLPYVRHLK<br>GEDDKPLPTS KPRKQYKMAKENRGDDGATERPKKAKEERRMDQM<br>MPGKTKADAADPAPLPSQEPNRNSTEQQLASGSSVSFVSGASC<br>PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG<br>CRHGAEPQASPAVHLPESPQSPKGLTENSRRHRLTPQEGLOAPGG<br>SLREEAQAGFCPAAPIFKGCPTHTPTEVLKPVSQHPRDFFSRLK<br>DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGI LYP<br>KPKACWVSPMAKVPASPTLPPTFPSSPGLGSKRSLEEEGAHS<br>GKRLRAVSFPLKEADAKKCGAKPAGSGLVSCLLGPAVGPPPEA<br>YRGTM LHCPLNFTGTPGLKGQALPFSPLVIPAPPAHFLATAG<br>PSPMAAGLMHFPPTS FDSALRHRLCPASSAWHAPPVTTYAAPHF<br>FHLNTKL |
| 6176       | 1040   | 402  | PLSALRAMAEVHVIGQIIGASGFSESLFCWGIHTGAAWKLLS<br>GVREGQTQVDTPOIGDMAYNSHPIDLHFATKGLQGWPRLHFQW<br>SQDSFGRCQLAGYGFCHVPSSPGTHOLACPTWRPLGWSREQLAR<br>AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLENFD<br>RYGVEC*GTLPTTSPPTPTPTPSDGGGWHSGQEHRL  |
| 6177       | 1400   | 992  | VPIESLVGKVHNFPLIAFYCCCKRQPHKSLHDCRFGALDPN<br>CSHCYLDQIKRSDFLGFGSGYSPHFVAISTNSEHKMQPSSMQQAL<br>PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPLPGTSGCSDRPP<br>VCPI  |
| 6178       | 1027   | 254  | STQRGGIKGVARAASLVGRRRAGTGMALLCLVCLTAALAHGCL<br>HCHSNFSKKFSFYRHVNFKSWWVGDI PVSGALLTDWSDDTMKE<br>LHLAIPAKITREKLDQVATAVYQMDQLYQGMYPFGYFPNELR<br>NIFREQVHLIQNAIESRIDCQHRCGIFQYETISCNCTDSHVA<br>CFGYNCESSAQWKS AVQGLLNYINNWHKQDTSMRPRSSAFSPWG<br>THRAAPAFVLVLPALRCLEPPHLANLSLEDA*CLKQH  |
| 6179       | 806  | 276  | RGETREMAGNLLSGAGRRRLWDNVPLACRSFSISGVPRLLIGIRLTL<br>PPPKVVDWRNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG<br>WKGNELQRCIRKRMVGSRMFADDLHNLKRIYLYKHFNHKGK<br>FR*KRKLRTSEKAHLSPPWRRETLPVVRKRLCIFSVIKWFFGI  |
| 6180       | 156  | 1833   | DHHILKAASHTHVCARGNIPAINTRCLEC*ATATPSSLECN*<br>SHLSLCLPLPATTSLGTPNSMIPKERNQIAERLLRVMCADLGAL<br>SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLP<br>MYNQVKVKVTCALGSNACLGIVTCHSQSVGPDSCYILTAYQAE   |

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|------------|--|--|---|
|            |  |  | GNHIKSYVLGVKADIRDSGDLVHHWVQNLSEFVMSEIRTVYV<br>TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE<br>VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDLSLLV<br>HERYEQICEFYSRACKMNLQSLNKHLLSNLAAITLTPVKQAVIE<br>LSNESQPTLQLVLPYVRLEKLFATAKANDAGTVSKLCHLFLEAL<br>KENFKVHPAHKVMILDPQQLRPVPPYQHEEIIIGKVCELINEV<br>KESWAEADFEPAKKPRSAAVENPAQAEDDRLGKNEVYDYLQE<br>PLFOATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN<br>MCEQALLIKRRRLSPEDMNKLMFLKSNML  |
| 6181       | 169  | 1032   | TRTLLSPVLLPGPRWKWPWRRRPMGPLALPAWLQPRYRNAYLFI<br>YLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS<br>VSLLELLHIYVGIESNHLPRFLQLTERIIILFVVITSQEEVQE<br>KYVVCVLPFVFNLLDMVRYTYGMLSVIGISYAVLTWLSQTLWMP<br>IYPLCVLAEAFIYQSLPYFESFGTYSTKLFPDLISYFPYVLKI<br>YIMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR<br>KDRLNIQCSK*NTGSILVEKFLVF   |
| 6182       | 1769   | 1224   | AS*IDYQLNTLLKEFQTEENTKLRYLTCSLIEDMAAAYFPDCI<br>VRPFGSSVNTFGKLGCDLDMFLDDETRNLNSAHKISGNFLMEFQ<br>VKNVPSEIATQKILSVLCECLDHPGPGCVGVQKILNARCPVLR<br>FSHQASGFOCDLTNNRIALTSSSELYIYGALDSRVRLVFSVR<br>CWARHSLTSSIPGAWITNFSITMMVIFFLQRRSPPIPLTDSL<br>KTLADAEDKCVIEGNCTFVRDLSRIKPSQNTETLELLLEKFEFE<br>YFGNFAFDKNSINIROGREQNKPDSSPLYIQNPFTSLNISKNV<br>SQSOLQKFVDLARESAILQEQEDTDRPSSISNRPWGLVSLLLPS<br>APNRKSFTKKKSNKFAIETVKNLLESKGNRTENFTKTSGRKTI<br>STQT  |
| 6183       | 1118   | 452  | HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRMGC CGCGSRGC<br>GSGCGCGSGSACGCGSGCGCGSGCGCGSGCGCGSSCGGCGS<br>RCYVPVCCCKPVCSWVPACSTSCGSGCGSGCGSGCGSGKGGC<br>GSCGCSQSSCCKPCCSSGCGSSCCQSSCCKPCCQSSCCVPVC<br>CQSSCCKPCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM<br>VP   |
| 6184       | 1  | 2191   | IYTVREEDGAPAVAPPVVVSRANKRSGAGPGSGGGGARGAEE<br>EPPPPQLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLLE<br>FLTATGVQETFFVCCWKAQIKHLLKSKWCRPTSLNVVRIITS<br>ELYRSLGDLVDVDAKALVRSDFLLVYGDVISNINITRALEEHR<br>LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVAVDSTTNRVL<br>HFQKTQGLRRFAFPLSLFQSSSDGVEVRYDLLDCHISICSPQVA<br>QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMVTAKEYGARVS<br>NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG<br>PEVSLGHGSIENVLGSGTVIGSNCFITNSVIGPGCHIEPGD<br>NVVLDQTYLWQGVRAAGAIIHQSLLCDNAEVKERVTLKPRSVL<br>TSQVVVGPNITLPEGSVISLHPPDAEEDDDGEFSDDSGADQEK<br>DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEELQQNLWGLKI<br>NMEEESESESEQSMDSSEPDSSRGSPQMDDIKVFONEVLGTQR<br>GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVLEFPPLQ<br>MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED<br>FFLEHEALGISMALVMAFYQLEILAEETILSWFSQRDITDKGQ<br>QLRKNQQLQRFIQWLKEABEESEDD |
| 6185       | 791  | 44   | PCTSCVLWATLHLPASTRKAPQAECCGMISITWQKIGVGITGFG<br>IFPILFGLTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFQR<br>HKLKGTSLGGGVIVLLRWPLLMFLETYGFPSLFKGFPPVAF<br>GFLGNVCNIPPLGALFRRLQGTSSMV*KTEMSSSLNDHWLKGAK<br>REEWEPPPPQSPALTHSPYFGPPQVQKERNAGELTSPNPQVDSR<br>GCQEAEMQTPRRLGWGWHYHTLTLYLWEEK   |
| 6186       | 569  | 238  | VYGDSSNTNTHGAERNRKLKHKWLCHAQSRLDVNGLALKMA   |

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|------------|--|--|--|
|            |  |  | KERKVKNKVKNKADTEEVFNNSPTNQEKMPSTAILPDPFSGSVIS<br>NIRNOMETLHSGPHQEENLCFENSFSLINLLPINAVEPTSSQOI<br>PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIKD<br>LEDCLMVGLHTCGDLAPNLTIRFTSNSEIKGCVSGCCYHLLSE<br>EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACALERV<br>AAGQGLPTESLFYRAVLQDIKDCYGITKCDRHVGKIYSKCSF<br>LDYVRRSLKKLGLDESKLEKIIMNYEYKPRMNELEAFNMLK<br>VVLAPCIETLILLDRCLCYLKEQEDIAWSALVKLPDPVKSPPRYA<br>VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGPPALRDAP<br>PSGSRVGSRYD                                |
| 6187       | 1701   | 771  | DAWGPETRLARILNPDSFIEPRPGRLEPELEATRPHEPKASCPA<br>AAPLMERKFHVLVGTGVSVAALKPLLLVSKLLDIPGLEVAVVTT<br>ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDDVLHIDLRRAWDL<br>LLVAPLDANTLGKVASGICDNLTCVMRAWDRSKPLLFPCPAMNT<br>AMWEHPITAQQVDQLKAFGYVEIPCAKKLVCGDEGLGMAEVEG<br>TIVDKVKEVLFQHSFGQS*PGISVMGVPLYSEWQAKSVKMDV<br>GKIGGYPHLLNGGPALS LPRGQACSRLNWTEGPGLSFFQPGEAA<br>A  |
| 6188       | 238  | 1534   | KGFVNAGPLMAELQVSPQWKAPEMSOICLSCGHPSA*GPRWASW<br>NIGVFCIRCAIGHRLGVHISRVKSVNLDQWTQEQIQCMQEMG<br>NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKEYEKKYMDRSLD<br>INAFRKEKDDKWKRGSEPVPEKKLEPVVPEKVKMPQKKEDPQLP<br>RKSSPKSTAPVMDLLGLDAPVACS IANSKTSNTLEKDLDLLASV<br>PSPSSSGSRKVVGSMP TAGSAGSV PENLNLFFEPGSKSEEIGKK<br>QLSKDSILSLYGSOTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP<br>PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG<br>VPNGMMTTQAGYMGAMAAMPQT VYGVQPAQQLQWNLQTMTQOM<br>AGMNFYANGMMNYGQSMSSGGBQAANQTLSPQMWK |
| 6189       | 1297   | 793  | LGEPLGDLCELI PGDVQQLQMGVHFGTGAQGSAAQSVAGEVQL<br>TQLSHARQRPSCQGSQIALDLQHMDISRQPRWQHVPVARQVQ<br>RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGKVFAANACDL<br>VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR<br>RVRAFMIHNLQITGIGREDFATTYFLSELNLSYNRITSPOVHRD<br>AFRKLRLRLSLDLSGNRLHMLPPGLPRNVHLVKVRNELAALAR<br>GALAGMAQLRELYLT SNRLRSRALGPRAWDLAHLQLLDIAGNQ<br>LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN<br>KLAVGVSVDFAFRRLKHLQVLDIEGNLEFGDISKDRGLGKEKE<br>EEBEDEVEEETR                              |
| 6190       | 66   | 1309   | ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTGTGQCECRPGYQ<br>GLHCETCKEGFYLYNTSGLCQPCDCSPHGALSI PCNSSGKCQCK<br>VGVIGSICDRCDQGYGFSKNGCLPCQCNRSASCDALTGACLN<br>CQENS KGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK<br>SSELEPCDQCKDGYIGPNCNKCENGYNFDSICRKCQCHGHVY<br>PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLBGNCIK<br>KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS<br>TSENSTALADVSWTQFNI IILTVIIIVVLLMGFVGAVMYRE<br>YQNRKLNAPPWTIELKEDNISFSSYHDSIPNADVSGLEDDGNE<br>VAPNGQLTLTPIHNYKA                        |
| 6191       | 1212   | 1511   | VNLCHGGLLHLSTHHLGKPSMH*LFLLMLSFPHLTPQPKCPS<br>MIDWIKKIWIYITMEYYATIKRNBIMFFAGTWMEAIILSKLM<br>QDYMFSLISGS  |
| 6192       | 3  | 950  | TRGCGNKMAGKKNVLSLAVYAEDSEFESDGEAGIEAVGSAEE<br>KGLVSDAYGEDDFSRIGDEDDGYEEEDENSRSQEDDDSETEK<br>PEADDPKDNTAEAKRDPQELVASFSERVNRMSPEIKIPPEPPG<br>RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPISYKLI<br>QFCAIDELGTNYPKDMFDPHGWSEDSYAEALAKAQKIEMDKLEK   |

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|------------|--|--|---|
|            |  |  | AKKERTKIEFVTGTGKGGTTTATSTTTTASTAVADAQKRKSKW<br>DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT<br>IVKKAKQ  |
| 6193       | 3  | 950  | TRGCGNKMAGKKNVLSLAVYAEDSEPESDGEAGIEAVGSAEE<br>KGGLVSDAYGEDDFSRLLGDEDDGYEEBEDENSRQSEDDDDSETEK<br>PEADDPKDNTEAEKRDPELVASFSEVRNMSPEIKIPPEPPG<br>RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI<br>QFCAIDELGTNYPKDMFDPHGWSSEDSYIEALAKAQKIEMDKLEK<br>AKKERTKIEFVTGTGKGGTTTATSTTTTASTAVADAQKRKSKW<br>DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT<br>IVKKAKQ  |
| 6194       | 3  | 950  | TRGCGNKMAGKKNVLSLAVYAEDSEPESDGEAGIEAVGSAEE<br>KGGLVSDAYGEDDFSRLLGDEDDGYEEBEDENSRQSEDDDDSETEK<br>PEADDPKDNTEAEKRDPELVASFSEVRNMSPEIKIPPEPPG<br>RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI<br>QFCAIDELGTNYPKDMFDPHGWSSEDSYIEALAKAQKIEMDKLEK<br>AKKERTKIEFVTGTGKGGTTTATSTTTTASTAVADAQKRKSKW<br>DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT<br>IVKKAKQ  |
| 6195       | 736  | 235  | VANGLQSNMFKFYCDYCDTYLTHDPSVRKTHCSGRKHKENVKD<br>YYQKWMEEQAQSLIDKTTAAFOQKGIPTTFFSAPPAGAMIPPP<br>PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPPVGPAPGMRP<br>PMGHPMPMPGPPMMRPPARPPMMVPTRPGMTTRPDR   |
| 6196       | 1512   | 623  | KTGKRRAAYVRNILDNAEQVINSLEARNLSPRLTPLLQZEDSH<br>QRLLMGLMVSELKDFLRHLQGVKKKIEQWVLDYISKLLDLIC<br>HIVETNWRKHNLSWVLFHNSRGSAAEFVHFHIMTRILEATNSL<br>FLPLPPGFHTLHTILGVQCLPLHNLHCIDSGVLLLTETAVIRL<br>MKDLNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR<br>NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS<br>NQALYPFEHNDVDAEFVBEAALKHTAMLLGL   |
| 6197       | 3  | 819  | ADPEGTEZAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG<br>PVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLRKWVCG<br>RQIEIQFAQGDRTPGQMSKERHPCSPDHRRSRSPSQRRTRS<br>RSSSWGRNRRRSDSLKESRHRFSYSQSKRSKSLPRRSTARSQ<br>SRTPRRNFGSRGRSRKSLQKRKSKSIGKSQSSSPQKQTSSSGTKS<br>RSHGRHSDSIARSCKSPKGYTNFETKVQTAHSHFRSHSRSR<br>YRHKNW   |
| 6198       | 111  | 1912   | SEALSPSFISPAFLRLKLPALDGTLPHPDTLGMNYEGARSE<br>RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAGLQDSQ<br>REMPPPPPPSPSDPAQKPPPRGAGSHSLTVRSSLCFAASQFL<br>LACGVLFWSGYGHIWSQATNLVSSLLTLKQLEPTAWLDSGTW<br>GVPSLLLVLVFLSGGLVLTTLVHLLRTPPEPPTPLPPEDRRQSV<br>SRQPSFTYSEWMBEKIEDDFLDLPVPETPVFDCVMDIKPEADP<br>TSLTVKSMGLQERRGSNVSLTDMCTPGCNEEGFGLMSPREES<br>AREYLLSASRVLAELHEKALDPFLQAEFFIIPMNFVDPKEY<br>DIPGLVRKNRYKTILPNPHSRVCLTSPDPPDPLSSYINANYIRG<br>YGEEKVYIATQGPVSTVADEFWRMVWQBHTPIIVMITNIEEMN<br>EKCTEYWPEEQVAYDGEITVQKVIHTEDYRLRLISLKSGETER<br>GLKHYWFTSWPDQKTPDRAPPLHLVREVEEAQQEGPHCAPII<br>VHCSAGIGRTGCFIATSIACCQQLRQEGVVDILKTTQCLRQDRGG<br>MIQHCEQYQFVHHVMSLYEKQLSHQSPE |
| 6199       | 144  | 1211   | MARENGESSSSWKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA<br>TGKLFVAKCI?KKALKGKESSIEIEIAVLRKIKHENIVALEDIY<br>BSPNHLYLVMLVSGGELFDRIVEKGFYTEKDASTLIRQVLDV<br>YYLHRMGIVHRDLKPENLLYSQDEESKIMISDFGLSKMEGKGD<br>VMSTACGTPGYVAPVLAQKPYSKAVDCWSIGVIAIYILLCGYPP  |



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|------------|--|--|--|
|            |  |  | FYDENDSKLFEQILKAEEYFDSPYWDIDSDAKDFIRNLMEKDP<br>NKRYTCEQAARHPWIAAGDTALNKNIHESVSAQIRKNFAKSKWRQ<br>AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF<br>HAL*   |
| 6200       | 702  | 96   | LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVIDLDYTLWPF<br>WVDTHVDPFFHKSSDGTVRDRRGQDVRLYPEVEVLKRLQSLGV<br>PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL<br>QOKTGIPFSQMIFFDDERRNIVDVSKLGVTCTIHIQNGMNLQTL<br>QGLETFAKAQGTGPLRSSLEESPFEEA   |
| 6201       | 2809   | 2383   | GQTPRVWKMRRSLRAGKRRQTAGRKSPPKVPVIVIQDSSLPA<br>GPPQIRILKRPTSNGVSSPNSTSRPTLPVKSQAQREAEYASA<br>RKRIKLSASPEEEQEKPIIDRPTIRISQPEDSRQPNVIRQPLGP<br>DGSQGFQRR  |
| 6202       | 2  | 426  | INADRAAVASSLLSRPTRKMAPOKDRKPKRSTWRFLDLTHPVE<br>DGIFDSGNFEQFLREKVKVNGKTGNLGNVHHIERFKNKITVVS<br>KQFSKRYLYLTKYLYLKNLRDLRVVADSKETVELRYFQISQ<br>DEDESESED   |
| 6203       | 419  | 2550   | RCPRPPATAGAAASRPDRSPSGISGSEAAAGAGAAAPASQHEA<br>TGTGAVQTEAMKQILGVIDKLRNLKKGKGLDDYQERMNKG<br>LNQDQLDAVSKYQEVNTNNLEFAKELQRSFMALSQDIQKTIKTA<br>RREQLMRBEAEQKRLKTVEQLQYVLDKLGDDVVRTDLKQGLNGV<br>PILSEELSLDDEFYKLVDPERDMSLRNLNQYEHASIHLDLLE<br>GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNLQGLCEESEAA<br>SAPAVEDQVPEAEPEAEYEQSEVESTEYVNRQFMAETQFTS<br>GEKEQVDEWTVETVEVNSLQQQQAASPSVPEPHSLTPVAQAD<br>PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPVISAQPM<br>NPTQNMMPQLVCPVHSESRQAQPNQVPVQPEATQVPLVSSTS<br>EGYTASQPLYQPSHATEQRPKBPIDQIQATISLNTDQTASSS<br>LPAASQPVQFQAGTSKPLHSSGINVNAAPFQSMQTVFKMNAFVP<br>PVNEPETLKQONQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG<br>TYHGSPPDQSHQVTGNHQQPPQNTGFPFRSNQPYNSRGVSRGGS<br>RGARGLMNGYRGPANGFRGGYDGYRPSFNTFNSGYTQSQFSAP<br>RDYSGYQRDGYQQNFKRSGSGSGPRGAPRGRGPPRPNRGMQPM<br>NTQQVN                   |
| 6204       | 2933   | 787  | CTHNLISLLGGRALIHFNRLNLKIQEGEAHNIFCPAYDCFLV<br>PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV<br>RLTKQGSNTSGSDTLSPFLLRAPAVDCGKGLFCWECLGEAHEP<br>CDQOTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC<br>ANCKSPIQKNEGCNMQCAKCYDFCWI CLEWKKHSFVHWEVI<br>YRCTRYEVIQHVVEEQSKEMTVEAEKKHFRFOELDRFMHYTRFK<br>NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFFIEDAV<br>HVLLKTRRILKCSYPYGFLEPKSTKKEIFELMQTDLEMVTEDL<br>AQVNRPYLRTPRHKI IKAACLVQQRQEPFLASVARGVAPADSP<br>EAPRRS FAGGTWDEYLFASPEEYAEFQYRRRRRQRRRGDVHS<br>LLSNPPDPDEPSESTLDI PEGGSSSRPPTS SVVSSASMSVLHSS<br>SLRDYTPASRSNQDSLQALSSLOEDDPNILLAIQLSLQESGLA<br>LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE<br>LLELGDSLMLGAENDPFSTDTLSSEPLSEARSDFCPSSSDPDS<br>AGQDPNINDNLLGNIMAWFDMNPQSIALIPATTEISADSQLP<br>CIKDGSEGVKDELVLVLPEDSMFEDASVSEGRGTQIEENPLEBNI<br>PGGGKQHPQAW |
| 6205       | 1  | 1200   | RAHRGKMALEVGMEDGQLSDSDSDMTVAPS DRPLQLPKVLGGD<br>SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCWLKR<br>KRQKCFNPPPKBPFPQGSQKPPVAGGKKNINIWAVLQEQN<br>QDAVATELGILGMEGTIDRSRQSETYNYLLAKLRKESQEHKTD<br>LDKELDEYMHGGKKMGSKKEENGQGHLLKRRKRPVKDRLGNRPEMN  |

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|------------|--|--|--|
|            |  |  | YKGRYEITAEDSQEKVADEISFRLOEPKKDLIARVVRIIGNKKA<br>IELLMETAEEVQNGGLFIMNGSRRTPGGVFLNLLKNTPSISEE<br>QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED<br>DDTSRETFASDTNEALASLDESQEGHAEAKLEAEAEI EVDHSHD<br>LDIF   |
| 6206       | 10   | 1442   | IISERRERSCLHLVLCIRCSCDVVEMGSLGLCSMASNIPCLCGS<br>APCLLCRCPCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ<br>LNKIPGFCENEGVPCNIVLVGYKAVYRLCFLAMFYLLSLLM<br>IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTTW<br>FYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKMEEGNSRCWYA<br>ALLSATALNYLLSLVAIVLFFVYVYTHPASCSENKAFISVNMLLC<br>VGASVMSILPKIQESQPRSGLLQSSVITVYTMVLTWSAMTNEPE<br>TNCNPSLLSIIGYNTTSTVPKEGQSVQWHAQGIIGLILFLLCV<br>FYSSIRTSNNSQVKNLILTSDESTLIEDGGARSDGSLDGDDVH<br>RAVDNERDGVITYSYSFHFMLFLASLYIMMTLTNWRYEPSREM<br>KSQWTAHVVKISSSWIGIVLYVWTLVAPLVLTNRDFD    |
| 6207       | 2924   | 1471   | TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG<br>GGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSFY<br>SVVCKYFORGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLA<br>SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEWDVNAIEFVP<br>GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA<br>VGECRYGENCVYLHGDSMDMGLQVLHPMDAAQRSQHIKSCIEA<br>HEKDMELSAVQSRKDMVCGICMEVVYEKANPSERRFGILSNEN<br>HTYCLKCIKWRSAKQFESKIKSCPECRITSNFVIPSEYVWVE<br>KEEKQKILILKYEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD<br>GRREEPQRQKVGTSRRYRAQRNRHFWELIEERENSNPFDNDEEE<br>VVTFLGEMLLMLLAAGGDELTDSEDEWDLFHDELEDFYDLDL |
| 6208       | 2924   | 1471   | TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG<br>GGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSFY<br>SVVCKYFORGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLA<br>SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEWDVNAIEFVP<br>GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA<br>VGECRYGENCVYLHGDSMDMGLQVLHPMDAAQRSQHIKSCIEA<br>HEKDMELSAVQSRKDMVCGICMEVVYEKANPSERRFGILSNEN<br>HTYCLKCIKWRSAKQFESKIKSCPECRITSNFVIPSEYVWVE<br>KEEKQKILILKYEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD<br>GRREEPQRQKVGTSRRYRAQRNRHFWELIEERENSNPFDNDEEE<br>VVTFLGEMLLMLLAAGGDELTDSEDEWDLFHDELEDFYDLDL |
| 6209       | 1758   | 829  | ERLCFPCMQSKIYSYMSPNKCSGMRFPLOEENSVTTHHEVKCQK<br>PLAGIYRKREKRNAGNAVRSAKSEEQIKDARKGPLVFPFNQ<br>KSEAAEPKTPPSSCDSTNAIAKQALKKPIKQKQAPRKAQKQ<br>TQNRKLTDFYPVRRSSRKSKAELQSEERKRIDELIESGKEEGM<br>KIDLIDGKGRGVIATKQFSRGDPVVEYHGDLEITDAKKREALY<br>AQDPSTGCMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ<br>TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL<br>KH  |
| 6210       | 3761   | 387  | IFGMSKLRMVLLLEDGSGSADFRHFVNLSPTTITVVLLLSACFVT<br>SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV<br>SVICNQLGCPPTAIAKPGWANSSAGSGRIWMDHVSRCGNESALWD<br>CKHDGKGKHSNCTHQDAGVTCSDGSNLEMLTRGONMCSGRIE<br>IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGE<br>SGPIWDDLICNGNESALWNCKHGGWKGKHNCDHAEDAGVICSKG<br>ADLSRLRLVDGVTCSGRLEVRFGGEWGTICDDGWSYDAAVACK<br>QLGCPPTAVTAIGRVNASKGFGHIWLDVSVCQGHFAVWQCKHHE<br>WGKHYCNHNEADAGVTCSDGSDLELRLRGGGSRCACTVEVEIQRL<br>LGKVCDRGWGLKEADVCRQLGCGSALKTSYQVYSKIQTNTWL  |

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|------------|--|--|---|
|            |  |  | <p>FLSSCNGNETSLWDCKNWQWGGGLTCDHYEAKITCSAHREPRLV<br/>GGDIPCSGRVEVKHGDWTGSI CDSDFSLEAASVLCRELQCGTVV<br/>SILGGAHFGEGNGQIWAEEFQCEGHESHLSCPVAPRPEGTC SH<br/>SRDVGVCVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD<br/>IEDAHVLCQQLKCGVALSTPGGARFGKNGQIWRHMFHCTGT EQ<br/>HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSSLGPT<br/>RPTIPESAVACIESGQLRLVNGGRCAGRVEIYHEGSGWTICD<br/>DSWDLSDAHVVCRLQCGEAINATGSAHFGEGTGP IWLDEMKN<br/>GKESRIWQCHSHGWGQNCNRHKEDAGVICSEFMSLRLTSEASRE<br/>ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGINP<br/>ASLDKAMSI PMWVDNVQCPKGPDTLWQCPSPWEKRLASPEET<br/>WITCDNKIRLQEGPTSCSGRVEIWHGSGWTVCDDSWDLDDAQV<br/>VCQQLGCGPALKAFKAEFGQGTGPIWLNVEVKCKGNESSLWDCP<br/>ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA<br/>VGILGVVLLAIFVALFPLTKRRRQRQLAVSSRGENLVHQIQYR<br/>EMNSCLNADDLDLMNSSGGHSEPH</p>  |
| 6211       | 3761   | 387  | <p>IFGMSKLRMVLLEDSDGSADFRRHFNLSPTITVVLSSACFVT<br/>SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV<br/>SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHIVSCRONESALWD<br/>CKHDGWGKHSNCTHQDAGVTCSDGSNLEMLTRGGNMCSGRIE<br/>IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG<br/>SOPIFWDDLICNGNESALWNCKHQGWGKHNCDAEDAGVICSKG<br/>ADLSLRLVDGVTECSGRLEVRFGQEWGTICDDGWDSYDAAVACK<br/>QLGCPTAVTAIGRVNASKGFHGIWLDVSVCQGHPEPAVWQCKGHE<br/>WGKHYCNHNEAGVTCSDGSLELRLRGGGSRCACTVEVEIQRL<br/>LGKVCDRGWGLKEADVCRQLGCGSALKTSYQVYSKIQTNTWL<br/>FLSSCNGNETSLWDCKNWQWGGGLTCDHYEAKITCSAHREPRLV<br/>GGDIPCSGRVEVKHGDWTGSI CDSDFSLEAASVLCRELQCGTVV<br/>SILGGAHFGEGNGQIWAEEFQCEGHESHLSCPVAPRPEGTC SH<br/>SRDVGVCVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD<br/>IEDAHVLCQQLKCGVALSTPGGARFGKNGQIWRHMFHCTGT EQ<br/>HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSSLGPT<br/>RPTIPESAVACIESGQLRLVNGGRCAGRVEIYHEGSGWTICD<br/>DSWDLSDAHVVCRLQCGEAINATGSAHFGEGTGP IWLDEMKN<br/>GKESRIWQCHSHGWGQNCNRHKEDAGVICSEFMSLRLTSEASRE<br/>ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGINP<br/>ASLDKAMSI PMWVDNVQCPKGPDTLWQCPSPWEKRLASPEET<br/>WITCDNKIRLQEGPTSCSGRVEIWHGSGWTVCDDSWDLDDAQV<br/>VCQQLGCGPALKAFKAEFGQGTGPIWLNVEVKCKGNESSLWDCP<br/>ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA<br/>VGILGVVLLAIFVALFPLTKRRRQRQLAVSSRGENLVHQIQYR<br/>EMNSCLNADDLDLMNSSGGHSEPH</p> |
| 6212       | 1  | 1134   | <p>LKWE LRPGGAVWGTGRGAGTGAPRSCCQTNPGPPSSLRRAFRR<br/>RELFPFACHEIGLGAEGSGPPPAPAARESRSRAMEEEASSPGL<br/>GCSKPHLEKLTIGITRILESSPGVTEVTII EKPPAERHMISSWE<br/>QKNNCVMPEDEVKNFYLMTNGFHMTWSVKLDEHII PLGSMAINS I<br/>SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS<br/>VIFELDS CNGSGKVLVYKSGKPALAEDTEIWFDRALYWHFLT<br/>DTFTAYYRLLI THLGLPQWQYAFTSYGISPQAKQRVSMYKPIY<br/>NTNLLTEETDSFVNKLDP SKVFKSKNIVIPKKKGPVQAGGQK<br/>GPSGSPGSPSTSSTSKSSSGSGNPKRK</p>   |
| 6213       | 1  | 1134   | <p>LKWE LRPGGAVWGTGRGAGTGAPRSCCQTNPGPPSSLRRAFRR<br/>RELFPFACHEIGLGAEGSGPPPAPAARESRSRAMEEEASSPGL<br/>GCSKPHLEKLTIGITRILESSPGVTEVTII EKPPAERHMISSWE<br/>QKNNCVMPEDEVKNFYLMTNGFHMTWSVKLDEHII PLGSMAINS I<br/>SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS</p>  |

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|------------|--|--|--|
|            |  |  | VIFELDSCNGSGKVCVLYKSGKPALAEDTEIWFLLDRALYWHFLT DTFTAYYRLLIHLGLPQWQYAFSTSYGISPOAKQVSMYKPITY NTNLLTEBTDSFVNKLDPSKVFKSKNKIVIPKKKGPVQVAGGQK GPSGSPSGPSTSTSKSSSGSGNPTK   |
| 6214       | 2  | 460  | HELAPSAIRRAARLGLGPARGWQSRRAAFYFVRGFRGTGWSFVGWV VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRRESKRFSAYN YRTYAVRRIRDAFRENKNVDPVBIQTLVNVKAKRDLGVIRRVQH IGQLYSTDKLIIENRDMPT  |
| 6215       | 2  | 1849   | FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNV MLDGCMHMGFNDDRRFPDFSYITQNGRI.TDFLDCVLIISHFLDH CGALPYFSENVGVDGPIYMTHTQAICPILLEDRKLAVDKKGE ANFFTSQMIKDCMKVAVHLHQTVQVDELEIKAYYAGHVLGA AMFQIKVGSSEVVYTGDNMTDPDRHLGAAWIDKCRPNLLITEST YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVAFALGRAELC ILLETFFWERNMLKVPYFSTGLTEKANHYKLFIPWTNQKIRKT FVQNMFEFKHIAFDRAFADNPGPMVVPATPGMLHAGQSLQIF RKWAGNEKNMVIMPGYCVQGTGHHKILSGQRKLEMEGRQVLEVK MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKMEFLKQ KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAQCL LPEAKKPRLLHGTLMKDSNFRVLSSEQALKELGLAEHQLRFTC RVHLHDTRKBOETALRVYSHLKSVLKDHCVQHLPDGSHVTVESVL LQAAAPSEDPGTKVLLVSWTYQDEELGSLTSLKKGLPQAPS |
| 6216       | 11   | 393  | QTTREPEPRNSALRQSRKMAVVGVSVSRLGRSRPQLGRPMSS GAHGEESARMWKTITFFVALPGVAVSMLNVYLSHGHGEHERPE FIAYPHLRIRTKPPFPWGDGNHTLFHNPVNPPLPTGYEDE  |
| 6217       | 9  | 1178   | TRVGRGESGLKMEVKPPGRFPQDSGRRRRRRGEEGHDPKEPEQ LRKLFIGGLSPETDDSLREHFKEKWTLTDCVVMRDPTKRSRG FGFVITYSCVEBDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEZYNLRDYFEKYKIEETIEVMEDRQSGK KRGFAPVTFDDHDTVDKIVVQKYHTINGHNCVKKALSQKQMS AGSQGRGRGGSGNFMGRGNFGGGGNGFRGNGFGRGGYGGGG GSGRGSYGGGDDGNGFGDGGNYGGGPGYSSRGGYGGGGPGYG NQGGGYGGGGYDGYNEGGNFGGGNYGGGNYNDFGNYSGQQQS NYGPMKGSFGRSSGSPYGGGYGGGGSGGGSGGYGSRFF   |
| 6218       | 1305   | 906  | SCERRGFIADDLKRFLYKLPVSEGLHAIIVSDRDGVFVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIIICYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS   |
| 6219       | 2  | 890  | AGPGEAGAGTRCAGAEAMASAGGEDCESPAPPADRPHQRFFL IGVSGGTASGKSTVCEKIMELLGQNEVEQRQKVVILSQDRFYK VLTAEQKAKALKQYNFDHPDAFDNDLMHRTLKNIVEGKTVVEP TVDFVTHSRLPETTVVYPADVLFEGILVFYSQEIIRDMFHLRLF VDTSDVRLSRRVLRDVRGRDLEQILTQYTTFFVKPAFSEFCLP TKKYADVIIPRGVDMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH   |
| 6220       | 227  | 764  | EONISLEMSCTIEKALADAKALVERLRDHDAAESLIEQTALN KRVEAMKQYQEEIQELNEVARHNPSTLVMGIQENRQIRELQQ ENKELRTSLEEHQSALELIMS KYREQMFRLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFLLDASRHILEAPQHGLERRHLEANQ NVH  |
| 6221       | 98   | 916  | RNIWDLNPFVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWAGLSNGLYFVFYNAIKSYKTEGRAERLEATEYLVSAEAG AMTLCITNPLWVTKTRMLQYDAVNSPHRQYKGMPTLVKIYK YEGVRGLYKGFVPLFGTSHGALQFMAYELLKLYNQHINRLPE AQLSTVEYISVAALS KIFAVAATYPYQVVRARLQDQHMFGYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHPL LDLREKRK   |

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|------------|--|--|---|
| 6222       | 2  | 2116   | MARELRALLWGRRLRPLLRAPALAAVPGGKPILCPRITTAQLG<br>PRRNPWSLQAGRLFTQTAEDEKEEPLHSIISSTESVQGSTSKH<br>EFOAETKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKL<br>SDGQALPEMEIHLQTAEGKGTITIQDTGIGMTQEELVSNLGTIA<br>RSGSKAFDLALQNAEASSKIIGQFGVGFYSAFMVADRVEVYSR<br>SAAPGSLGYQWLSGSGVFEIAEASGVRTGKIIHLKSDCKEF<br>SSEARVDRVVTKYSNFVSPFLVNGRRMNTLQAIWMDPKDVR<br>WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFFVPMKPSM<br>FDVSRLEGSSVALYSRKVLIOQTATDILPKNLRFRIGVDSEDI<br>PLNLSRELLOESALIRKLRDVLQORLIKPFIDQSKKDAEKYAKF<br>FEDYGLFMREGIVTATEQEVKEDIKLLRYESSALPSGQLTSL<br>EYASRMPAGTRNIYYLCAPNRHLAEHSPYEAAMKKKDETEVLCF<br>EQFDELTLHLREFDKKLISVETDIVVDHYKEEFEDRSPAAE<br>CLSEKETEELMAWMNRNLGSRVTNVKVLRLDTHPAMVTVLEMG<br>AARHFLRMQQLAKTOEERAQLLOPTLEINPRHALIKKLNQLRAS<br>EPGLAQLLDVQIYENAMIAAGLVDDPRAMVGRINELLVKALERH   |
| 6223       | 3  | 715  | DAWARTMAGMVDQDEEQVKSFLENMEVECNHYHCYHEKDPDGCY<br>RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDDCYKLGAYVVTGK<br>GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNB<br>GQPDLGKARDYYTRACDGGYTSSCFNLNANFLQAGPFPKMDML<br>ACKYSMKACDLGHIWACANASRMVKLGDGVDKVEAKAEVLKNRA<br>QQVHKEQQKGQVPLTFG   |
| 6224       | 1  | 133  | LRTISSMAWGPLLTLTLLAHCTGSAQSVLTQPPSVSGARIPHEK  |
| 6225       | 3259   | 938  | LLSCHRLAICKLFFSVESRKTVMGPOGARRQAFLAGDVTVDFT<br>QKEWRLLSPAQRALYREVLTENYSHLVSLGILHNSKPELIRLEQ<br>GEVPMGEERRRRPGPCAGIYAEHVLRPKNLGLAHQROQQLQFSD<br>QSFSQSDTAEGQEKESTKPMAPSSPPLRHAVSSRRRNSVVEIES<br>SQGQRENPTIDKVLKGIENSRWGAFKCAERGQDFSRKMMVVIH<br>KKAHSRQKLPTCRECHQGFREDSALLHONHTHTEKSYVCSVCG<br>RGFSLKANLLRHQRTHSGEKPFCLKVCGRGYTSKSYLTVHERTH<br>TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFFVCKECCGRGYT<br>NKSYPVVKRIHSGEKPYPYRCQECGRGFSNKSHLITHQRTHSGEK<br>PFACRQCKQSFSVKGSLLRHQRTHSGEKPFFVKDCERSFSQKST<br>LVYHQRTHSGEKPFFVCRECGQGIQKSTLVKHQITHSEKPFVC<br>KDCGRGFIQKSTFTLHQRTHSEBKPYGCRECGRRFRDKSSYNKH<br>LRAHIGEKRFRCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE<br>KSFSLKANLLRHQWTHSGERPFNCKDCGRGFIKSTLLFHQKTH<br>SGBKPFICSECGQGF IWKSNLVKHQLAHSGKQPFVCKECCGRGFN<br>WKNLLTHQRTHSGEKPFFVNCVCGGFSWKRSLTRHHWRIRHSKE<br>KPFVCOECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS<br>YYSKHLKRHLREKRFCTGSVGEASS |
| 6226       | 29   | 266  | TKVSELGGSQLFFLPLWRLRCRGLGPRVSPMAGPRVEVDGS<br>IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA  |
| 6227       | 2581   | 890  | MSASSLLEQRPKGQGNKVQNGSVHQDGLNDDDFEPYLSPOARP<br>NNAYTAMSDSYLPSYSPSIGFSYSLGEAAWSTGGDTAMPYLT<br>YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFPPSGIDFS<br>AWGNNSQGGSTQSSGYSSNYAYAPSSLGAMIDGSAFANETL<br>NKAPGMNTIDQMAALKLGSTEVASNVPKVVGSAVSGSITSNI<br>VASNSLPPATIAPPKPASWADIASKPAKQPKLKTNGIAGSS<br>PPPIKHNMDIGTWDNKGFPVAKAPSQALVQNIQPTQGSQPQVG<br>QQANNSPPVAQASVGQQTQPLPPPPPPQAQLSVQQQAQPTRW<br>APNRNGSGFGHNGVDGNGVGQSQAGSGSTPSEPHVLEKLRSIN<br>NYPKDFDWNLKHGRVFIKSYSEDDIHRSIKYNICWSTEHNK<br>RLDAAYSRMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG<br>VNSQDKWKGFRDVRWIFVKDVPNSQLRHRLNENKPVNTSRD<br>TQEVPLEKARQVLKI IASYKHTTSIPDDFSHYEKRQ  |

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|------------|--|--|---|
| 6228       | 47   | 1978   | GRRRCRRRGAVMELAQEARELGCWAVEEMGVPAARAPESTLRLRL<br>CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDPSQVRRKL<br>ELEAAVTLRLRAEIQELDQSELMERDTEAQDTAMEQARQHTQDT<br>QRRALLLRAQAGAMRRQOHTLRDPMQRLQNLRLQDMERKAKV<br>DVTFGSLTSAALGLEPVLRLDVRTACTLRAQFLQNLRLPQAKRG<br>SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALHLEHAAER<br>EAEIRSLCSGDLGDTAISRPQAPDQSDSSQTLPSMVHLIQEGW<br>RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL<br>ILGLRCCNLNTELKALHDQSQELQDAAGHRQLLRELAQAKQRI<br>LHWRQLVEETEQQVRLIKGNSASKTRLCSRPGEVLAIVQRKVV<br>PTFEAVAPQSRRELLRCLEBEVRHLPHILLGTLRLHRRPGELKPLP<br>TVLPSIHQLHPASPRGSSFIASHKLGPPGKASELLPAAASL<br>RQDLILLQDQRLWCWDLHMKTSLPPLPTQELLQIQASQSKQ<br>QENLGQALKRLEKLLKQALERIPELQGIQVGDWWEQPGQAALSE<br>ELCQGLSLPQWRRLRWVQAQALQKLS   |
| 6229       | 1571   | 560  | GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAVDDLQFEFG<br>NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREDELLG<br>NDDSDKTELLAGQKSSPFWTFEYQTFDFVDVYQVFDRIKGS<br>LPPIGKNFVRLYIRSNPDLYGPFWICATLVFAAISGNLSNFI<br>HLGKTYHYVPEFKVSIATIIYAWLWPLALWGLMWRNSK<br>VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIIPHKAVRWILVMI<br>ALGISGSLAMTFWPAVEDNRNRVALATIVTIVLLHMLLSVGCL<br>AYFFDAPEMDHLPTTTATPNQTVAAAKSS   |
| 6230       | 1723   | 600  | SKMSGRSGKKKMSKLSRSARAGVIFPVGRMLRMVLRKGTFRYRIS<br>VGAPVYMAAVIEYLAELILELAGNAARDNKKARIAPRHILLAVA<br>NDEELNQLLKGVTIASGGVLPRIHPPELLAKKRGTKGKSETILSP<br>PPEKRGKATSGKGGGKSKAKAPRTSKKSKPKDSKKEGTSNST<br>SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP<br>TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSQGLEVAEAAV<br>SQSSGLAAKFVICHIPQWGSCKCEEQLEETIKNCLSAABDKKL<br>KSAVAFPPFSGRNCFPKQTAQVTLKAISAHFDDSSASSLKNVY<br>FLLFDSSEIGIYVQEMAKLDAK   |
| 6231       | 149  | 870  | LIFSSTMDRSLRNVLVVSFGFLLFTAYGGLQSLQSSLYSEEG<br>LGVLTALSTLYGGMLLSSMFLPPLIERLGCKGTIILSMCGYVAF<br>SVGNFFASWYTLIPTSIILLGLGAAPLWSAQCTYLTITGNTHAEK<br>AGKRKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL<br>PEBQLTSCGASDCLMATTTTNTSTQPSQQLVYTLGITYTSGSVL<br>AVLMIAAFLQPIRDVQRESE  |
| 6232       | 3679   | 1476   | FVAGTTMAGFWGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL<br>YYSRQCLMVSRNLGSGVYDPNEKTFDKILVANRGEIACRVIRTC<br>KMGIKTVAIHSDVDASSVHVMADEAVCVGPAPTSKSYLNMDA<br>IMEAIIKKTAAVHPGYGFLSENKEFARCLAAEDVVFIPGPDTHA<br>IQAMGDKIESKLLAKAEVNTIPGFDGVVKDAEBAVRIAREIGY<br>PVMIKASAGGGGKMRIAWDDEETRDGFRLLSSQEAASSFGDDRLL<br>LIEKFIDNPRHIEIQVLGDKHGNALWLNRECSIQRRNQKVVEE<br>APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY<br>FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHQKQDIR<br>INGWAVECRVYADPYKSFGLPSIGRLSQYQEPHLPLGVRVDSG<br>IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV<br>THNIALLEVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK<br>NQLLAIASLFAVQLRAQHFQENSMPVVKPDIANWELSVKLH<br>DKVHTVVASNNGSVFSVEVDGSKLNVSTWNLASPLLSVSDGT<br>QRTVQCLSRAGGNMSIQFLGTVYKVNILRLAAELNKFMLEKV<br>TEDTSSVLRSPMPGVVAVSVKPGDAVAEGQEICVIEAMKNQNS<br>MTAGKTGTVKSVMHQAQAGTVGEGDLLVELE |
| 6233       | 1  | 2654   | HSTRENLNAGNPNFPSEGHVLRSTGPGGSFAKHMVAQCVPKGP   |

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|------------|--|--|--|
|            |  |  | LACSRTYFFGATHVPYLGSDSKLPKKTEQIRLLSQIYAAVIEAV<br>LAGIACYAKTSSSLTKAEVAEQTLGSGLDSELIIPFKAALRSKM<br>TFHIHAVMNOGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC<br>LGSVVFSESLTSQILVKEKDGTVTTETSSVVLTAAPFRFCSWL<br>VEDNEVKLSEKTHQAVRGDESFLGTLYLTGEGAYLYSSNLQSWP<br>EEGNVHFFSSGGLFESHCRHGSIIISKDHMNSISFYDGDSTSTVA<br>ALLIDFKSSLLPHLPVHFHSGSNFLMIALFPKSKIYQAFYSEVF<br>SLWKQDNGSISLKVIEDGLSVEQKRLHSSAQKLSALSQAPAG<br>EKRSSLKLLSAKLPELDWFLQHFATSSISQEPVMRTHLPVLLQO<br>AEINTHRIESDKVIIISIVTGLPGCHASELCALVTLHKECGRW<br>MYYRQINDSSECFHAHFQRYLSSALEAQNRARSQAYIRKKT<br>RLLVVLQGYTDVIDVQALQTHPDSNVKASFTIGAITACVEPMS<br>CYMEHRFLFPKCLDQCSQGLVSNVVFSTHTTEQRHPLLVLQQLS<br>IRANPAAAFILAENGIVTRNEDIELISENSFSSPEMLRSRYL<br>MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRPVAKCKAIQS<br>SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL<br>EGPTPPDPSKSVSQDSSGQCEYLFIGCSLKEDSIKDWLRQSA<br>KQKQKALKTRGMLTQOEIRSIHVKRHLEPLPAGYFYNGTQFV<br>NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQEQEQEYHDLF<br>ELKP |
| 6234       | 1731   | 404  | PRVREDMDHKSPGNKGLVYAGIKSIVKSSLSGMVESSRHNSGL<br>DKQSDIQNLNEERILALQLCGWIKKGTDDVGVFFLNSLVQEGW<br>ERAAVALFNLDIRRAIQILNEGASSEKGDNLNVVAMALSGYT<br>DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN<br>KVAVRDRVAFACKPLSDTQLNRYIEKLTNEMKEAGNLEGILLTG<br>LTKDGVLDLMEYSVDRTGDDVQTASYCMIQGSPLDVLKDERVQYWI<br>ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVVFVSCNFCG<br>KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC<br>ALCLINMGTPVSSCPGCTKSDEKVDLSKDKKLAQFNWFTWCHN<br>CRHGGHAGHMLSWFRDHAECVPVSACTCKCMQLDTTGNLVPATV<br>QP   |
| 6235       | 1  | 571  | EKRDRHRLPSWPRALKVPGRGGRVGTTPELAAGGIMATRNPPPQ<br>DYESDDDSYEVLDLLEYARRHQWNNRVFGHSGPMVEKYSVATQ<br>IVMGVGTGWCAGFLFQXVGKLAATAVGGGFLLLQIASHSGYVQI<br>DWKRVEKDVNKAQRQIKKRANKAAPEINNLEIETEPIKQNI<br>SSGFVGGFLLGLAS   |
| 6236       | 1  | 703  | WDQNKGAAGSGSLTLPSPSARFSAGPPTQRSRPTMSNMEKHLF<br>NLKFAAKELSRSAKCDKEEKAEEKAKIKKAIQKGNMEVARIAE<br>NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK<br>SMDATLKTMLNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT<br>LTTFQNVQVDMLLQEMADEAGLDLNMELPQGTGSGVGTSVASAEQ<br>DELSQRLARLRDQV   |
| 6237       | 312  | 720  | PTAMAEGLAAGGVMDVNTALQEVLTALIHDLGARGIREAAKA<br>LDKRAHLCLVLANCDEPMYVKLVEALCABHQINLIKVDNKKL<br>GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK<br>CKK  |
| 6238       | 2  | 4566   | EEVPTQESVKWEINVIKKNPEIVFVADMTKNDAPALVITTQCEI<br>CYKGNLENSMTAAIKDLQVRACFPFLPVKRGKITTVLQPCDLF<br>YQTTQKGTDPQVIDMSVKSLLTKVSPVIINTMITITSALYTTKE<br>TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP<br>KGEMIKMNIIDIFIVLEAGIGHRTVPMLLAKSRFSGEGKQWSSL<br>INLHCQLELEVHYNYEMFGVWEPLLEPLEIDQTEDFRPWNIGIK<br>MKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG<br>LVMLNNLVKAFTEAATGSSADFKDLAPFMILNSLGLTISVSPS<br>DSFVNLNIPMAKSYVLKNGESLSMDYIRTKDNDFNMTSLSSK<br>LPFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI  |

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|------------|--|--|---|
|            |  |  | <p>DTVEGSKKVTIRSPVQIRNHFVPLSVYEGDTLLGTASPENEFN<br/> IPLGSYRSFIFLKPEDENYQCEGIDFSEIINKDGALLKKKCRS<br/> KNPSKESFLINIVPEKDNLTSLSVYSEGDGWDLPYIMHLWPPILL<br/> RNLLPYKIAYYIEGIENSFVTLSEGHSAQICTAQLGKARLHLKL<br/> LDYLNHDWKSEYHIKPNQDDISFVSFTCTVEMEKTDLDIAVHMT<br/> YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHFPNKKPVL<br/> FSFQPNHFFNNNKVQLMVTDSLSNQFSIDTVQSHGAVKCKGLK<br/> MDYQVGVITDLSSEFNITRIVTFTPFYMIKNKSKYHISVAEENGD<br/> KWLSDLLEQCI PFWEYASSKLLIQVERSEDPPKRIYFNKQENC<br/> ILLRLDNELGGIIEVNLAEHSTVITFLDYHDGAATFLLINHTK<br/> NELVQYNQSSLSIEDSLPPGKAVFYTWADPVGSRRLLKWRCKRS<br/> HCEVTQKDDMMMPIDLGEKTIYLVSEFFGLQRIILFTEDPRVPK<br/> VTYESEKAEIAEQEIAVALQDVGISLVNNYTKQEVAYIGITSSD<br/> VWVETKPKKKARWKPMKSVKHTKLEREFKYTESSPSEDKVIQL<br/> DTNPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQ<br/> SFRIQIYRIQIQNHGAVFFVFPVKPPKSVTMDAPKPFID<br/> VSIWMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLME<br/> AEVTENTLEVELFHDKIEAFKEEYKTASLVQSQVSLYEYFHSIP<br/> IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLNLLKLSIGATLTD<br/> VQDVVFKLAFFELNYQFHTSDLQSEVIRHYSKQAIKQMYVLIL<br/> GLDLVGNPFGLIREFSEGEAFPEPYQGAIQGPEEFVEGMALG<br/> LKALVGGAVGCLACAASKITGAMAKGVAAMTDEYQQRREAM<br/> NKQPAQFREGITRGKGKLVSGFVSGITGIVTKPIKGAQKGAAG<br/> FFKGVGKGLVGAVARPTGGIIDMASSTFGQIKRATETSEVESLR<br/> PPRFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD<br/> DDDDDDDESDELNH</p> |
| 6239       | 2108   | 634  | <p>KPGMAGKSSGRRPLLLGLLVAATVHLVICPYTKVEESFNLOA<br/> THDLLYHWQDLEQYDHLFPGVVPRTFLGPVVIIVFSSPAVYVL<br/> SLEMSKFYSQLIVRGVGLGVIFGLWTLQKEVRRHFGAMVATM<br/> FCWVTAMQPHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI<br/> WLSAFAIIVFRVELCLFLGLLLLLLALGNRRKSVVRALRHAVPAG<br/> ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSNNWGTSPLL<br/> WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVALGFMALYSLL<br/> PHKELRFIIYAFPLMNI TAARGCSYLLNNYKKSPLYKAGSLLVI<br/> GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI<br/> DVAAAQGTGVSRLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA<br/> PGLLALYRDTHRVLASVVGTTGVSLLNLTLQLPFFNVHLQTKLVLL<br/> ERLPRPS</p>  |
| 6240       | 2202   | 1176   | <p>HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTEGKSFHF<br/> DPLSSGSRSSSLKSAQGTGFELGQLQSI RSEGTTSYKSLANQ<br/> TRNGSLSYDLSLT'PSDSDPFESVQAGPEPDPLGYTSPFLSARL<br/> AQQREAEHRPRLVPTGPTHREPSPVRYDNL SRHIVASLQEREKL<br/> LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP<br/> LGKTPLRGPVAVRPFKPDGLRGRGVSGPEPGPTAPYLGRSMSYS<br/> SQKAQPGVSBTEEVALQPLLT PKDEVQLKTTYKSNQPKSLGS<br/> ASPGPGQPLSSPTRGGVKVSGVGGTTYEISV</p>   |
| 6241       | 3  | 1341   | <p>RNABEKKRLSLQREKIIARVSDNRTALVOALRRTTDPKLCIT<br/> RVEELTFHLLFPEGKGVAVKERIIPYLLRLRQIKDETLLQAQVR<br/> EILALIGYVDPVKGRGIRILSIDGGTRGVVALQTLRKLVELTQ<br/> KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGS DV<br/> FSQNVIVGTVMKSWSHAFYDSQTWENILKDRMGSAIMETARNP<br/> TCPKVAAVSTIVNRGITPKAFVFRNYGHFFGINSHYLGCGQYKM<br/> WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNPSALAMHECKC<br/> LWPDVPLECIVSLGTGRYESDVNTVTYTSKTKLSNVINSATD<br/> TEEVHIMLDGLLPDPTYFRFNPVMCENIPLDESRNEKLDQLQLE<br/> GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP</p>   |



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|------------|--|--|---|
| 6242       | 198  | 1310   | FFSKL<br>QHFLPGAETWSPGAAVCTARRFPGRSLAAPPRAAPRAVEMGE<br>SSEDIDQMFTLLGEMDLLTQSLGVDTLPPDPNPRAEFNYSV<br>GFKDLNESLNALEDODDLADMADLVADISEAEQRTIQAQKESLQ<br>NQHHSASLQASIFSGAASLGYGTVNAAATGISQYEDDLLPPPPADP<br>VLDLPLPPPPPEPLSQEESQAQKADKIKLAEKLEKAKVKKLV<br>VKVMNDNSTKSLMVDERQLARDVLDNLPBKTHCDNVDWCLYE<br>IYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEKEEKYAVF<br>KNPQNFYLDNRGKKESKETNEKMNNAKNKESLLEVLRLIQSGRKE<br>KDVCSIFKSFASENNGKI   |
| 6243       | 1509   | 614  | RSASRFSGCWSRDSTCCCPSTCWSRSSASCPRARWPPSSAPAT<br>TSRASSRRLACGPQTRAGAETRTAMIRAKSAARDTRRATCRSA<br>AGTPSPITMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA<br>MQAGAGPAGRGKSEAGGGPSRAHHAHPSPLPREPRVRTGPPAH<br>SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR<br>RVFFFFYQHLTFFSIQPPPPCHAFHPRDPAGTKRQLILVPLK<br>GPPILAPILSLTPIILSRWSCYFPRSRIAQGWHL   |
| 6244       | 2119   | 1745   | FEHAYASQFGTFLGNNESECKLKLQOKTMSLWSWVNQPSLSK<br>FTNPLFEANNLVIWQSVAPQSLPLWEGIFLRWNRSKKYLDEAYE<br>EMVNIIEYNKELQAKVNIILRRQLAELETEDGMQESP   |
| 6245       | 81   | 1148   | LSLRNAKYSFPQELISLFSMTDLNDNICKRYIRMITNIVLSLI<br>ICISLAFWIISMTASTYYGNLRPISPRWLFVSVVPLIVSNGL<br>KKSLDHSGLGGLVVGFIITIANFSFSTSLMFLSSSKLTKW<br>KGEVKKRLDSEYKEGGQRNWWQVPCNGAVPTLALLYMIENGGP<br>EIPVDFSKQYSASWMLCSLLAALACSAGDTWASEVGPVLSKSSP<br>RLITTWKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV<br>NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG<br>MVVNSPTNKARHLAGKPILDNNNAVNLFSSVLLALLLPTAANGFW<br>PRG   |
| 6246       | 1177   | 359  | SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV<br>QATHRGAVNSLMLCILKLASQMPLENTTVQOMVFMLLSNLALS<br>HDCKGVIQKSNFLQNLFLSLALPKGGNKHLSNLTILWLKLLNLS<br>SGEDGQQMILRLDGLDLDTMSKYKHSSPLLPLLIHNVCFSS<br>PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ<br>KAKTALKSPSVKRRVDEAYSLAKKTFPNSKANPLNAYLYKLEL<br>LVQLNNS  |
| 6247       | 3  | 1678   | NSRVHGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP<br>PGPGRALLECDHLRSQVPGRRRKDWSSCLLVASLAGAFSSFL<br>YGYNLVSVNAPTPIYIKAFYNESWERRHGRIPDPTLTLWSVTV<br>SIFAIGGLVGLTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS<br>LQAGAFEMLIWGRFIMGIDGGVALSVLPMYLSIISPKIIRGSLG<br>QVTAIFICIGVFTGQLLGLPELLGKESTWPLYFGVIVVPAVVQL<br>LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQVEBEVL<br>AESRVQRSIRLVSVLELLRAPYVRWQVVTIVITMACYQLCGLNA<br>IWFYTNISIFGKAGIPPAKIPIYVTLSTGGIETLAAVFSGLVIEHL<br>GRRPPLLIGGFGMLGFLFTGLTITLLODHAPVVPYLSIVGILAI<br>IASFCSPGGIPFILTGFEEFQOSQRPAAFIAGTVNNLSNFAVG<br>LLFPPIQKSLDTCYCLVFATICITGAIYLYFVLPETKNTRYAEI<br>SQAFSKRNKAYPPEEKIDSAVTDGKINGRP |
| 6248       | 56   | 1773   | VPPPRMMAAVPPGLEPWRNRVIPKAGNRSAVTVQNPGAALDLICI<br>AAVIKECHLVLSLKSQTLDAETDVLCAVLYSNHNMRGRHKPHL<br>ALKQVEQCLKRLKNMNELEGSIQDLFELFSSNENQPLTTKVCVVP<br>SQPVVELVLMKVLGACKLLRLDCCCKTFLLTVKHLGLQEFII<br>LNLVMVGLVSRLLVLYKGVLLKRLILLYEPLFGLLQEVARIQPM<br>YFKDFTFPSDITEFLGQPYFEAFKKMPIAFAAKGINLLNKLFL<br>LINEQSPRASEETLLGISKKAKQMKINQNVNVDLGPVKNRVP  |

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|------------|--|--|---|
|            |  |  | KEESSEFDVRAFCNQLKHKATQETSFDKCSQSRLKTKYSSQK<br>VIGTPHAKSFVQRFREAESFTQLSBEIQMAVVWCRSKKLKAQAI<br>FLGNKLLKSNRLKHLEAOGTSLPKKLECIKTSICNHLRSGSGIK<br>TSKHHLRQRRSQNKFLRRQRPQRLQSTLLREIQQFSQGTGRKS<br>ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPIQTKEKMI<br>HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDI PALMGV   |
| 6249       | 56   | 1773   | VPPPRMAAVPPGLEPWNVRVIPKAGNRSVAVTQVNGAALDLICI<br>AAVIEKCHLVILSLKSQTLDAETDVLCAVLYSNHNRMRHKLPHL<br>ALKQVEQCLKRLKMNMLEGSIQDLFELFSSNENQPLTTKVCVVP<br>SQPVVLEVLKVLGACKLLRLLDCCCKTFLLTVKHLGLQEFII<br>LNLVMVGLVSRLLVLYKGVLRLLILLYBPLFGLLQEVARIQPMF<br>YFKDFTFSDITEFLGQPYFEAFKKKMPIAFAAGINKLNLKLF<br>LINEQSPRASEETLLGISKKAKQMKINQVNNVDLQGPVKNKRVF<br>KEESSEFDVRAFCNQLKHKATQETSFDKCSQSRLKTKYSSQK<br>VIGTPHAKSFVQRFREAESFTQLSBEIQMAVVWCRSKKLKAQAI<br>FLGNKLLKSNRLKHLEAOGTSLPKKLECIKTSICNHLRSGSGIK<br>TSKHHLRQRRSQNKFLRRQRPQRLQSTLLREIQQFSQGTGRKS<br>ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPIQTKEKMI<br>HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDI PALMGV   |
| 6250       | 232  | 1306   | LAALHIMALPFRKOLEKYKOLDEDELLGNLSETELKQLETVLDD<br>LDPENALLPAGFRQKNQTSKSTTGPFDRHLLSYLEKEALEHKD<br>REDYVPYTGKKGKIFIPKQKPVQTFTEEKVSLDPELEALTS<br>SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG<br>EKILPVFDEPPNPTNVEESLKRTKENDAHLEVNLNINIKIPIPI<br>TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK<br>SLNVESNFITGVGILALIDALRDNETLAEKIDNQROQLGTAVE<br>LEMAKMLEENTNILKFGYQFTQQGPRTAAANITKNNDLVRKRR<br>VEGDHQ  |
| 6251       | 62   | 972  | TPGSGPMSAWAAASLSRAARCLLARGPGVRAAPPRDPRPSHPE<br>PRGCGAAPGRTLHFTAAVPAHGNKWSKVRHIKGPKDVERSRIFS<br>KLCLNIRLAVKEGGNPENHNSNLANILEVCRSKHMPKSTIETAL<br>KMEKSKDTYLLYEGRGPGGSSLLIEALSNSHKKQADIRHILNK<br>NGGVMVAGARHSFDKKGVI VVEVEDREKKAVNLERALEMAIEAG<br>AEDVKETEDBEERNVPKFCIDASSLHQVRKKLDSGLCSVSCAL<br>EFIPNSKVQLAEPDLEQAHLIQALS NHEDVIHVYDNIE   |
| 6252       | 27   | 1897   | EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE<br>ETVPTTAGASPGPPRNKNREL RPQRPKNAYILKKSRI SKKPQV<br>PKKPREWKNPESQRLSGAQDPFPGPAPVVPVEVQKFCRIDKSR<br>KLPHSKAKTRSRLEVABEABEEETS IKAARSELLLAEPGFLEGE<br>DGEDTAKICQADIVEAVD IASAAKHFDLNLRFQGPYRLNYSRTG<br>RHLEAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL<br>AVAQNRNLHIYDNQGIELHCIRRCRDVTRLEFLPFHLLATASE<br>TGFLTLYLDVSVGKI VAALNARAGRLDVMSQNPYNAVIHLGHSNG<br>TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL<br>KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA<br>GQKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT<br>SMLVPGAGEPNFDGLESNPYRSRKQREWEVKALLEKVPABELIC<br>LDPRALAEVDVISLEQKKKEQIERLGYDPOAKAPFQPKPKQKGR<br>SSTASLVKRRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS<br>ALDRFVR |
| 6253       | 27   | 1897   | EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE<br>ETVPTTAGASPGPPRNKNREL RPQRPKNAYILKKSRI SKKPQV<br>PKKPREWKNPESQRLSGAQDPFPGPAPVVPVEVQKFCRIDKSR<br>KLPHSKAKTRSRLEVABEABEEETS IKAARSELLLAEPGFLEGE<br>DGEDTAKICQADIVEAVD IASAAKHFDLNLRFQGPYRLNYSRTG<br>RHLEAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL   |

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|------------|--|--|--|
|            |  |  | AVAQRNRLHIYDNOGIELHCIRRCORVTRLEFLPFHPLLATASE<br>TGFLTYLDVSVGKIVAALNARAGRLDVMSONPYNAVIHLGHSNG<br>TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTVMATSGLDHQL<br>KIFDLRGTYQPLSTRTPHAGHLAFSQRGLLVAGMGDVVNIWA<br>GQKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT<br>SMLVPGAGEPNFDGLESNPYRSRKQRQEWVKALLEKVPALIC<br>LDPRALAEVDVISLEQGGKEQIERLGYPQAKAPFQPKPKQKGR<br>SSTASLVKRRKVMDEHRDKVRSLOQQHHEAKAKPTGARPS<br>ALDRFVR  |
| 6254       | 155  | 1139   | HALGRRGGSQELSAACGCFALRLRAPGSGRPALAPGAAAFAGL<br>GGAPRFPFPGSAAGRTMLLKEYRICMPLTVDEYKIGQLYMISKH<br>SHEQSDRGEVGVVQNEPFEDPHHNGQFTEKRVYLSKLPSWA<br>RAVVPKIFYVTEKAWNYPYTITEYTCSPLPKFSIHETKYEDN<br>KGSNDTIFDNEAKDVEREVCFIDIADEIPERYKESQEDPKHFK<br>SEKTRGRQLREGWRDSDHQPIMCSYKLVTVKFEVWGLQTRVEQFV<br>HKVVRDILLIGHRQAPAVVDEYDMDTDDVREYKKNMHEQTNIK<br>VCNQHSSPVDDIESHAQTS   |
| 6255       | 1  | 1444   | PTRPQQLLVSLATVIFVASQKALSVEKAVIKQLESVSNWGT<br>VYRIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS<br>HAEQCLTGLQENYSSALS CIAESLKFYHKGIAASLTAASTPLNP<br>LSFQCEVFKLRIDLLQAFSQLICTNSLKTSPFPAIATTIAMTL<br>GNDLQRCGRISNQMKQSMEEFRSLASRYGDLQASFDADSATLR<br>NVELOQQSCLLISHAIEALILDPESASFQYEGSTGTAHADSEYE<br>RRMMSVYNHVLREVESLNGKYTPVSYMHTACLCAIALLKVP<br>SFQRYFFQKLQSTS IKLALSPPRNPAPPIAVQNNQQLALKVEG<br>VVQHGSKPGLFRKIQSVCLNVSSLTQSKSGQDYKIPIDNMTNEM<br>EQRVEPHNDYFSTQFLNFAILGTHNITVESSVKDANGIVWKTG<br>BRTTIFVKSLEDPYSSQIRLQQQQAQPLQQQQQRNAYTRF   |
| 6256       | 1  | 1542   | CRGAGAEPAANPRSPRSLVPSLESTSTVPPAFPGTMATDSWALA<br>VDEQEAAAESLNLHLKEEKIKPDTNGAVVKTANAEKTDDEEK<br>EDRAAQSLLNKLIRSNLVDNTNQVEVLQDPNSPLYSVKSFEEL<br>RLKPOLQGVYAMGFNRP SKIQENALPLMLAEPQNLIAQSQSG<br>TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM<br>GKFPYELKLAYAVRGNKLERGQKISEQIVIGTPTGLDWCSSKLK<br>FIDPKKIKVFLDEADVMIATQGHQDQSIIRIQRLMPLRNCQMLLF<br>SATPEDSVWKFAQKVVPDPNVIKLKEEETLDTIKQYVVLCSR<br>DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAELSKEGHQVA<br>LLSGEMMVEQRAAVIERFREGKEKVLVTNNVCARGIDVEQVSVV<br>INFDLPVDKDGNPDNETYLRHIGRTGRFGKRGGLAVNMVDSKHS<br>NILNRIQEHFNKKIERLDTDDLDEIEKIAN |
| 6257       | 210  | 615  | AFIPAMAEIQQKKLQGEVEKYQQQLQKDLSSKMSGRQKLEAQLTE<br>NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI<br>TAEIKRYESQLRDLERQSEQQRET LAQLQGEFQRAQAAGAGP<br>KA   |
| 6258       | 210  | 615  | AFIPAMAEIQQKKLQGEVEKYQQQLQKDLSSKMSGRQKLEAQLTE<br>NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI<br>TAEIKRYESQLRDLERQSEQQRET LAQLQGEFQRAQAAGAGP<br>KA   |
| 6259       | 2  | 1540   | ILEKGFPSQCHPERKWKVDDVLESSQENEDHFWELLFHNKTV<br>SVENGDRGSKTFNLGTDVPSLRNYPYKICDSCEMNLKNISGLII<br>SKNCNSRKKPDEFNVCEKLLDIRHEKIPIGESYKYDQKRNAI<br>NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK<br>YNECGRTFIESLKLNISQRPHLEMEPYGCSI CGKSFCMNLRFHG<br>QRALTNDNPEYNEYGEIFCDNSAFIHHQAYTRKILREYKVSD<br>KTWKSALLKHQIVHMGKSYDYNENGSNFSKKSHTQLRRAHT<br>GEKTFECGECGKTFWEKSNLQHQHRTHTGKPYECTECGKAFQ   |

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|------------|--|--|---|
|            |  |  | KPHLTNHQRTHTGEKPYECKQCGKTFVCVSNLTHQRTHTGEKPYECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFVCVSNLIVHQRTHTGEKPYKCNCEGKTFCEKSALTQHRTHTGEKPYECNACGKTSQRSVLTQKHQRIHTRVKALSTS  |
| 6260       | 2081   | 1436   | GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVWRFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF RALAPMYRGSAAAIIVYDITKEETFSTLKNWVKELRQHGPPI NVVAIAGNKCDLIDVREVMERDAKDYADSIHAI FVETSAKNAINI NELFIEISRRI PSTDANLPSGGKGFKLRRQPSEPKRSCC   |
| 6261       | 3  | 1188   | FWYRLGPGTRSRWPRRGSWAASLVPRGSPALVTSPCPDPLRSPACEPCRPDFAPRPALLRSGPRAPAVTGKPKLQGPWPWGMAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS NVQRNRLVQHDLOVAKLQEEEDLKAQAQLQKRYKDLEQQDCBIA QEIQEKLAIEAERRRIQEKDEDIARLLQEKELQEEKRRKHFP EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA ETARKLQEBELLATQVDMRAAQVAQDEEIARLLMAEEKKAYKKA KEREKSSLDKRRQDPBWKPKTAKAANSKSKESDEPHHSKNERPA RPPPPIMTDGEDADYTHFTNQSSSTRHFSKSESSHKGPHYKH   |
| 6262       | 2  | 1759   | PGCHSOGLCVHRPFGKVPQARMSSGLVLGORDEPAGHRLSQEETL GSTRVLSQGLEALRSBHQAVLQSI.SQTIECLQGGHEEGLVHEK ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRQAVRR LCQENQWLRDELQAGTQQRLLQRSEQAVAQLEEEKHLEFLGQLRQ YDEGHTSBEKEGDATKDSLDDLPNEEEDPSNGLSRGGQATA AQOQGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALDLEL TSGRGHDPDVATMLNIALVYRDQNKYEAHLLNDALSIRESTL GPDPHVAATLNNLAVLYGKRGKYKEAPLCQORALEIREKVLGT NHPDVAKQLNNLALLCONOGKYEAVERYQORALAIYEGQLGPDN PNVARTKNNLASCYLKQGGKYAEABTYKEILTRAHVQFEGSVDD DHKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV NTTLRNLGALYRRQCKLEAAETLEECALRSRRQGTDPISQTKVA ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVESGDSGGTQLQR GSGLGKIRDVLRR   |
| 6263       | 1  | 2408   | RELDLADLPERIKPPYANGLSTSHLRSSSVEDVKLIIEGRPT IEVRRCSMPSVICEHTKQFOTISEESNOGSLLTVPGDTSPPSKP EVFNVNPERDLNVSNIHSSFATSPGTASNSKYVSADRNLKNT APVNTVMDSPPVHLEPSSQGVVIQNKSWEMPVDRLETSTRDFIC PNSNIPDQESSLQSFNCSENKVLKENADFLSLRQTELPGNCAQ DPASFMPPPQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQ KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK SSSGHEVENSTDTQVISHEKENKLESVLVTHLSRCDSDLCERN AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQOSILSSLENHSQ QSTQPEMHKYGLVKVLEENAEDDKTENQIPORMTRNKANTMA NQSKQILASCTLLSEKDSSESSPRGRIRLTEDDDPQIHHPKRK VSRVPQPVQVSPSLLOAKEKTQQSLAAIVDSLKLDEIQPYSSER ANPYFEYLHIRKKIEEKRKLCSVIQAPQYDEYVTFNGSYLL DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRQLHSIE REKLIVSNEQEVLRVHYRAARTLANQTLPPSACTVLLDAEVYNV PLDSQSDSKTSVRDRFNARQFMSWLQDVDDKFDKLTCLLMRQ QHEAALNAVORLEWQLKLQELDPATYKSISYIEIQEFYVPLVD VNDDFELTPI |
| 6264       | 143  | 1960   | KHRQENNALDAPETIHMTPMCLIENTNGELVANPEALKILSAI TQPVVVVAIVGLYRTGKSYLMNKLAKENKGFSLGSTVKSHTKGI WMWCVPHPKPEHTLVLLDTEGLGDVKKGDNDQNSWIFTLAVLL SSTLVYNSMGTINQQAMDQLYVTELTHIRSKSSPDENENEDS ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTOGT  |

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|------------|--|--|--|
|            |  |  | SQKDKNFNLPRLCIRKFFPKKKCFVFDLPPIHRRKLAQLEKLQDE<br>ELDPEFVQQVADFCSYIFSNSKTKLSSGGIKVNGPRLESVLTY<br>INAI SRGDLPCMENAVLALAQIENSAAVQKAI AHYDQMGQKQV<br>LPAETLQELLDLHRVSEEREATEVYMKNPKDQVHLFQKLAQAL<br>DKKRDDFCQKQNEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG<br>YCLFIQKLQDLKYYEPRKGIQAEIILQTYLKSSESVDAIL<br>QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK<br>EKSYQEHVKQLTEKMERERARQLLEEQKTLTSKLQEQARVLKER<br>CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI  |
| 6265       | 143  | 1960   | KHRQENNALDPAPEIHTMTGPMCLIENTNGELVANPEALKILSAI<br>TQPVVVVAIVGLYRTGKSYLMNKLAKNGFSLGSTVKSHTKGI<br>WMWCVPHPKKPEHTLVLLDTEGLGDVKKGNQNDSWIFTLAVLL<br>SSTLVNSMGTINQAMQDLYYVTELTHRIRSKSSPDENENEDS<br>ADVFVFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT<br>SQKDKNFNLPRLCIRKFFPKKKCFVFDLPPIHRRKLAQLEKLQDE<br>ELDPEFVQQVADFCSYIFSNSKTKLSSGGIKVNGPRLESVLTY<br>INAI SRGDLPCMENAVLALAQIENSAAVQKAI AHYDQMGQKQV<br>LPAETLQELLDLHRVSEEREATEVYMKNPKDQVHLFQKLAQAL<br>DKKRDDFCQKQNEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG<br>YCLFIQKLQDLKYYEPRKGIQAEIILQTYLKSSESVDAIL<br>QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK<br>EKSYQEHVKQLTEKMERERARQLLEEQKTLTSKLQEQARVLKER<br>CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI |
| 6266       | 276  | 1421   | GSHQKQMLVPCPLYSQNRKPSLYGSLTCQGGIGLDGIPVETASE<br>GFTVNEINKSKIHSCKPENASSKFLAPYTTFSRIHTKSITCLD<br>ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCRRFF<br>PSGLVVLSSGMDAQLKIWSAEDASCVVTFKGHKGGLDITAVDR<br>GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN<br>SINLGSPEQMPSEREVGTEAKMILLAREDDKQLQCLGLOSRLVF<br>LFIGSDAFNCCTFLSGFLLLAGTQDGNIVQLDVRSPRAPVQVIH<br>RSGAPVLSLLSVRDGFASQGDGSCFIVQDLDLYVTELTGADCD<br>PVYKVATWEKQIYTCRCDGLVRRYQLSDL   |
| 6267       | 3  | 622  | LGMMKKNNASAKRGPQDGNQFPAPPEKVGWVRKFCGRGIFREIWK<br>NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSYKCEELRKS<br>RSKKNHKSFTLAHSKQPGNTAPNLI FLAVSPEEKESWINALNSA<br>ITRAKNRILDEVTVEDDSYLAHPTRDRAKIQHSRRPPTRGHLM<br>VASTSTSDGMLTDLIQEEDFSPPEPTSLC   |
| 6268       | 160  | 1368   | HRELQNLPAGLSSALIDNPLTLLSIDTYVMLQEPVTFQDVAV<br>DFSREEWGLLGPTQRTYRDVMLETFGHLVSVGWETTLENKELA<br>PNSDIPEEPAPSLKVQESSRDCALSTLEDTLQGGVQEVQDTV<br>LKQMESAQEKDLPQKKHFDNRESQANSALDTNQVSLQKIDNPE<br>SQANSALDTNQVLLHKIPPRKRLRKRDSSQVSKMHNRSVKIHQ<br>KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCECGK<br>IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS<br>GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKQDCGKAFRQ<br>SSHLIRHQRTHTGERPYACNCKGKAFQSSHLIGHQRTHNRTRK<br>KKKQPTS  |
| 6269       | 2886   | 1449   | HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL<br>TQYVVKWINDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT<br>GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVS AVETFANGN<br>FPKACELWEQILQDHPTDMLAKFSDHAYFYLYGQEQMRDVAR<br>IYFPWTPDIPLSVVKGIYSFGLMETNFYDQAEKLAKALSINP<br>TDAWSVHTVAIHMKAEIKDGLEFMQHSETLWKDSDMLACHNY<br>WHWALYLIEKGEYAALTIYDTHILPSLQANDAMLDDVDSCSML<br>YRLQMEGVSVGQRWQDVLVPARKHSRDHILLFNDAHFLMASLGA<br>HDPQTTQELLTTLRDAESPGENCQHLLARDVGLPLCQALVEAE   |

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|------------|--|--|--|
|            |  |  | DGNPDRVLELLLPYRIVQLGGSSNAQRDVFNQLLIHAALNCTSVHKVNVARSLMERDALKPNSPLTERLIRKAATVHLMQ   |
| 6270       | 23   | 2086   | SVTVTLGSEGDGRPPPTYHLEEMEQEPQNGEPAETKIITREAYKKAFLFVNKGLNTDELQKKEAKNYYKQIGHLLRGISISSKESEHTGPGWESARQMQQMKETLQNVTRLEILEKGLATSLQNDLQEVPKLYPEFPKDMCEKLEPQSFSSAPQAEVNGNTSTPSAGAVAAPASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDGSEFSSVGE EYFNHNSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPSYPGYLRIVRFLDNLDTVLNRPFGFLQVCDWLYPLVPDRSPVLKCTAGAYMFPDMLQAAAGCFVGVVLSSELPEDDRELFEDLLRQMSDLRLQANWNRAEEENEFCQIPGRTRPSSDQLKEASGTDVKQLDQGNKDVRHKGKRGKRAKDTSSSEVNLSHIVPCEPVPEEKPELPEWSEKVAHNILSGASVWSGLVKGAETGKAIQKGASKLRERIQPE EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGKELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFSTVWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDASAVNVGVTAYNINNIGIKAMVKKATATQGTHTLLEDYQIVDNSQRENQEGAANVNVRGEKDEQTEKVEKAKKDK |
| 6271       | 32   | 1058   | GCGVKTAGMVGREKELSIHFVPGSCLVEEENIPNRRVLVTGATGLLGRAVHKEFQNNNHAVGCGFRARRPKFEQVNLDSNAVHHI IHDQPHVIVHCAAERPDVVENQPDAAASQLNVDASGNLAKAEEAAVGAFLIYISSDYVFDGNTPPYREEDIPAPLNLYGKTKLDGKAVLENNLGAVALRIPILYGEVEKLEESAVTMFDKVQFSNKSANMDHWQORFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQMTKYEMACAIADAFNLPSHLRPTDPSVLGAQRPRNAQLDCSKLBTLGIGQRTPFPRIGIKESLWPFLLDKRWRQTVFH   |
| 6272       | 1136   | 528  | CAVMEDAAAPGRTEGVLERQGAAPAGQGGALVELTPTPGGLALVSPYHTRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQI QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKRESGQ QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAKISMDTLLSQSVLPPCTEPNFQGLTH   |
| 6273       | 256  | 843  | SCPRVSPSCRSLGCQVMFSLPLNCSPDHIRRGSCWGRPDQLKIASAANWSKCHPGAGAMARQHARTLWYDRPRYVFMFCVEDSTDVHVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSR SITCFVRKWKVKVAVPRLTKEDIKPVWLSVDFDNWRDWEGBEEMELAHVEHYAEVRDNTYCVLPT  |
| 6274       | 56   | 1142   | AAAAAAAAGGGAGAAARSLSRFRGCLAGALGDCVGSFYEAHDTVDLTSVLRHVQSLPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQYKQKDPDRGYGAGVTVFKLLNPKCRDVFEPARAQFNGKSGYNGGAMRVAGISLAYSSVDVQKFARLS AQLTHASSLGYNAILQALAVHLALQGESSSKHFLKQLLGHMEDLEGDAQSVLDARELGMEERPYSRLKKIGELLDQASVTRBEVVS ELGNGIAAFESVPTAIYCFRLCMEPDPEIPSAFNSLQRTLIYSI SLGGDDTDIATMAGAIAGAYYGMDQVPESWQQSCGEYEETDILA QSLHRVFQKS  |
| 6275       | 20   | 565  | SRGRARCLARGSRPVRPAKTMAMFVKTVMVGGQLKNTGSLG GGEDKGDGKSAAEAQMSREYEEYQKQLVEEKMERDAQFTOR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQTLDGLKQSAE KCHVM   |
| 6276       | 797  | 97   | TLLPLPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE SCLQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP VMVGAKEI SHGSFSPVGHVAGRELLTAVAEVFPHTVAPGWPEEV LGSGYREQLLTDMLELQGLWQPVSFQMQAMLLGHSTAGAI GRL LASSPRATVTEHNPAAGGDYASVRTALLAARAVDRTRVYYRLPQ GYHKDLLAHVGRN  |

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|------------|--|--|--|
| 6277       | 4600   | 2744   | MAFRTEMGLYYSYFKTIVEAPSPFLNGVNMIMNDKLTETPLVINT LKRFNLYPEVILASWYRIYTKIMDLIGIQTKICWTVTIGEGISP TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSCSRLGGL VTVLCFFFNHGECTRMWTPPLRESFSYPFLVLQMLLVTHILRA TKLYRGSLLIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVG YIDICKLRKIIYHIMISLALCFVLMFGNSMLLTSYASSLVIWNG ILMKPHFLKINVSELSLWVIQGCFLWFGTVILKYLTSKI FGA NDAHIGNLLTSKTFYSYKDFDTLLYTCAAEDFMEKETPLRYTKT LLLPVVLVGFVAIVRKIISDMWGVLAQOQTHVRKHQFDHGELVY HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRLPGWLFC KVHPGAIVFAILAAMSIOGSANLQTQWNIVGEFSNLPQEEELIEW IKYSTKPDVAFAGAMPTMASVKLSALRPVNHPHYEDAGLRART KIVYSWYSRKAAEEVKRELILKKNVYIILEESWCVRRSKPGCSM PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLV EVV KE |
| 6278       | 3  | 823  | ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL IRIILEYCGQVDNIPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG ALQVVGKLTITTKNALSSRCLQIVHYIPVIRAHFEARLPKQ YSMLRHFDPHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVA PVPSACFRNICKQMTKMHEAIFDLLPEEQTQMLFLRINASYKLH LKKQLSHLVINDGGPQNGLVLTADVAFYTGNLQALKGLKDLDLN MAEIQEQXR   |
| 6279       | 127  | 1687   | GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLHGT L RSTAKMPTTPVKAKRVSTFQEFESNTSDANDAGEDDELLAMA AESLNSEVVMETANRVLNRHSRQGRPTLQEGPGLQKPRPEAE PPSPPSGDLRLVKSVSSEHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPMTWKLLSGYLPANVDRRPTLQKQKEYFAFI EHYYSRNDVHQDTYRQIHIDIIPRMSPEALILQPKVTEIFER LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEABEVDTVDS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNLLMREVPRLCTIR LWDTYQSEPDGFSHFHLYVCAAFVLRWRKEILEEKDFQELLLFL QNLPTAHWDEDISLLLAAYRLKPAFADAPNHYKK  |
| 6280       | 857  | 2515   | ECCDQKMGSRNSSAGSGSDPSEGLPRRGAGLRRSEEEEEDE DVDLAQVLA YLLRRGQVRLVQCGGAANLQFIQALLDSEENDRA WDGRLGDRYNPPVDATPDTRLEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQREGLCHRGFSLSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTI RLYDCRYGRFRKFSIKA RDVGWSVLDAFTPDGNHFLYSSWSYIHCNIYEGDTH TALD LRPDERRFVAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVDRRTMREDDPK PVGALAGHQDGTITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQONWDIRWQVPPKAWRKLKLPDSSSLMTYRGH GVLHTLIRCRFSPHISTGQQFIYSGCSTGKVVVYDLSGHI VVK LTNHKACVRDVSNHFPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPO   |
| 6281       | 857  | 2515   | ECCDQKMGSRNSSAGSGSDPSEGLPRRGAGLRRSEEEEEDE DVDLAQVLA YLLRRGQVRLVQCGGAANLQFIQALLDSEENDRA WDGRLGDRYNPPVDATPDTRLEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQREGLCHRGFSLSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTI RLYDCRYGRFRKFSIKA RDVGWSVLDAFTPDGNHFLYSSWSYIHCNIYEGDTH TALD LRPDERRFVAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVDRRTMREDDPK PVGALAGHQDGTITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR   |

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|------------|--|--|---|
|            |  |  | EGMEASRQAATOONWDYRWQQVPKKAWRKLLKPGDSSLMTRYGH<br>GVLHTLIRCRFSPHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK<br>LTNHKACVRDVSHPFEEKIVSSWDGNLRWLQVYRQAEYFQDDM<br>PESEECASAPAPVPQSSSTPFSSPQ   |
| 6282       | 125  | 906  | RMAACRALKAVLVDSGLTHIEDAAVPGAQEAALKRLRGASVIR<br>FVTNTTKESQDQLERLRKLEFDISEDEIFTSLTAARSLERKQ<br>VRPMLLVDDRALPDFKGIQTSDFNAVVMGLAPEHFHYQILNQAF<br>RLLDGAPLIAIHKARYKRDGLALGPGPFVTALEYATDTKAT<br>VVGKPEKTFLEALRGTCPEEAVMIGDDCRDDVGGADQVGM<br>GILVKTGKYRASDEEKNPPYLTCESEFPAVDHILQHL   |
| 6283       | 140  | 1043   | LSLFGIHVMNPFWSMSTSSVRKRSEGEERTLTGDVKTSPPTAP<br>KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPFLEYSL<br>AEFTLVVKQLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVFKF<br>TVYIPDNYPDGDPCRLVFDIPVFNPLVDPTSGELDVKRAF<br>RNNHIWQVLMYARRVYKIDTASPLNPEAAVLYEKDIQLFKSK<br>VVDVSVKCTARLFDQPKIEDPYAISFPWNPSVHDEAREKMLTQ<br>KKKPEEQHNKSVHAGLSWVKPGSVQPFSSKEEKTAT   |
| 6284       | 1  | 2879   | RSVTPGSTISSRWPGLSRPRFMAAHEWDFQREELIGQISDIRV<br>QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI<br>LMALLEVLSSGRNLLHEYKSSSHRIFRLNNIAKALKFLED<br>SNVKLVSIDAEEIADGNPSLVGLIWNILFFQIKELTGNLSRNSPSS<br>LAPGSGGTDSDFPTPTAERSVAISVKDQKAKALLAWVQR<br>KTRKYGVAVQDFAGSWRSLAFLAVIKADPSLVDMKQALENST<br>RENLEKAPSIADALHIPRLEPEDIMVDTPEQSIMTYVAQFL<br>ERFPELEAEDIFDSKKEVPIESTFVRIKETPSEQESKVFVTEN<br>GERTYTVNHETSHPPSKVFCVKPESMKERLGDVSSHALSDS<br>STEFMHQIIDQVLQGGPGKTSIDISEPSPSSILSSRKENGSRNS<br>LPIKKTVHFEADTYKDFCSKNLSLCEGSPRVAKESLRQDGHV<br>LAVEVAEEKEQKQESSKIPSSSDKVAGDIFLVEGTNNSSQSS<br>CNGALESTARHDEESHLSPPGENTVMADSFQIKVNLMTVEALE<br>EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPEDA<br>EAFENHAEKLGKRSIKSAHKKKDSPEQVKMDKHEPHQDSGEA<br>EGCPSAPEETPVKKPEVHEKAKRKRSTRPHYEEEGEDDLQGVG<br>EELSSSPSSCVSLETLSHSEGLDFKPSPLSKSVSIPHDLF<br>YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEPEGYMPDLSRE<br>EEADGSQSSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP<br>LAPHEDHQRETENDPMDSHQSQSPNLENIANPLEENVTKES<br>ISSKKKEKRKHVDHVESLFLVAPGSVQSSDDLLEDSSDYSIPSR<br>TSHSDSSIYLRRHTRHSSSDHFLCSVEERSRSG |
| 6285       | 2157   | 1331   | SKTENLLEMMWFQQLSFLPSALVIWTSAAFIYSYITAVTLHI<br>IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYVRYKQVH<br>ALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAAHVS<br>GAVLTFGMGSLYMFVQTILSYQMCPKIHGQVFWIRLLVWCG<br>VSALSMLTCSVLSHSGNFGTDLEQKLHWNPEDKGYVLHMITTA<br>EWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPIN<br>NERTRLLSRDI  |
| 6286       | 1619   | 276  | KAGASCCGSANFYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV<br>PFSIPAASEIADLSNIINKLLKDKNEFHKVEFDLIKQFLRM<br>PLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIK<br>GAEEWILTGSYDKTSRIWSLEGKSIIMTIVGHTDVVKDVAWVKD<br>SLSCLLLSASMDQITLLWEWNVERNKVKALHCCRGHAGSVDSIA<br>VDGSGTKFCGSGWDKMLKIWSTVPTDEEDEMESTNRPKQKQ<br>EQLGLTRTPIVTSLGHMEAVSSVLWSDAEEICSAWDHTIRVWD<br>VESGSLKSTLTGNKVFNCISYSPCKRLASGSTDRIHRLWDPRT<br>KDGLSVLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT<br>RSCKAPLYDLAAHEDKVLSDVWDTDTGLLLSGGADNKLYSYRSP   |



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|------------|--|--|---|
| 6287       | 278  | 1482   | TTSHVGA<br>MQFFPNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF<br>APAKLVQVKILCDLLPENLKEGLKRESSWSSLPCTKNRPFDFHS<br>VMEESQSLNEPSPKQSEIEPTSEPVKGSINRAQSAQSINSTE<br>MPAREDCIKRVSSSEPVLSVQEKGVLLKRLSLLQDVIWNEDGR<br>NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMLRFFE<br>PVTTPCGHSFCKNCLERCLDHAPYCPCKESLKEYLADRRYCVT<br>QLLEELIVKYLDELSEKRIYDEETAELSHLTKNVPIFVCTMA<br>YPTVPCPLHVFEPYRLMIRRSIQGTGKQFGMCVSDTQNSFADY<br>GCMLQIRNVHFLPDGRSVVDTVGGKRFVLKRGMKDGYCTADIE<br>YLEDV  |
| 6288       | 1  | 743  | VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECRL<br>MLDSGADYHLVDMDGHFVPNITFGHPVVESLRKQLGQDPFFDM<br>HMMVSKPEQWVKPMAGAVAGANYTFHLEATENPGALIKDIRNGM<br>KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDM<br>PKVHNLRTQFPPLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM<br>RSEDPKRSVINLLRNVCSEAAQKRSILDR   |
| 6289       | 1  | 743  | VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECRL<br>MLDSGADYHLVDMDGHFVPNITFGHPVVESLRKQLGQDPFFDM<br>HMMVSKPEQWVKPMAGAVAGANYTFHLEATENPGALIKDIRNGM<br>KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDM<br>PKVHNLRTQFPPLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM<br>RSEDPKRSVINLLRNVCSEAAQKRSILDR   |
| 6290       | 3  | 1856   | TLGRWLLGVYETVAPTACLPRPRLRRRRRRRRRRMISRYTRKA<br>VPQSLELKGITKHALNHPPPEKLEIISPTSDSHEKDTSSQS<br>DITRESSPTSADTGNLSAFPSTGAGISTEGSSDFSWGYGELD<br>QNATEKVQTMFTAIDELLYEQKLSVHTKSLOECQOWTASFPHL<br>RILGRQIITPSEGYRLYPRSPSAVSASYETTLQERDSTIFGIR<br>GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY<br>LAPDHIIDIEEGFHGKKSEATEKQKLYPPIAPFYCMKEDVLAY<br>VDSVWCKVVSCEQLTRSHWEGFASDDESNAVATRPDSESSCV<br>LSELHPLVLPVPQSKVLYITSNPMSLCOASRHQPNVNDLLVHG<br>MPLQPRNLMLDKLLDLDDKLLMRPGSSTILSTRNWPNAVEFS<br>TSSLSYTVQSTRRRNPPRTHLPITSHSCAETPRSEIEILRGA<br>RVVPAPDSLSSPSTPLSRNNLLPPIGTAEVHVSTVGFQRMK<br>PHGDSRAQSAVVDEPNYQPPQERLLLPDFFPNPNTTQSFLD<br>QYRRSCAVEYPHQAQPGRSAGPQLHGSTKSQSGRPVSRTRQG<br>P |
| 6291       | 1732   | 602  | LVAKMASSASARTPAGKRVINQEEELRLMKKQRLSTSRKRIBS<br>PPAKYNRLGQLSCALCNTPVKSELLWQTHVLGKHREKVAELKG<br>AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVQVQVQST<br>SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEGD<br>GERKRGDASKPLSDAQGKEHSVSSREVTSSVLPNDFFSTNPPK<br>APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV<br>RKVDAPKDQMDKEWDEFQKAMQVNTISEAIVAEDEEGRLDRQ<br>IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKKEEN<br>ADSDDEGELQDLSQDWRVKGALL   |
| 6292       | 1835   | 1142   | TCPGAMKMVAPWTRFYNSNCCCHVVRTGTILLGVWYLIINAVV<br>LLILLSALADPDQYNFSSSELGGDFEFMDANMCIAIAISLLMI<br>LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN<br>SIQEYIRQLPPNFPYRDDVMSVNTCLVLIILFISIIILTFKGY<br>LISCWNCYRYINGRNSDVLVYVTSNDTTLVLPYDDATVNGA<br>AKEPPPPYVSA   |
| 6293       | 2382   | 1035   | FWCTLGTVDVHPIGWCAINSKILVFPRTIHAFTDWKGYLMKRL<br>VGSRTLVPDFHIKMEVSMKYPFRQGMRLVVDKSVQSRTRMAVV<br>DTVIGGRLRLLYEDGSDDDFWCHMWSPLIHPVGSRRRVGHGK  |

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|------------|--|--|---|
|            |  |  | MSERRSDMAHHTPRKIYCDVPPYLFKKVRAVYTEGGWFEEGMK<br>LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY<br>HASSHAIFPATFCQKNDIELTPPKGYEAQTFNWNYLEKTKSKA<br>APSRLEFMDCPNHGFVKVGMKLEAVDLMEPRLICVATVKRVVHRL<br>LSIHFDGWDSEYDQWVDCESPDYIPVGVWCELTYQLQPPVAAEP<br>ATPLKAKEATKKKKQFGKKRKRIPTKTRPLRQGSKKPLLEDD<br>PQGARKISSEPVGEI IAVRVKEEHLDVASPDKASSPELPVSVE<br>NIKQETDD   |
| 6294       | 354  | 1814   | AQLTTRGRTVAGGVRWIPSPFPDLLEYSCCLGTDRGFPELSHHC<br>KNVIATASDYDMAEITNIRPSFDVSPVAVGLIGASVLVVCVSVT<br>VFWSCCHQQAQKHKKNPPYKFHMLKGISYIPETLSNKKKIIK<br>VRRDKDGPREGGRNLLVDAAEAGLLSRDKDPRGSSGSCIDQ<br>LPIKMDYGEELRSPITSLTPGESKITSPSSPEEDVMLGSLTFSV<br>DYNFPKKALVVTIQEAHGLPVMDDQQTQGSDDPYIKMTILPKRHR<br>VKTRVLRKTLDPVDETFYFYGIYPSQLQDLVLHFLVLSFDRFS<br>RDDVIGVMVPLAGVDPSTGKVQLTRDIKRNQKICISRGELQV<br>SLSYQFVQARMTVVVLKARHLQKMDIAGLSGNPVYKVNYYGRK<br>RIAKKTHVKCTLNPINFESFIYDIPTDLLPDISIEFLVIDFD<br>RTTKNEVVGRLLIGAHSVTASGAHWEVCESPRKPKVAKWHSLS<br>EY   |
| 6295       | 2795   | 617  | VSSALLTGATSGSDAAKSEGASAPLSCTNAVAMDPRDEGPPAK<br>TRRLSSSESQRDPPIPPPPPPPLRLPLPFPQQRPRLQEETAA<br>QVLADMGRVGLGPALEPPPPYVILEEGGIRAYFTLGAECPGWDS<br>TIESGYGEAPPPTESLEALPTPEASGGSLIDFQVVQSSSFGGE<br>GALETCSAVGWAPQRLVDPKSKKEAIIIVEDEDEDERESMRSSR<br>RRRRRRRRKQKVKRESRERNAERMESILQALEDIQLDLEAVNI<br>KAGAFRLRLKRFQIMRRPFLERRDLIIQHIPGFVWKAFLNHPR<br>ISILINRRDEDI FRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT<br>NMVIVKEFQRNRSRGLVSHSTPIRWHRGQEPQARRHGNQDASHS<br>FFSWFSNHSLEADRIAETIKNDLWVNPLRYLRRGSRIRKRRK<br>QEMKKRKTGRCEVVIMEDAPDYAVEDIFSEISIDIDETIHDIK<br>ISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETDN<br>NESADDHETTDNNEADDNNENPEDNNKNTDDNEENPNNNENTY<br>GNFFFKGGFWGSHGNQDSSDSNEADEASDDEDDNGNEGDNEG<br>SDDGNEGDNESDDDDRDIEYEEKVIEDFDKQADYEDVIEII<br>SDESVEEGIEEGIQQDEDIYEEGNYEEGESDVEEGEDSDSDS<br>DLEDVLQVPNGWANPGKRGKTG |
| 6296       | 727  | 1199   | RHCGDAAGACDSLPTGTSSPVTARNAPPEARCCVWLLDGTTV<br>EAVRPARERLARKELRQKRMQQFSRDSAYSSNKDSTCLLTERDT<br>LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK<br>KWALIHKRVRLSVFGARWGRIYFGK   |
| 6297       | 1  | 922  | QRAAAASPSSCGPRGAEVGALMAMEGYWRFALLGSALLVGLS<br>VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAT<br>VYRLPWTWKCSKLLMKSIHAGLNAVAAILAISVAVFENHNVN<br>NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL<br>MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGV<br>FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEQ<br>GARGSMPAYSGNNMDKSDSELNNEVAARKRNALDEAGQRSTM   |
| 6298       | 3  | 985  | SVPLRRLSLSGTLQAGTTTKMAVARLAAVAAPVPCRSWGWAAV<br>PFGPHRGLSVLLARIPQAPRWLPACRQKTSLSFLNRPDLNLA<br>YKCLKGKSGPIIFIPGYLSYMGTKALAEFCKSLGHACIRFD<br>YSGVGSSDGNSEESTLKGWRKDVLSIIDLADGPQILVGSLSGG<br>WLMLHAAIARPEKVVALIGVATAADTLVTKFNQLPVELKKEVEM<br>KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL<br>LHGMKDDIVPWHSTMQVADRVLSTDDVILRKHSDHRMREKADI<br>QLLVYTIDDLIDKLSTIVN   |

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|------------|--|--|--|
| 6299       | 512  | 814  | ECDEGIMPVNTISLSLPTNGSPQLQDILVHPCVTSLSAAILTSS<br>SIDAMDESAFSGPYKFPFTPPLSFNLCFYTSQVPPVPPILGFYQ<br>MKEEEVQLRNNH   |
| 6300       | 121  | 692  | AAPSCWSQRGVPAAGTPSSPRLLVSRRAAPSAWPAGAWRQAGARA<br>AQSPSPISNSSSVPYGSDSVHSSPEDGGGGRRDPVGGSPGGPR<br>LVIGSLPAHLSPHMFPGPKCPVCSKFVSSDEMHLVCLTKPR<br>ITYNEDVLSKDGECALCLEELQQGDTIARLPCLCIYHKGCIIDE<br>WFEVNRSCPEHPSD  |
| 6301       | 616  | 284  | GKFPVNVNWPFPQLFFPKYLRCYRCLLETKELGCLLSDICLTP<br>AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW<br>IFSQYCFDLFCNDPQNRGLYTP  |
| 6302       | 490  | 745  | IFGFLHLFHNEHSFLLVLCALFAHVFFSSSCGSSVALHSDPCLLS<br>PVLNCLPGDLRLPLDELYAQKLKYKATSEELDHALNDMTSL   |
| 6303       | 2  | 1961   | YWNIEYGGGLLWQSWOEKHPGQALSSPEWNPFDTEKEWEQHSYQL<br>YWYLEQFQYWEAQGWTFDASQSCDITDITYTSKTEADKNDKCM<br>KDLVSLSSPIMGDNSSGTSKDKHSEILDGINSIKLNSEEV<br>QSQLDSCSTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS<br>SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK<br>PSKLKRSHELDIDENPASDFDDSGSLGFRYGSQKYGIPNFS<br>HRQVRYLEKNVCLKSKYLDMMRRQIKMKNNKHIFFTESEKPFKK<br>SKILSKVEKFLTWVKNPMDEEASQESSSHDNGHDASTSCDSEEQ<br>DMSVKKGDLLLETNNPEPEKCSQSVSSAGELETENYERDSLALAT<br>PDEODCVTQEVDPDSRQAETEAEVKKKKNNKKNNKVNGLPPEIAA<br>VPELAKYWAQRYRLFSPRFDGKLDREGWFSVTPEKIAEHIAGR<br>VSQSFKCDVVDAFCVGCGNTIQFALTGMRVIAIDIDPVKIALA<br>RNNAEVYGIADKIEFICGDFLLASFLKADVFLSPPWGGPDYA<br>TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS<br>LAGPGGQVEIEQNFLNNKLKITAYFGDLIRRPASET |
| 6304       | 1  | 1438   | HRARVDRSRESFPGDLRHFGRVRRDITLSGHPRLSTQHVVLLRE<br>DEVGDPGTGKDLGHPQHGSPIQETQSEVVTLVSPPLPGSDMAALPA<br>NRATSGTLWPHPTAEGRDLLGAENRALTGQQAEDPTLASGAYQ<br>WPGSVEKLQGSVWCDAETLLSSRTGGQAPPWLTQHDVQMLRL<br>AQGEVVDKARVPAHQVQLQVGFSTEAALQDLSSPRLSQCSCGL<br>CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPFLPYRY<br>TDGGARPVIIWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN<br>WPGQAPCPGIHHTEWARLALFDLLQVHDLRLDRYCCGFEPSPD<br>PCVEERLREKCRNPAELRLVHILVRSSDPFSLVYIDNAGNLQHP<br>EDKLNFRLLLEGIDGF2ESAVKVLASGCLQNMMLKSLQMDPVFWE<br>SQGGAQGLKQVLQTLQQRGQVLLGHIQKHNLTFRDEDP   |
| 6305       | 99   | 420  | NMIWRGRSTYRPRRRSVPPPELIGPMLEPGDEEPQEEPPPTES<br>RDPAPQGEREDQGAETQVPDLEADLQELSQSKTGDECGDGP<br>VQGKILTKEQFKMPEGR  |
| 6306       | 1  | 1874   | PTRPSKVVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDC<br>KFNCHKRCATRVPNDCLEALINGDVPMEATDFSEADKSALMD<br>ESEDGVI PGSHSENALHASEEEEGEGGAQSSSLGYIPLMRVVQ<br>SVRHTRKSSTTLREGWVHYSNKDTLRKRHYWRDLCKCITLQ<br>NNTTNRYKIEIPLSEILTVESAQNFSLVPPGTNPFCFIVTANA<br>TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILQDAPS<br>APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF<br>GVVYGGKHKRKTGRDVAVKVIDKLRFP TKQESQLRNEVAILQSLR<br>HPGI NVLECMFETPEKV FVVMKELHGDMLEMILSSEKGRRLPERL<br>TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADFPQVKLC<br>DFGFARIIGEKSFRRSVVGTTPAYLAPEVLLNQGYNRSLDMWSVG<br>VIMYVSLSGTFFPNEDEDINDQIQNAAFMYPASPWSHISAGAI<br>LINLLQVKMRKRYSDKSLSHPLQEQYTWLDLRELEGKMGGR<br>YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMMQ  |

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|------------|--|--|--|
|            |  |  | LAERISVL   |
| 6307       | 2136   | 589  | CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKFRHVFG<br>QPVKNDCCYEDIRVSRVTWSTFCVAVNPKFLAVIVEASGGGAFL<br>VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC<br>TVMVWQIPENGLTSPLTEPVVLEGTTRKVGIIAMHPTARNVLL<br>SAGCDNVVLEWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS<br>ACKDKSVRIIDPRRGLVAEREKAHEGAPMRAIFLADGKVFTT<br>GFSRMSERQALWDPENLEEPALQELDSSNGALLPFYDPDTSV<br>VYVCGKGDSSIRYFEITEEPYIHFLNTFTSKEPQRMGMSMPKR<br>GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQODLYPDTAG<br>PEAALEAEWVSGRDADPILISLREAYVPSKQRDLLKISRRNVLS<br>DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEV<br>QELRALRALVKEQGDRI CRLEEQLGRMENGDA |
| 6308       | 2  | 1118   | GRPTRPEKMLLSLVLTYSMRYLLPSVVLGTAPTYVLAWGVWR<br>LLSAFLPARFYQALDDRLYCVYQSMVLEFFENYTGVIILLYGDL<br>PKNKENIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK<br>WLPLYGWYFAQHGGIYVKRSKAFNEKEMKNKLQSYVDAGTPMYL<br>VIFPEGTRYNPEQTKVLSASQAPAAQRGLAVLKHVLTPIKATH<br>VAFDCMKNYLDAIYDVTVVYEGKDDGGQRRSPMTTEFLCKECP<br>KIHIIHIDRIDKDVPEEQEHMRRWLHERFEIKDKMLIEFYESP<br>PERRKRFPKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL<br>YVNTWIYGTLLGCLWVTIKA  |
| 6309       | 220  | 563  | LVAEVKEPCSLPMLSVDMENKENGSGVGVKNMENGRRPPDPADWA<br>VMDVVNYFRTVGFEQASAFQEQEIDGKSLLLMTNDVLTGLQL<br>KLGPALKIYEHYVKPLQTKHLKNSS   |
| 6310       | 36   | 979  | GPRCWFILILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE<br>AQRGSLA3LNVAAGLWADCDQPLYDCPMGLICTNYHILQEHV<br>DLHLEENSFQQGMDRVQCSGDLQLAHQEQEEDRRRSEESRQE<br>IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPEFHR<br>KADMMESLALGFDDGKTKTSGIIEALHRYQNAATDVRVWLSS<br>VVDHFHSSLGDKGWGCGYRNFQMLSSLLQNDAYNDCIKGMLIP<br>CIPKIQSMIEDAWKEGFDPOGASQLIIRLQGTKAWIGACEVYIL<br>LTSLRV  |
| 6311       | 1  | 675  | PVWNNSCEGPRLAAAARTGHGVGRRARLACLGEPVKAAMVLT<br>ASKLRDDGLKGSRTAATASDSTRVSVRDKLLVKEVALEANL<br>PCTCKVHFDPNKLHCFQLTVPDEGYQGGKFQFETEVDPAYN<br>MVPPVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL<br>KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI<br>KRYAR   |
| 6312       | 213  | 1400   | GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRABGFTVEALW<br>GKTEEAQKLAEMNIAFYTSRTDDILLHQDVLDVCISIPPLT<br>RQISVKALGIGKNVCEKAATSVDAFRMVTASRYYPQLMSLVGN<br>VLRFLPAFVRMKQLISEHYGAVMICDARIYSGSLLSPSYGWIC<br>DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFFVRONAA<br>IRGIRHVTSDDFCFQMLMGGGVCSVTTLNFMMPGAFVHEVMV<br>GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD<br>VPLLKGMVYMQALRQSFQGGQDRRTWDRTPVSMASFEEDGL<br>YMQSVVDAIKRSSRSGEWEAVEVLTEPDNTQNLCEALQRNNL  |
| 6313       | 2  | 2071   | QRSGAARLAFLPSPFPACVHRSPLSFHGCWFYFVVVFMPLGLV<br>FIHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHKKMILD<br>RLNEQREQDRFTDITLIVDGHFKAHKAVLAACSKFFYKFQEF<br>TOEPLVEIEGVSKMAFRHLIEFTYAKLMIQGEEDANDVWKA<br>FLQMLEAIKALEVRNKENSAPLENTTGKNBAKKRKIAETSNVI<br>TSLPSAESEPEVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK<br>YIQTSGSSDDSLALLADITSKYRQGRKQIQEDGCPSPDPTSK<br>QVEGIEIVELQLSHVKDLFHCCKNRSFKLPYHFKHEMKSHSTE  |

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|------------|--|--|---|
|            |  |  | SFKCEICNKRYLRESAWKQHLNLCYHLEEGGVSKKQRTGKKIHVC<br>QYCEKQFDHFGHFKEHLRKHTEGKPFECPCNCHERFARNSTLKCH<br>LTACQTVGVGAKKGRKKLYECQVCNSVFNWDQFKDHLVIHTGDK<br>PNHCTLCDLWFMQGNELRRHLSDAHNISRVLTEEVLSVETRVQ<br>TEPVTSMITIEQVGKVVHLPPLQVQVDSAQVTVEQVHPDLLQDS<br>QVHDSHMSLPEQVQVSYLEVGRITTEEGTEVHVEELHVERVNO<br>MPVEVQTELEADLDHVTPEIMNQBERESSQADAAEAAREDHED<br>AEDLETKPTVDSEAEKAENEDRTALPVL   |
| 6314       | 2  | 2071   | QRSGAARLAFPLSPFSPACVHRSPLSFHGCWFYFVVVFMPLGV<br>FRRRAHAGCTLSCSSFVEQPTAMEAETMECLQEFPEHHKMLD<br>RLNEQREODRFTDITLIVDGHFKAHKAVALAACSKFFYKFFQEF<br>TQEPVLEIEGVSKMAFRHLIEFTYAKLMIQGEEDNDVWKAEE<br>FLQMLEAIKALEVRNKNENSALEENTTGKNEAKKRKIAETSNVI<br>TESLPSAESEPVIEVEIAEGTIEVEDEGIEETLEEVASAKOSVK<br>YIQSTGSSDDALALLADITSKYRQGDGRGQIKEDGCPSPDTSK<br>QVEGIEIIVELQLSHVKDLFCEKCNRSFKLFYHFKHEMKSHSTE<br>SFKCEICNKRYLRESAWKQHLNLCYHLEEGGVSKKQRTGKKIHVC<br>QYCEKQFDHFGHFKEHLRKHTEGKPFECPCNCHERFARNSTLKCH<br>LTACQTVGVGAKKGRKKLYECQVCNSVFNWDQFKDHLVIHTGDK<br>PNHCTLCDLWFMQGNELRRHLSDAHNISRVLTEEVLSVETRVQ<br>TEPVTSMITIEQVGKVVHLPPLQVQVDSAQVTVEQVHPDLLQDS<br>QVHDSHMSLPEQVQVSYLEVGRITTEEGTEVHVEELHVERVNO<br>MPVEVQTELEADLDHVTPEIMNQBERESSQADAAEAAREDHED<br>AEDLETKPTVDSEAEKAENEDRTALPVL |
| 6315       | 1  | 1015   | IGLAVNVVTTLVLSYCPATETEEAPYWTYLLCALGLFIYQSLDA<br>IDGQARRTNSCSPGLGELFDHGCDLSLTVFMVAGASIAARLGT<br>PDWFFSCSFIGMFVYCAHWQTVVSGMLRFGKVDVTEIQIALVI<br>VFVLSAFGGATMWDYTIPILEIKLILPVLGFLGGVIFSCSNYF<br>HVILHGGVGKNGSTIAGTSLVSPGLHIGLIIILAIMIYKKSATD<br>VFEEKHPCLYILMFGCVFAKVSQKLVAHMTKSELYLQDVTFLGP<br>GLLFLDQYFNNFIDEXVVLWMMAMVSSFDMMVIYFSALCLQISR<br>HLNIFKTACHQAPEQVQVLSKSHQNNMD   |
| 6316       | 1503   | 792  | VSAGAGTGIMGGTTSTRRTFEADENENITVVKGIRLSENVDR<br>MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALQAKKES<br>EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEBERAKAKHL<br>ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTEQYQKAA<br>EEVEAKFKRYESHPCADLQAKILQCYRENTHTLTKCSALATQY<br>MHCNVHAKQSMLEKGG  |
| 6317       | 102  | 839  | PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSDDQN<br>FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK<br>TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGANGFILMYDITN<br>EESFNVAQDWSQIKTYSWDNAQVILVGNKCDMEDERVISTERG<br>QHLGEQLGFEFFETSADKNINVKQTFERLVDIICDKMSSELETD<br>PAITAQKQNTLKETPPPPQPNAC  |
| 6318       | 1765   | 733  | PWHPLRTLPLHHPHPRPPHAEAGREGADSMHLPGLRLRREAPPL<br>LGPLLSPPPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI<br>LAPVRRDRVLAELPQCLRKEALHGHKDFHPRVTCACQEHRTGT<br>VGFKISKVIVGDLVSGKTCILNRFCKDTFDKNYKATIGVDFEM<br>ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIVFNLN<br>DVASLEHTKQWLADALKENDPSSVLLFLVSGSKDLSTPAQYALM<br>EKDALQVAQEMKAEYWAWSSTLGENVREFFRVAALTFEANVLA<br>ELEKSGARRIGDVVRINSDSNLYLTASKKKPTCCP   |
| 6319       | 88   | 717  | AATMRLNQNTLLGKKVVLVPYTSSEHVPSRYHEWMKSEELQRLT<br>ASEPLTLEQYAMQCSNQEDADKCTFIVLDAEKWQAQPGATEES<br>CMVGDVNLPLTDLEDLTGIEIVMIAEPSRCRKGGLGTEAVLAML<br>SYGVTTLGLTKFEAKIGQGNBPSIRMFQKLHFEQVATSSVFQEV   |

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|------------|--|--|--|
| 6320       | 90   | 1111   | TLRLTVSESEHQWLLLEQTSHVEEKPYRDGSAEPC<br>RPRGTGREKVMAAVDSFYLLYREIARSCNCEALALVGAWYTA<br>RKSITVICDPYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG<br>IGKAYAEELASRGLNIIILSRNEEKLVAKDIADTYKVETDII<br>VADFSSGREIYLPPIREALKDKDVGLVNNVGVFPYQYFTQLS<br>BDKLWDIINVNIAAASLMVHVLPGMVERKKGAIVTISGSCCK<br>PTPQLAASFASKAYLDHFSRALQYAYASKGIFVQSLIPFYVATS<br>MTAPSNFLHRCWSLVPSPKVYAHAVSTLGISKRTTGYWSHSIQ<br>FLFAQYMPPEWLWVVGANILNRSRLRKEALSCTA   |
| 6321       | 1418   | 341  | HRKAALGALMAGRLGKALAASVLSLALASVTIRSSRCRGIQAF<br>RNSFSSSWFHLNTNVMGSGNGSKENSHNKARTSPYPGSKVERSQ<br>VPNEKVGWLVWQDYKPEYTAVSVLGPRWADPQISESNFSPK<br>FNEKDGHVVERKSKNGLYEIEGRPRNPAGRTGLVGRGLLGRWGP<br>NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA<br>IPGGMVDPGEKISATLKREFGEBALNSLOKTSAEKREIEEKLHK<br>LFSQDHLVYKGVVDDPRNTDANWMETEAVNYHDETGEIMDNLM<br>LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSSEDS<br>EADCHAL  |
| 6322       | 2047   | 1083   | NQELKNVESSRTVQPHFLEPLSLGWSVDVGRHPGWTGHVSTS<br>WSINCCDDGEGSQEEVISEDIGASIFNGQKKVLYADALTEI<br>AFVVPSPVESLTDLSLESNISDQSDSDNMDLMPGILKQPSLTLEL<br>FPNHTDNLNSSQRLSPSSRMKLPQGRPVPLGPETRVSVVWVE<br>RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF<br>IHPLNTGLFRIKIQGATGKFMVPLVDGMIVSRRALGFLVRQT<br>VINICRRKRLSDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT<br>SLFQEVGLKNCS  |
| 6323       | 1  | 656  | PASTTDGAQEAVPLDGAFWIPRPAGSPKGCFAVSKPPALQA<br>PAAPAPEPSASPMAPTLFPMESKSSKTDVRAAGAPPACKHLA<br>EKKTMTNPTTVIEVYPTTEVNDYLLWSIFNFVYLNFCCLGFIA<br>LAYSLLKVRDKLLNDLNGAVEDAKTDRLINITRSLGAASCIMLW<br>MALSVIATHRGLRSSASILVAEPHDWINTERPQVTFREPCAL   |
| 6324       | 1  | 2061   | EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGRRRQPGQO<br>RPGPGAGAPAGRPEGGPWARTGSSSLHSEPERAGLGAPAGTES<br>PQAEFWTDGQTEPAAAGLVETERPKQKTEPDRSSLRTHLEWSW<br>SELGTTCLWTETGTDGLWTDPHRSDLQFQPEEASPTWQPGVHG<br>WTELETHGSQTQPERVKSADNLWTHQNSSSLQTHPEGACPSKE<br>PSADGSWKELYTDGSRTOQDIEGPWTEPYTDGSQKKQDTEAARK<br>QPGTGGFQIQDTDGSWTQPTDGSQTAPGTDCLLGEPEDGPLE<br>EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPAQPVGPPS<br>RVEGGSGGFSSASSFDESDVAGGGGASDPEDRSGSKPWKKL<br>KTVLKYSFPVVSFRKHYFWVQLSGHAGNFQAGEDGRILKRFQC<br>EQRSLEQLMKDPLRPFPVAYYGMVLQDQGTFNQMEDLLADFE<br>SIMDCKMGSRTYLEEELVKARERPRPRKDMYKMWAVDPGAPT<br>EEHAQGAUTKPRYMOWRETMSSSTSLGFRIEIGIKKADGTCNINF<br>KKTQALEQVTKVLEDFVDGDHVLQKYVACLEELREALEISPF<br>KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP<br>WAEGNREDGYLWGLDNMICLLQGLAQS |
| 6325       | 165  | 944  | GLRDPFRKRRLKPKQVKMSNYVNDMWFGSPQEKDPSSTSRSGGS<br>SRLSSRSRSRSFSSRSRSHSVSSRFSSRSRKSRSRSRRRHQ<br>RKYRRYSRSYSRSRSRSRRYRERYGFTRRYRSRSRYRSRS<br>RSRSRSRGRSYCGRAYAIARGQRYGFGRTVYPEHSRWRDRSR<br>TRRSRTPFRLESEKDRMELLEIAKTAALKALGTTNIDLPA<br>SLRTVPSAKETSRGIGVSSNGAKPEVSIILGLEQNFOKANCQI   |
| 6326       | 238  | 680  | GEPSPATQQKPSATGAGVLHQHFSGGHIYVLMGLLPPFWTISFT<br>VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAKRTQTL<br>GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPVSLTA   |

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|------------|--|--|--|
|            |  |  | QAWGGVGQEAASSGVP   |
| 6327       | 1  | 1337   | SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLGSLCALFSDA<br>DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQKKRKEEK<br>GAEPETGSVAASAAQCGPTRELPESGIQLGTPREKVPAGRSKAE<br>LRAERRAKQEAERALKQARKGEQGGPPPKASPTAGETPSGVKR<br>LPEYPQVDDLLRLRVKKPERQVPTRKDYGSKVSLFSLHPQYS<br>RQNSLTQFMSSVHPAMVRLGLQYSQGLVRGNSNARCIALLR<br>ALQOVIQDYTTTPNEELSRDLVNKLKPYMSFLTQCRPLSASMHV<br>AIKFLNKEITSVGSSEKREEEAKSELRAAIDRYVQEKIVLAAQAI<br>SRFAYQKISNGDVLVYGCSLSVSRILQEANTEGRRFRVVVDS<br>RPWLEGRHTLRSLVHAGVPASYLLIPAASVVLPEVSTEEKDSKV<br>GGEKV  |
| 6328       | 1030   | 276  | HASAEVTTAAARGLOAMEEEMHTDAKIRAENGTSPPRGPGCSL<br>RHFACQNLSSRPDGSASFLOQDTSVLAVGYGPAEVKVSKEIFN<br>KATLEVLIRPKIGLPGVAEKSRERLRNCEAVVLGTLHPRTSI<br>TVVLQVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD<br>SDGTLVLDPTSKQEKARAVLTFALDSVERKLLMSSTKGLYSST<br>ELQOCLAAQAASQHVFRFYRESLQRRYSKS   |
| 6329       | 3  | 2016   | SSEVAAGGGTRSAEAGSGEVTVSATGAANGLNNGAGGTSATT<br>SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSRLTRNL<br>RGDIERKSLAINEEFVSIFKEVKEELESIEDVQAMSNCCQDMT<br>SRLQAAKEQTODLIVKTKLQSESQKLEIRAQVADAFLSKFQLT<br>SDEMILLRGTRREGPITEDFFKALGRVKQIHNDVKVLLRTNQTA<br>GLEIMEQMALLQETAYERLYRWAQSECRILTQESCDVSPVLTOA<br>MEALQDRPVLYKYTLDEFGTARRSTVVRGFI DALTRGGPGGT<br>PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGE<br>ENIQEVVGHITGVCRPLKVRIEQVIVAEFPAVLLYKISNLLKF<br>YHHTISGIVGNSATALLTTIEMHLLSKKIFFNLSLSLHASKLMD<br>KVELPPDLGPSSALNQTLMLLREVLASHDSSVPLDARQADVF<br>QVLSCLVDPLLMCTVSASNLGTADMATFMVNSLYMMKTTLALF<br>EFTDRRLEMLQFQIEAHLDTLINEQASYVLTTRVGLSYIYNTVQQ<br>HKPEQGS LANMPNLDVTLKAAMVQFDRLSAPDNLLIPQLNFI<br>LSATVKEQIVKQSTELVCRAYPEVAAVMNPINEYKDPENILHR<br>SPQQVQTLLS |
| 6330       | 1151   | 333  | FFYYTFYBNKTSFRKMVAEKETLSLNKCPDKMPKRTKLLAQOPL<br>PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR<br>KPYERGDFFIALEHDSKGNKIAWKVEIEKLDYHHYLPFFDGLC<br>EMTFPYEFFARQGIHDMLEHGGNKILPVLPLQIIPINAKNALNRN<br>RQVICVTLKVLQHLVVSAMVGKALVPYRQILPVLNIFKNMNV<br>NSGDGIDYSQQKRENIQDLIQETLEAFERYGGENAFINIKYVVP<br>TYESCLLN   |
| 6331       | 3  | 495  | QGGQVRTRGRRACASATPLEGCVDSLSPRTHAALLKVAQMVTL<br>LIAFICVRSSLWNYSAYSYSFEVVTICDLIMILAFYLVHLFRFY<br>RVLTCSISWPLSELLHYLIGTLLLIASIVAASKSYNQSGLVAGA<br>IKGFMATFLCMASIWLSYKISCVTQSTDAAV   |
| 6332       | 1  | 878  | VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI<br>NLLDYLPEILDGLFQILGDNCKEIRKMCVVLGEFLKEIKKNPS<br>SVKPAEMANILVIHCQTDDLIQLTAMCWMREFIQLAGRVMPLPY<br>SSGILTAVLPCLAYDDRKKSIIKEVANVCNQSLMKLVTPEDDEL<br>BLRPGQROAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREDP<br>VIGVALGPHLSNQDYFMYVTHTIVAATORSGSSGSPFFCRQDTG<br>KLSTMATHSQLVKTGTGLEPRQAVSSSH  |
| 6333       | 3  | 1467   | TRTPSEAEAGGESQSCVSAHSDWTAGKPVSLAPLIPFRSAG<br>QPLTFSPGGRQPLRSLLVGMCSGSGRRSSLSPTMRPGTGAERG<br>GLMMGHGPMHYAPMGMPGMRANMPVPHGMMPPQMPMPGPP<br>MGQMPGMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS  |

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|------------|--|--|---|
|            |  |  | GAKSMWTEHKSPDGRYYYNTETKQSTWEEKPDDLKTPAEQLLSK<br>CPWKYKSDSGKPYYYNSQTKESRWAKPKELEDLEGYQNTIVAG<br>SLITKSNLHAMIKAEESKQEECTTTSTAPVPTTEIPTTMTMA<br>AAEAAAAVVAAAAAANANASTSANTVSGTVPVVPP<br>EVTISIVATVVDNENTVTISTEEQAQLTSTPAIQDQSVESVNTG<br>EBTSKQETVADFTPKKEEESQPAKTTYTWTKEEAKQAFKELL<br>KEKRVPSNASWEQAMKMI INDPYSALAKLSEKKQAPNAYKVQT<br>EKK   |
| 6334       | 17   | 644  | GGNPSGRAAGFAAAAMPSSPLRVAVVCSSNQNRSM EAHN1LSKR<br>GFSVRSFGTGHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDK<br>ELYTQNGILHMLDRNKRIKPRPERFQNCCKDLFDLILTCEERVYD<br>QVEDLNSREQETCQPVHVNVVDIQDNHEBATLGAF LICELCQC<br>IQHTEDMENEIDELLQEFEEKSGRTFLHTVCFY  |
| 6335       | 82   | 529  | AARARPGVLCCLLGAALGDQSRVEMSYIPGQPVTA VVQVREIH<br>KLROGENLILGFSIGGGIDQDPSQNPFFSEDKTKDGIYVTRVSEG<br>GPAEIAGLQIGDKIMQVNGMDMTMVTHDQARKRLTKRSEEVRL<br>LVTRQSLQAVQQSMLS  |
| 6336       | 1003   | 438  | HEPASKGRAEVGNMRLSVA AAI SHGRVFRMRGLGPESRIHLRN<br>LLTGLVRHERIEAPWARVDEMRGYAEKLIDYKLGDTNERAMRM<br>ADFWLTEKDLIPKLQVLA PRYKDQTTGGYTRMLQIPNRLDRAK<br>MAVIEYKGNCLPPLPLPRRDSHLTLNQLLQGLRQDLRQSQEAS<br>NHSSHTAQTPGI   |
| 6337       | 76   | 524  | EGIQMLSVQPDTPKPGCAGCNRIKDRYLLKALDKYWHEDCLKC<br>ACCCRLGEVGS TLYTKANLILCRRDYLRLEFGVTGNCACSKLI<br>PAFEMVMRAKDNVYHLDCFACQLCNQRCVCGDKFPLKNNMILCQ<br>TDYBEGLMKEGYAPQVR  |
| 6338       | 66   | 1349   | APNSESQTGGPLPTPANLFWTRRANPDPTTSM SATDRMGPKAVP<br>GLRLALLLLGLGTPKSGVQGGEGLDFFEYDGVDRVINVNAKNY<br>KNVFKKYEVLLALLYHEPPEDDKASQRFEMEELILELAAQVLED<br>KGVGFGLVDSEKDA AVAKKLGLTEVDSMYVFKGDEVIEYDGEFS<br>ADTIVEFLLDVLEDPELIEGERELQAFENIEDEIKLIGYFKSK<br>DSEHYKAFEDAAEEFHPYIPFFATFDSKGAKKLT LKNEIDFYE<br>AFMEEPVTIPDKPNSEEEIVNFVEHRRSTLRKLKPESMYETWE<br>DDMDGIHIVAFEEADPDGFLETLKAVAQDNTENPDL SIWI<br>DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE<br>DLPSAEELEDWLEDVLEGEINTEDDDDDDDD   |
| 6339       | 246  | 1813   | NRCDRGGGGQAERQAGQGCRTQAGPGFGHSPFSQGAMKAPH<br>TFCVVLLVFGSVSEAKFDDFEDEEIV EYDNDFAEFEDVMEDE<br>VTESQPRVIITEDDEDET TVELEGQDENQEGDFEDADTQEGDTE<br>SEPYDDEEFEGYEDKPTDTSSSKNKDPTITVDVPAHLQNSWESYY<br>LEILMVTGLLAYIMNYITGKNKNSRLAQAWFNTHRELLESNFTL<br>VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQRLFL<br>KRQDLLNVLARMMPVSDQVQIKVIMNDEDMDTYVFAVGTRKAL<br>VRLQKEMQDLSEPCSDPKPSGAKYGLPDSLAILSEMGEVTDGMM<br>DTKMVHFLTHYADKIESVHFSDDQFSGPKIMQEEGQPLKLPDTPKR<br>TLLLTFNVPQSGNTY PKDMEALLPLMNMVIYSIDKAKKFRNLRE<br>GKQKADKNRARBENFLKLT HVQREQAAQSRREEKKRAEKERIM<br>NEEDPEKQRRLEBAALRREQKLEKKQMKMKQIKVKAM |
| 6340       | 2  | 583  | BACHTLSCPAFARLGRARRRPWMSHRTSTSFRAERSFHSSSSS<br>SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF<br>PARPGGAGNIKTLDGAYEFAVDVDFSPEDII VTTSNNHIEVRA<br>EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR<br>HPHTEHVQQTFRTEIKI  |
| 6341       | 2  | 645  | KMAVLSAPGLRGFRILGLRSSVGPVAVQARGVHQSVATDGPSSSTQ<br>PALPKARAVAPKPSRGEYVVAKLDDLNVNARRSSLWPMTFGLA<br>CCAEMMHMAAPRYDMDFRGVVFRA SPQSDVMIVAGTLTNKMA  |



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|------------|--|--|--|
|            |  |  | PALRKVVYDQMPEPRYVSMGSCANGGGYHYHSYSVVRGCDRIVP<br>VDIYIPGCPPTAEALLYGILQLQORKIKRERRLOIWIYRR   |
| 6342       | 2  | 1191   | DPRVRAMLATLARVAALRKTCLFSGRGGGRLWTGRPQSDMNNI<br>KPLEGVKILDLTRVLGPPFATMNLGDLGAEVIKVERPGAGDDTR<br>TWGPPFVGTESTYYSVNRNKSIAVNIKDPKGVKIIKELAAVC<br>DVFVENYVPGKLSAMGLGYEDIDEIAPHIYCSITGYGQTGPIS<br>QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG<br>TAHGSIVPYQAFKTKDGYIVVGAGNNQPFATVCKILDPELIDN<br>SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG<br>PINNMKNVFAEPQVLHNGLVMEHEPTVGKISVPGPAVRYSKFK<br>MSEARPPPLQGHTTHILKEVLRVDDRAIGELLSAGVVDQHEH   |
| 6343       | 2  | 936  | GTAMVSEDELENLIVVDANPIWGWKQALKESQFTLSKCIDAV<br>MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDPFGDP<br>GNPPEFNPSGSKDGYELLTSANEVIVEIKDLMTKSDIKGQHT<br>ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALO<br>YMFNMNVI PAAQKQNILIDACVLDSDSLQACDITGGLYLKV<br>POMPSLLQYLLWVFLPDODQRSOLILPPVHVVDYRAACFCHRL<br>IBIGYVCSVCLSI PCNFSPICCTTCETAFKISLPPVLKAKKKLKVSA  |
| 6344       | 2508   | 147  | TMPTATLGNLRGYGMASPLAAPS LTPPQLATPNLQOFPQATR<br>QSLGLGPPFVGVPMPNPSQFNLSGRNPQKQARTSSSTPNRNDSSS<br>QTMPVEDKSDPPEGSEAEAEPRMDTPEDQDLPPCPEDIAKEKRT<br>PAPEPEPCEASELPKRLRSSEEPTKEPPGQLQVKAQPOARMT<br>VPKQTQTPDLIPEALEAQVLPFRFQPRVLQVQAQVQSOTQPRI PS<br>TDTQVQPKLOQAQTQTSPEHLVLQKQVQVQLQQAEPQKQVQ<br>PQVQPOAHSQGPQVQLQQAEPPLKQVQVQVQVQVQVQVQVQVQ<br>LQLQKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ<br>PHTQVQ<br>VGTQVSMEEIQNESACGLDVGEENRAREMPGVWAGGSLKVTI<br>LQSSDSRAFTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY<br>ICKASCSSQGEFQDHMSEPHQQRLEI QHMSQACLLSLLPVPR<br>DVLETEDEEPPRRNCNTCLQYIMGDLIQHRTQDQDKIAKQSLR<br>PFCTVCNRYFKTPRKFEVHVKSQGHKDKAKELKSLEKEIAGQDE<br>DHFITVDVAGCFEGDEEEEDDEDEEIEVEERLCKQVRSRDIS<br>REWKGSSETYSPNTAYGVDFLVPVMGYICRICHKFYHNSGAQL<br>SHCKSLGHFENLQYKAAKNPSPTTRPVSRRCAINARNALTALF<br>TSSGRPPSQPNTQDKTTPSKVTARPSQPPLPRRSTRLKT   |
| 6345       | 2  | 3483   | PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEEMEIEQLQEKV<br>HELEKQNDTLKNRLISAKQQLQTOGYRQTPYNNVQSRINTGRRK<br>ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE<br>IRNLENVISQSQRGQIELEHLAEILKTQLRRKENEIELSLLQLR<br>EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK<br>QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER<br>RIEELQDRINDLEKERELLKENYDKLYDSAFSAHEEQWKLKEQ<br>QLKVQIAQLETAALKSDLTDKTEILDRLKTERDQNEKLVQENREL<br>QLQYLEQKQQLDELKKRIKLYNQENDINADELSEALLIKAQKE<br>QKNGDLSFLVKVDSEINKDLBSMRRELQATHAETVQELEKTRNM<br>LIMQHKINKDYQMEVEAVTRKMENLOODYELKVEQYVHLLDIRA<br>ARIHLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIIHLERG<br>ENLFEIHKVTFSSVLQASGDKEPVTFTYAFYDFELQITTPV<br>VRGLHPEYNFTSQYLHVNDLFLOYIQKNTITLEVHQAYSTEYE<br>TIAACQLKFHEILEKSGRIFCTASLIGTKGDI PNFGTVVEYWFRL<br>RVZMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQAPKTAQL<br>SSTDSTDGNLNLHITIRCCNLHLSRASHLQPHYPVYVYKFFDFA<br>DHDTAIIPSSNDPFDHMYFPVPMNMDLDRLKSESLSFYVDF<br>DSDTQENIYIGKVNPLISLAHDCISGIFELTDHQKHPAGTIH |

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|------------|--|--|---|
|            |  |  | VILKNKPAYLPFGSITTEDLGNFIRSEEPVQRLPPASSVST<br>LVLAPRPKPRQRLTPVDKKVSPVDIMPHQSDVSQEGSVDEVKEN<br>TEKMQQKDDVSLSEGQLAEQSLASSEDETEITEDLEPEVEED<br>MSASDDDCIIPGPISKNIKQPSKIRIETIALLSNDQSQTMD<br>TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYNNYNNVIYVDK<br>ENNAKARDILKAILQKQEMPNSRLRFTVVSDDPEDEQDLECEDI<br>GVAHVDLADMFQEGRDLEIQNDIVFDARADGEGIGKLRVTVEAL<br>HALQSVYKQYRDDLEA  |
| 6346       | 2921   | 533  | QDRRLRLLELQKTCQPTSTMSGSHTPACGPFSAITPSIWPQETL<br>AKYTQKEESAEPQEFYDFGFRVYKEEGDEPGSSLLANSPLME<br>DAPQRLRWQAHLFTTHNDVGLTWDKIAVSLPRSEKLSLVLA<br>GIPHGMRPQLWMRLSGALQKRNSELSYREIVKNSNDETIAAK<br>QIEKDLLRTMPSNACFASMGSIGVPRRLRRVLRALAWLYPEIGYC<br>QGTGMVAACLLLFLEEDAFWMSAI IEDLLPASYSFTLLGVQ<br>TDQVLRHLIVQYLPRLDKLQEHDIELSITLHWFLTAFAVSV<br>DIKLLRIWDLFFYEGSRVLFQTLGMLHLKEEELIQSENSASI<br>FNTLSDI PSQMEDAELLGVAMRLAGSLTDVAVETQRRKHLAYL<br>IADQGQLLGAGTLTNLSQVVRRTQRRKSTITALLFGEDDLEAL<br>KAKNIKQTELVDLREAILRVARHFQCTDPKNCSSVSRQLPGLL<br>PNTALTPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH<br>RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL<br>RGWFFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK<br>ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL<br>CKTFRLEDGKVLTPPELLYRAVQSVNVTHDAVHAQMDVKLRSL<br>ICVGLNEQVLHLWLEVLCSLPTVEKWKYQWPSFLRSPGWVQIKC<br>ELRVLCFFAFSLSQDWELPAKREAQQLKEGVDRMLVKHHLFSW<br>DVDG |
| 6347       | 2921   | 533  | QDRRLRLLELQKTCQPTSTMSGSHTPACGPFSAITPSIWPQETL<br>AKYTQKEESAEPQEFYDFGFRVYKEEGDEPGSSLLANSPLME<br>DAPQRLRWQAHLFTTHNDVGLTWDKIAVSLPRSEKLSLVLA<br>GIPHGMRPQLWMRLSGALQKRNSELSYREIVKNSNDETIAAK<br>QIEKDLLRTMPSNACFASMGSIGVPRRLRRVLRALAWLYPEIGYC<br>QGTGMVAACLLLFLEEDAFWMSAI IEDLLPASYSFTLLGVQ<br>TDQVLRHLIVQYLPRLDKLQEHDIELSITLHWFLTAFAVSV<br>DIKLLRIWDLFFYEGSRVLFQTLGMLHLKEEELIQSENSASI<br>FNTLSDI PSQMEDAELLGVAMRLAGSLTDVAVETQRRKHLAYL<br>IADQGQLLGAGTLTNLSQVVRRTQRRKSTITALLFGEDDLEAL<br>KAKNIKQTELVDLREAILRVARHFQCTDPKNCSSVSRQLPGLL<br>PNTALTPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH<br>RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL<br>RGWFFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK<br>ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL<br>CKTFRLEDGKVLTPPELLYRAVQSVNVTHDAVHAQMDVKLRSL<br>ICVGLNEQVLHLWLEVLCSLPTVEKWKYQWPSFLRSPGWVQIKC<br>ELRVLCFFAFSLSQDWELPAKREAQQLKEGVDRMLVKHHLFSW<br>DVDG |
| 6348       | 3  | 3679   | AGAECFVTLTACFLAKQNKYKYECKDLIKSMLRNELQFKEE<br>KLAELQKQAEELRQYKVLVHSQERELTQREKLREGRDASRSLN<br>EHLQALLTPDEPKSQGDLQEQLAEGCRLAQHLVQKLSPENDN<br>DDDEDVQVEVAEKVQKSSSPREMQKAEKEVPEDSLECAITCS<br>NSHGFCDSNQPHKNIKITFEDEVNSTLVVDRESSHDECQDALN<br>ILPVPPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA<br>EKKQQRNLKEKCFLTQACFLANQNKYKYECKDLIKFMLRN<br>ERQFKEBKLAELQKQAEELRQYKVLVHSQERELTQREKLREGR<br>DASRSLNEHLQALLTPDEPKSQGDLQEQLAEGCRLAQHLVQK<br>LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEKEVPEDSLE  |

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|------------|--|--|--|
|            |  |  | ECAITCSNSHGPYDSNQPHRKTITFEEDKVDSTLIGSSSHVEW<br>EDAVHIIPENESDDEEEEEKGPVSPRNLQSEEEVPEQSWDEG<br>YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVDIGRHRWDQVK<br>KEDHEATGPRLSRELLDEKGPVQLQDSLDRCYSTPSGCLELTDS<br>CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR<br>ELLDEKEPEVLQDSLGRCYSTPSGYLELPLDGPYSSAVYSLEB<br>QYLGLALDVDRIKKDQEEBEDQPPCPRLSRELLVEVEPEVLQD<br>SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE<br>KKGKGGKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG<br>PEVLQDSLDRCYSTPSGCLELTDSQCPYRSAFYILEQQRVGLAV<br>DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCY<br>TSGCLELTDSQCPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE<br>DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPLDGP<br>PYSSAVYSLEEQLGLALDVDRIKKDQEEBEDQPPCPRLSRELL<br>LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH<br>VGFSLDVGEIEKKGKGGKRRGRRSKKERRRGRKEGEEDQNPPCP<br>RLNSMLMEVEEPEVLQDSLDRCYSTPSMYFELPDSFQHYRSVVFY<br>SFEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ  |
| 6349       | 3  | 3679   | AGAEKCFVTLACFLAKQONKYKYECKDLIKSMLRNELOPKKEE<br>KLAELQKQAEELRQYKVLVHSQERELTQREKLREGRDASRLN<br>EHLQALLTPDEPKSQGDLQEQLAEGCRLAQHLVQKLSPENDN<br>DDDDEDVQVEVAEKVQKSSSPREMKAEEKEVPEDSLECAITCS<br>NSHGPCDSNQPHKNIKITFEDEVNSTLVVDRESSHDECQDALN<br>ILPVPGPTSSATNVSMVVSAGPLSGEKAANILEINEKLRLPQLA<br>EKKQQFRNLKEKCFLTQLACFLANQONKYKYECKDLIKFMLRN<br>ERQFKKEKLAELQKQAEELRQYKVLVHSQERELTQREKLREGR<br>DASRLNEHLQALLTPDEPKSQGDLQEQLAEGCRLAQHLVQK<br>LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAAEEKEVPEDSLE<br>ECAITCSNSHGPYDSNQPHRKTITFEEDKVDSTLIGSSSHVEW<br>EDAVHIIPENESDDEEEEEKGPVSPRNLQSEEEVPEQSWDEG<br>YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVDIGRHRWDQVK<br>KEDHEATGPRLSRELLDEKGPVQLQDSLDRCYSTPSGCLELTDS<br>CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR<br>ELLDEKEPEVLQDSLGRCYSTPSGYLELPLDGPYSSAVYSLEB<br>QYLGLALDVDRIKKDQEEBEDQPPCPRLSRELLVEVEPEVLQD<br>SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE<br>KKGKGGKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG<br>PEVLQDSLDRCYSTPSGCLELTDSQCPYRSAFYILEQQRVGLAV<br>DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCY<br>TSGCLELTDSQCPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE<br>DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPLDGP<br>PYSSAVYSLEEQLGLALDVDRIKKDQEEBEDQPPCPRLSRELL<br>LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH<br>VGFSLDVGEIEKKGKGGKRRGRRSKKERRRGRKEGEEDQNPPCP<br>RLNSMLMEVEEPEVLQDSLDRCYSTPSMYFELPDSFQHYRSVVFY<br>SFEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ |
| 6350       | 3  | 3679   | AGAEKCFVTLACFLAKQONKYKYECKDLIKSMLRNELOPKKEE<br>KLAELQKQAEELRQYKVLVHSQERELTQREKLREGRDASRLN<br>EHLQALLTPDEPKSQGDLQEQLAEGCRLAQHLVQKLSPENDN<br>DDDDEDVQVEVAEKVQKSSSPREMKAEEKEVPEDSLECAITCS<br>NSHGPCDSNQPHKNIKITFEDEVNSTLVVDRESSHDECQDALN<br>ILPVPGPTSSATNVSMVVSAGPLSGEKAANILEINEKLRLPQLA<br>EKKQQFRNLKEKCFLTQLACFLANQONKYKYECKDLIKFMLRN<br>ERQFKKEKLAELQKQAEELRQYKVLVHSQERELTQREKLREGR<br>DASRLNEHLQALLTPDEPKSQGDLQEQLAEGCRLAQHLVQK<br>LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAAEEKEVPEDSLE  |

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|------------|--|--|---|
|            |  |  | <p>ECATCSNSHGYPYDSNQPHRKTITFEEDKVDSTLIGSSSHVEW<br/>           EDVAVHIIPENESDDEEEEEKGPVSPRNLQSEEEBEVPQESWDEG<br/>           YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVADIGRHRWDQVK<br/>           KEDHEATGPRLSRELLDEKGPVQLQDSLDRCYSTPSGCLELTD<br/>           CQPYRSAPYVLEQQRVGLAVNMDEIEKYQEVEEDQPPSCPRLSR<br/>           ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE<br/>           QYLGLALDVDRIKKQDEEEEDQPPCPRLSRELLEVEVEPEVLQ<br/>           SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE<br/>           KKGKGGKRRGRRSKKERRRRKKEGEDQNPPCPRLSRELLDEK<br/>           PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAPYVLEQQRVGLAV<br/>           DMDEIEKYQEVEEDQPPSCPRLSGELLDEKEPEVLQESLDRCY<br/>           TSGCLELTDSCQPYRSAPYVLEQQRVGLAVDMDEIEKYQEVEE<br/>           DQPPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ<br/>           PYSSAVYSLEEQYLGLALDVDRIKKQDEEEEDQPPCPRLSREL<br/>           LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH<br/>           VGFSLDVGEIEKKGKGGKRRGRRSKKERRRRKKEGEDQNPPCP<br/>           RLNSMLMEVEPEVLQDSLDRCYSTPSMYFELPDSFQHYRSVVF<br/>           SFEETHISFALYVDNRRFTLTVTSLHLVFMGVIFPQ</p> |
| 6351       | 1291   | 319  | <p>REARRRTERSQLGRMLVVEVANGRLVWGAEAQALRERLGVGG<br/>           RTVGALPRGPRQNSRLGLPLLMPEARLLAIGAVTLVSAPRP<br/>           DSRHHSALATSPFRQEEESFQEQSALAAARETRRQELLEKITE<br/>           GQAACKQKLEQASGASSSQEAGSSQAAKEDTSDGQASGEQEA<br/>           GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS<br/>           KDWPAGRAPAHELRYSIYRDLWERGFLLSAGKFGDFLVYPGD<br/>           PLRFHAHYIAQCWAPEDTIPLODLVAAGRLGTSVRKTLTLLCSPQ<br/>           PDGKVVTSLQWASLQ</p>   |
| 6352       | 235  | 923  | <p>WSEWLSPCAACKCKGLSMLRITMKTRAISSLAADATEFVQGRSAP<br/>           AMARSLVHDTVYCLSVYQVKISPTPQLGAASSAEGHVGGGAPG<br/>           LMGMNMPGGVNHENGMNRDGGMIPEGGGNQEPQOQPQPPPEE<br/>           PAQAAMEGFPQENMQPRTTRTKFTLLQVEELESVFRHTQYPDVP<br/>           TRRELAENLGVTEDEKVRVWFKNKRARCRRHQRELMLANELRADP<br/>           DDCVYIVVD</p>   |
| 6353       | 65   | 672  | <p>RFAGAGATPEARARPDVQAAEEEEKEMDLPDSASRVFCGRILSM<br/>           VNTDDVNAILAQNMLDRFEKTNEMLLNFNNLSSARLQOMSER<br/>           FLHHTRTLVEMKRDLDSIFRRIRTLKGLARQHPEAFSHIPEAS<br/>           FLEEDEDPIPPSTTTTIIATSEQSTGSCDTSPTTVSPSLSPGFE<br/>           DLSHVQGPSPAINGRSQTDDEEMTGE</p>  |
| 6354       | 965  | 510  | <p>PSLRPMEPTRDCPLFGGAFSAYLPMGATIDVSDLRPVDPNQEVFC<br/>           HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVQGARAVHVE<br/>           SVQPLSLLENLALRGRCQEAWVLSGKQQIAKENQQVAKDVTLLHQA<br/>           LLRLPQYQTDLLLTENQPP</p>   |
| 6355       | 158  | 1662   | <p>RGSSAARFGSGLRGAMIRRVLPHGMRGLLTRRPGTRRGGSILD<br/>           WDGKVSIEIKKIKSILPGRSCDLLQDTSHLPEHSDVVI VGGGV<br/>           LGLSVAYWLKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQ<br/>           QFSLPENIQLSLFSASFRLNINEYLAVVDAPPLDLRFNPSGYLL<br/>           LASEKDAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTGCV<br/>           ALASYGMEDEGWFDPCWLLQGLRRKVQSLGVLCQGEVTRFVSS<br/>           SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVCAIVINAAGA<br/>           WSAQIAALAGVGEPPGTQGTGLPVEPRKRYVYVWHCPQGPGL<br/>           ETPLVADTSGAYFRREGLSNYLGGRSPTEQEEPPANLEVDHD<br/>           FFQDKVWPHLALRVPAFETLKVQSAWAGYDYNTFDQNGVVGPH<br/>           PLVVNNMYFATGFGSGHGLQAPGIGRAVAEMVLKGRFQTDLSPP<br/>           LPTFRYLGEKIQENNI</p>   |
| 6356       | 354  | 633  | <p>TGLTSSCLPLQVMMTKRDKMGKFSSTVSTIDEEEIEAREV<br/>           ADSYQNAKVIEKQLERKGMKRRRLQELAELEAKKARKMGTLLID<br/>           NQFK</p>   |

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|------------|--|--|---|
| 6357       | 2  | 915  | GLLRNMALLVRVLRNQTSSISQWVPVCSRLIPVSPTQGGDRALS<br>RTSQWPQMSQSQACGGSEQIPGIDIQLNRYHTTRKLTSTTKDSP<br>QPVEEKVGAF TKIIEAMGFTGPLKYSKWKIKIAALRMYTSCVEK<br>TDFEEFFLRQMPDTFNSWFLITLLHVWNCVLRMKQEGRSKGKYM<br>CRIIVHFMWEDVQQRGRVMGVNPIYILKNNILMTNHFYAAILGY<br>DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL<br>DSMNGEDLLLTGVEVSWRPLVEKNPQSILKPHSPTYNDEGL  |
| 6358       | 2009   | 1040   | ASDALHSLAPVLRLLSSRSARPATMTEQASFAKDFLAGGIAA<br>AISKTA VAPIERVKLLQVQHASKQIAADKQYKGVDCIVRIPK<br>EOGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT<br>QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLADVGKSGTE<br>REFRGLGDCLVKITKSDGIRGLYQGFVSQVQIIYRAAYFGVY<br>DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRMM<br>MQSGRGKADIMYTGTVDCWRKIFRDEGGKAFKGAWSNVLRGMG<br>GAFVLVLYDELKTVI  |
| 6359       | 98   | 1086   | VCRQEEEMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCEYH<br>GKSFQLRHREEGTLIIIEGLLNIAWGLRRPIRLQMQDDREQVHL<br>PSTSWMPRRPSCPLKEPSQNGNITAQGPSIQPVHKAESSTDSS<br>GPLLEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIIRHRFS<br>INGHFYNHKTSVFTPAYGSVTVNRVNSTMTTLQVLTLLLNKFRV<br>EDGPSEFALYIVHESGERTKLKDCYPLISRIHLHGPFCEKIARIF<br>LMEADLGVEVPHEVAQYIKPEMPVLDSFVEKLKEEEREI I KLT<br>MKFQALRLTMLQRLEQLVEAK   |
| 6360       | 1  | 345  | GTRGAVPSTLEEVLFPFRSCRVFWIHSGTTMSKVSFKITLTSDF<br>RLPYKVLVPESTPFTAVLKFAAEFEKVPAAITNDGIGIN<br>PAQTAGNVFLKHGSELRIIPRDRVGC   |
| 6361       | 615  | 158  | RPGLGQLQHCALAPQAGNRRCRPHGRHLALTRSTRHGKPMISMQ<br>FKDTLNTPLPDSFPVAVPLGAPIAVASTLSVEHNDGVETGIWAC<br>APGRWRRQITSQEFCHFIQGRCTFTPDDGETLHIQAGDALMLFA<br>NSTGIWDIQETVRKTYVLIL  |
| 6362       | 350  | 1576   | TTMDGSHSAALKLQQLPPTSSSSAVSEASFYKENLIGALLAYF<br>GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWLGLFLMLLG<br>ELGVFASVAFAPLSLIVPLSAVSVIASAIIIGIIFIKEKWKPKDF<br>LRRYVLSFVGCGLAVVGTYYLLVTFAPNSHEKMTGENVTRHLVSW<br>PFLYMLVEIILFCLLLFYKEKNANNIIVILLVALLGSSMTVV<br>TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ<br>ASQMYDSSSLIASVGYLSTTIAITAGAI FYLDFIGEDVLHICMF<br>ALGCLIAFLGVFLITRNRKKPIPEFYISMAMPGMQNMHDKGM<br>TVQPELKASFSYGALENNNDNISEIYAPATLPVMOQEEHGSRSASG<br>VPYRVLEHTKKE |
| 6363       | 21   | 1201   | RRTRLGSSFFRRRDSSAMESYDVIANQPVVINDNGSGVIKAGFAG<br>DQIPKYCFPNYVGRPKHVRVMAGALEGDI FIGPKAEHRGLLSI<br>RYPMEHGI V KDWN DMERIWQYVYSKDQLQTFSEHVPVLLTEAPL<br>NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD<br>SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLKKEGY<br>DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS<br>TIEIGPSRFRAPPELLFRPDLIGEESGIEHVLVFAIQKSDMDLR<br>RTLFSNIVLSGGSTLFKGFCDRLLEVKKLAPKDVKIRISAPQE<br>RLYSTWIGGSILASLDTFKMMNVSKKEYEDGARSIRKTF                  |
| 6364       | 21   | 1201   | RRTRLGSSFFRRRDSSAMESYDVIANQPVVINDNGSGVIKAGFAG<br>DQIPKYCFPNYVGRPKHVRVMAGALEGDI FIGPKAEHRGLLSI<br>RYPMEHGI V KDWN DMERIWQYVYSKDQLQTFSEHVPVLLTEAPL<br>NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD<br>SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLKKEGY<br>DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS<br>TIEIGPSRFRAPPELLFRPDLIGEESGIEHVLVFAIQKSDMDLR  |

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|------------|--|--|--|
|            |  |  | RTLFSTNIVLSGGSTLFGKFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMVSKKEYEEDGARSIHRRKTF  |
| 6365       | 234  | 1989   | KHKSRAACAARAQAFGPSREREVHSRFRSGLRRLGESNSGCC TM ASMGTLAFDEYGRPFLLIKDQDRKSRLMGLKSHIMAAKAVA NTMRTSLGPNGLDKMMDVKGDDVTVTNDGATILSMMDVDHQIAK LMVELSKSQDDSIGDGTGTVVVLGALLLEAEQLLDGRIHPRI ADGYEQAAARVAIEHLDKISDSVLVDIKDTEPLIQAKTTLGSKV VNSCHROMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLEFD TKLIKGVIVDKDFSHQMPKPKVEDAKIAILTCPPFPKPKTKKHK LDVTSVEDYKALQKYRKEKFEEMIQQIKETGANLAICQWGFDD ANHLLQNNLPVVRWVGGEIELIAIATGGRIVPRFSELTAELK GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIEE AKRSLHDALCVIRNLIRDNRVVYGGGAEEISCALAVSQEADKCP TLEQYAMRAFADALEVIMPALENSGSMNPQTMTTEVRARQVKEM NPALGIDCLHKGNTDMKQHVIEITLIGKKQQLSLATQVMVRMLK IDDIRKPGSEEE |
| 6366       | 257  | 1898   | GNKEGAHSSTFWVLLSIFLGAVAMLCKEGGITVLGLNAVFDILV IGKPNVLEIVQVLHKDKSLENGLMLRNGGLFRMTLLTSGGAG MLYVRNRIMGTGPPAFTEVDNPASFADSMVRAVNYNYYSLNA WLLCPWWLCFDWSMGCIPLIKSISDRVIALAALNFCILGLIC QALCEDGHKRRILTLGLGLFVIFPLPASNLFFRVGVVAERVL YLPSVGYCVLLTFGOALS KHTKKKKLIAAVVLGILFINTLRCLV LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAI RYYREAVRLNPKYVHAMNNGNILKERNELQAEELLSLAVQIQ PDFAAAMNGLIVQNSLKRFEAAEQSYRTAKHRRKYPDCYYNL GRLYADLNRHVDALNAWRNATVLKPEHSLAWNMIILLDNTGNL AQAEAVGREALELIPNDHSLMFLANVLGKSQKYKESALFLKA IKANPNAASYHGNLAVLYHRNGHLDLAKKHYEISLQLDPTASGT KENYGLLRRLKLELMQKKA   |
| 6367       | 287  | 1934   | SIGFPVMLVLSILLYTCMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTKVQNIIEDEYKNPRNLSLMRE KLCESKESHHCGESFNQIADDMNRRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFIHSCIQHRVMHSGDGPYCKCF CGKAFYFLNLCLIHERIHTGVKPYCKQCGKAFTRSTTLPVHER THTGVDNADECKEKGNAFSPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHG EKPYECCRQCGKAFRCTSDLRHEKTHETEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKEKGKVFYFSSLRHERHTHTGEKPH ECKQCGKAFRYFSSLRHERHTHTGDKPYECKVCGKAFCTCSSIR YHERHTHTGEKPYECKHCGKAFISNYIRYHERHTHTGEKPYQCKQC GKAFIRASSCREHERHTHTINR                                  |
| 6368       | 1  | 327  | RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVBIEDFQYDE DSEYFYPCPGDNFSITKEDLNGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC   |
| 6369       | 1  | 1745   | AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSFPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTKVQNIIEDEYKNPRNLSLMREKLCESKESHHC ESPNQIADDMNRRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFIHSCIQHRVMHSGDGPYCKFCGKAFYFLNLCL IHERIHTGVKPYCKQCGKAFTRSTTLPVHERHTHTGVNADECKE CGNAFSPSEIRRHKRSHTGEKPYECKQCGKVIFSSIQYHKM THTGKPYECKQCGKAFRCGSHLQKHGRTHTGKPYECCRQCGKA FRCTSDLRHEKTHETEDKPYGCKQCGKGFRCA SQLQIHERTHSG EKPYECKEKGKVFYFSSLRHERHTHTGEKPYECKQCGKAFRYF  |

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|------------|--|--|--|
|            |  |  | SSLHIHERHTHTGDKPYECKVCGKAPTCSSSIRYHERHTHTGEKPY<br>ECKHCKGKAFISNYIRYHERHTHTGEKPYQCKQCGKAFIRASSCRE<br>HERHTHTINR   |
| 6370       | 1711   | 329  | FVLSEQLRLTERTWPRSPGLGRGAAAGARTAGAGLLRLLLGCG<br>ALVGGGLRPVMTTPANAQNASKTWELSLYELHRTPOEAIMDGT<br>IAVSPRSLHSELMCPICLDMKNTMTTKECLHRFCSDCIVTALR<br>SGNKECPTCRKKLVSKRSLRDPNFDALISKIYPSREYEAHQD<br>RVLIRLSRLHNQALSSSIEEGLRMQAMHRAQVRPRPIPGSDQT<br>TMSGGEGEPGEGEGEDGSDSDSAPDSAPGPAPKRPGRGGGAGG<br>SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS<br>PPEPGGIELVFRPHPLLVKEGEYCQTRYVKTGNATVDHLSKY<br>LALRIALERRQQQEAGEPGPGGGASDTGGPDGCGGEGGGAGGG<br>DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE<br>KFWKVSRLPLELCYAPTIDPK  |
| 6371       | 3  | 288  | GVANMSTAMNFGTKSFQPRPDKGSFPLDHLGECKSFREKEMKC<br>LHNNNFENALCRKESKEYLECRMERKMLQBLEKLGFGLTSG<br>KSEAAX   |
| 6372       | 2141   | 625  | RVSATASEGKAERYKKLEDLLEKSFSLVKMPSLQPVVMCMKH<br>LPKVPEKKLKLVMADKELYRACAVEVRRQIQWQNALFGDEVSP<br>LLKQYILEKESALFSTELSVLHNFSPSPKTRRQGEVVRQLTRM<br>VGKVKLYDMVLQFLRFLRTRNVHYCTLRAEELMSLDLQV<br>EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFQVKKQGE<br>QVLGDLMSILCDPFAINTLALSTVRHLQELVQETLPRDSPDLL<br>LLRLLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSPLVD<br>DYTFNVQKLPAEEKAPVSYNTLPESFTKFLQEQRMACEVGLY<br>YVLHITKQRNKNALLRLPLGLVETFGDLAFGDI FLHLLTGNLAL<br>LADEFALEDFCSSSLFDGFFLTASPRKENVHRHALRLIHLHPRV<br>APSKLEALQKALEPTQSGEAVKELYSQLEKLEQLDHRKPSPA<br>QAETPALELPLPSVPAPAPL                              |
| 6373       | 67   | 711  | PSRAARASPARL2AMVSWIISRLVVLIFGTLYPAYYSYKAVKSK<br>DIKEYVKMMWYIIFALFTTAETFTDIFLCWPPFYELKIAFVA<br>WLLSPYTKGSSLLYRKFFVHPTLSSKEKEIDDCVQAKDRSYDAL<br>VHFGKRGVLNVAATAAVMAASKGQALSERLRSFSMQDLTTIRGD<br>GAPAPSGPPPPGSGRASGKHQPKMSRSASESASSSGTA   |
| 6374       | 535  | 2105   | HKLFCSYISTSEFFPSSTRHSCPTHTFCNYTSSTIFLSSTRDHS<br>CPTHTFCNYTSSTIFLSSTRDHSCTHTSCNYTSSTIFLSSTRD<br>HSCPTHTSCNYTSSTIFLSSTRDHSCTHTFCNYPRPIRLSSC<br>CPAELQTEGSNGKKEVLSGFQVLEDTVLFPPEGGGQPDGRGTIN<br>DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH<br>SQOHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA<br>IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR<br>VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGGKNRTNLIPL<br>SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL<br>QKNNLNLRLDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII<br>ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRAEVL<br>EGKGAGKKGRFQKATKMSRRMEAQALLQDYISTQSAKE |
| 6375       | 1  | 1535   | AIMAAATRPVRLPEAGCEGRERCWNPSSRSRSHSGEGGLAAWSRT<br>CPGRPRRPQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK<br>PPGRACSNPSFLRFQLDFYQVYFLAALADWLOAPYLYKLYQHYY<br>FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY<br>SLCCLTKLSQDYFVLLVGRALGGLSTALLFSFAFEAWYIHEHVER<br>HDFPAEWIPATFARAFAFNHVLAVVAGVAAEAVASWIGLGPVAP<br>FVAIPLLLALAGALALRNWGENYDRQAFSRTCAGGLRCLLSDR<br>RVLLGTIQALFESVIFIFVFLWTPVLDPHGAFILGIISSFMAA<br>SLGSSSLYRIATSKRYHLQPNHLLSLAVLIVVFSLFMLTFSTSP<br>QGESPVESFIAFLLELACGLYFSPMSFLRRKVIPETEQAGVLN   |

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|------------|--|--|---|
|            |  |  | WFRVPLHSLACLGLLVLDHSDRKTGTRNMFISCSAVMMALLAV<br>VGLFTVVRHDAELRVSPTEEPYAPEL   |
| 6376       | 380  | 1437   | ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSQEGRO<br>QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQSLTSLVRRATLKE<br>NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC<br>GLNVHKQCSKMVPNDCKPDLKHVKVYSCDLTTLVKAHTTKRPM<br>VDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD<br>ISVNMVEDINIITGALKLYFRDLPIPLITYDAYPKFIESAKIMD<br>PDEQLETLHEALKLPPAHCELTLYRLMAHLKRVTLHEKENLMNA<br>ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEIDILF   |
| 6377       | 2311   | 1845   | SRIRRRSSRRPREPPGPPSRRRRRRRDPRTMPSEKTFKQRTTPE<br>QRVEDVRLIREQHPKIPVIERYKGEKQLPVLDTKTKFLVPDHV<br>NMSLKIIRRRQLNANQAFLLVNGHSMVSVSTPISEVYESE<br>KDEGDFLYMVYASQETFGMKLSV  |
| 6378       | 686  | 191  | GAGPWAEAFPDGIGRRSRRLRLOPKRPPGRVGGGDSGRNMAVA<br>DLALIPDVDDSDGVFKYVLIRVHSAPRSGAPAESKEIVRGYK<br>WAEYHADIDYKVSQDMQKQGCDCCLGGGRISHQSQDKKIHYVG<br>YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY   |
| 6379       | 35   | 378  | BRAGSPSPSRAALRRCAPQRSQAPRWPDRAACRRSFGSQGRAY<br>LFNSVVNVGCGPAEERVLLTGLHAVADIYCECKTTLGWKYEHA<br>FESSQKYKEGKYIIELAHMIKDNWD   |
| 6380       | 1414   | 462  | PAVQGORGAGPPTGRGSGNMAFALTIVVRHGETRFNKEKIQGQ<br>GVDEPLSETGFKQAAAAGIFLNNVKFTAFSSDLMRKQTMHGI<br>LERSKFKCDMTVKYDSRLRERKYGVEGKALSELRAMAKAAREE<br>CPVFTPPGGGETLDQVKMRGIDFFEFLLCQLILKEADQKEQFSQGS<br>PSNCLSETSLAEIFPLGKNHSSKVNDSGIPGLAASVLVSHGAY<br>MRSFLDYFLTDLKCSLPATLSRSELSVTPNTGMSLFIINFEEG<br>REVKPTVQCICMNLQDHLNGLTENSGLNLPSKSNHFEPLKGV<br>LALFTSLLC   |
| 6381       | 1668   | 218  | AVVRAQGSRGFSGAGWRPQAAAMNFSEVFKLSLLCKFSPDGK<br>YLASCVQYRLVVRDVTNLQILQLYTCLDQIQHIEWSADSLFILC<br>AMKRGVLQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT<br>TEFLRLITVWSLCTKSYSYIKYPKACLOGITFTRDRYMALAER<br>RDCKDYVSI FVCSQDWQLRHFTDTQDLTGIEWAPNGCVLAVWD<br>TCLEBYKILLYSLDGRLLSTYSAYEWSLGKSVAVSPSSQFLAVG<br>SYDGKVRILNHWTKMITEFGHPAAINDPKIVVYKEAEKSPQLG<br>LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDNRANP<br>KIGIGMLAFSPDSYFLATRNDNIPNAVWVDIQKLRLFAVLEQL<br>SPVRAFQWDPQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA<br>VLSLCWHLSGDSMALLSKDHFCLCFLEAVVGTACRQLGGHT |
| 6382       | 2  | 1062   | FEEDDRNLCLIAIYPLKGDHGIIVDVSNDCEPKSKLLRWTTNK<br>KHVLETEKTPKDWVROHRKEEKMKSHKLEEFELKKSEVLYY<br>TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL<br>LENLTSRYEPCVLDLKMGTQHGDDASEEKAANQIRKQCSSTS<br>AVIGVRVCGMQVYQAGSGQLMFNMKYHGRKLSVQGFKEALFQFF<br>HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLVYIDG<br>KERPEVVLSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM<br>IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG<br>E   |
| 6383       | 3159   | 1061   | SPAPGRPSPHGSQPAARAAAAAPAMPSAKQSGSKGGHGAASPEK<br>GAHPSAARPLAAPTAPACRSPSPGGAPASFPGRAPRSLASQP<br>AARAAAAAPAMPSAKQSGSKGGHGAASPEKGAHPSGGADDVAKK<br>PPAPQPPPPPPAPHPQHPQHPQHPQHPQHPQHPQHPQHPQHPQ<br>SSSSSASAAAAAASSASCSRRRLGRALNFLFYALVAAAAFS<br>GWCVHVLEEVQVRRSHQDFSRQREELGQGLQGVQKQVQSLQA<br>TFGTPEILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNB  |



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|------------|--|--|--|
|            |  |  | LKDLSGDIHVVKDARERDFTSLENTVEERLTETLTKSINDNIAIF<br>TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTS<br>AKSREWDMEALRSTLQTMESDIYTEVRELVS LKQEQQAFKEAAD<br>TERLALQALTEKLLRSESVSR LPEIRRLLEEELRQLKSDSHGP<br>KEDGGFRHSEAFEALQOKSQGLDSRLQHVEDGVLSMQVASARQT<br>ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRS L<br>GETQLVLYGDVEELKRSVGE LPTVESLQKVQEQVHTLLSQDOA<br>QAARLPQDFLDRLSSLDNLKASVSQVEADLKMRLTAVDLSLVAY<br>SVKIETNENNLESAGKGLDDLRNDLRLFVKVEKIEHKV  |
| 6384       | 738  | 1904   | IWEVPUCLTHLLHQANQPLPPSSSINEEDADEANRAIGEKR<br>AAPDSGKKPKTPKTKQKQDPNEPQKPVSA YALFFRDQAAIKQG<br>NPATFGEVSQIVASMWDSLGEQKQVYKRTKTEAAKKEYLKALA<br>AYRASLVSKAAESA EAQTIRSVQQT LASTNLSSLLNTPLSQ<br>HGTVASPQTLQQLSPRSIAPKPLTMR LPMNQIVTSVTIAANMP<br>SNIGAPLIISSMGTTMVGSA PSTQVSPSVQTQQHQMQLQQQQQQQ<br>QQQMQQMQQQLQQHQMHHQQIQQQMQQQH FQHMQHQLQQQQQH<br>LQQQINQQQLQQQLQQLQLQLQQLQHMHQSQSPSPRQHS PVASQI<br>TSPIPAIGSPQASQQHQSQIQSQSQTQTQVLSQVSI P  |
| 6385       | 2  | 1584   | PRVRAADVAAQAQAVVSAGMAKSNGENGFRA PAAGESLSGTRES<br>LAQGPDAATDELSSSLGSDSEANGFAERRIDKFGFIVGSQGAEG<br>ALEEVPLEVLQRQESKWLDMNNWDKMAKHKKIRLRCKQGIIP<br>PSLRGRAWQYLSGGKVKLQONPGKFDELDMS PGDPKWLVDVIER<br>LHRQFPFHEMFVSRGGHQQDLFRVLKAYTL YRPEEGYCQAQAP<br>IAAVLLMHMPAEQAFWLQV ICEKYLPGYYSEKLEAIQLDGEIL<br>FSLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTL PWSSVL<br>RVWDMFFCEGVKII PRVGLVLLKHALGSPEKVKACQGYETIER<br>LRLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG<br>ELQCRSPRLHGAKAILDAEPGRPALQPSPSIRLPDAPLPGS<br>KAKPKPPKQAQKEQRKQKGRGQLEKPPAPNQAMVVAAGDACP<br>PQHVPKDSAPKDSAPQDLAPQVSAHRSQESLTSQES EDTYL |
| 6386       | 819  | 195  | TVCGSFYLGIMQASRLKRELHMLATEPPPGITCWQDKDQMDL<br>RAQLGGANTPYEKG VFKLEVIIPERYPFEPPIRELTPIYHPN<br>IDSAGRICLDVLKLPKGAWRPSLNIATVLTSIQLLMSEPNPDD<br>PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKAD EEEMLDNL<br>PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV   |
| 6387       | 1  | 662  | PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAE LVKR<br>KQELAETLANLERQIYAFEGSYLED TQMYGNIIRGWDRYLTNQK<br>NSNSKNDRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQ LIEK<br>REPGSGTESDTS P DFNQENEPSQEDPEDLDG SVQGVKPKAAS<br>STSSGSHHSHKRRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY   |
| 6388       | 1  | 662  | PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAE LVKR<br>KQELAETLANLERQIYAFEGSYLED TQMYGNIIRGWDRYLTNQK<br>NSNSKNDRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQ LIEK<br>REPGSGTESDTS P DFNQENEPSQEDPEDLDG SVQGVKPKAAS<br>STSSGSHHSHKRRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY   |
| 6389       | 1074   | 497  | AEPGDRMAGHRLVVLGDLHIFHRCNSLP AKFKKLLVPKIQHI<br>LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG<br>QFKIGLIHGQVIPWGDMA SLALLQRFQDVIDILISGHTHKPEAF<br>EHENKFYINPGSATGAYNALETNIIPSFV LMDIQASTVVTYVYQ<br>LIGDDVKVERIEYKKP  |
| 6390       | 158  | 535  | GEERKEGRAPGKAFAPERNPAKMEKERTRELLLPNWQSGSHG<br>L TIAQRDDGVFVQEV TQNSPAARTGVVKEGDQIVGATIYFDNLQ<br>SGEVTQLLNTMGHHTVGLKLHRKGRDRFFPSLGQTDWP   |
| 6391       | 5386   | 2897   | VRWNSKTECYLSIQTQENFPANLNLVNCIVISSLVTTQRKLKA<br>MSLLGSRNQLARAVLNP NPMDFCTKDLLTTT SERIIAYLRDFNE<br>DQKKAIETAYAMVKHSPSAKICLIHGPPGTGSKSTIVGLLYRL   |

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|------------|--|--|---|
|            |  |  | LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF<br>KECKDKKNPLGNCGDINLVRIGPERKINSSEVLKFSLDQVNH<br>MKKELPSHVQAMHKKRKEFLDYQLDELRSQRALCRGGREIQRQEL<br>DENISKVSKERQELASKIKVQGRPKQTQSIIILESHIICCTLS<br>TSGGLLLESFAFRGQGGVPPFSCVIVDEAGQSCIEITLPLIHRN<br>KLILVGDPKQLPPTVISMKAQEGYDQSMARFCRLLEENVEHN<br>MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTRNQTEAIRC<br>SSDWPPFPYLVFDVGDGSEBRDNDSDYINVQEIKLVMIEIKLIK<br>KRKDVSRNIGIITHYKAQKTMIOKDLDEKFDKGPVAVDTVDA<br>FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVITIRAKYSLF<br>ILGHLRLTMENQHNQLIQDAQKRGAIKTCCKNYRHDAVKILK<br>LKPVLQRSLTHPPTIAPEGSRPQGGPSSKLDGFAKTSVAASL<br>YHTPSSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKG<br>IFLWDPPQSSPQHPGATPPTGEPGFVVHVDLSHVQQAFAVAA<br>LSSHKPPVRGEPFAASPEASTCQSKCDDPEELCHRRARAFSE<br>GEQEKCGSETHHTRNSRWDRKRTLEQEDSSSKKRKLL |
| 6392       | 972  | 186  | GRTGVDLASSMAHRLQIRLLTWDVKOTLLRLRHLGEAYATKAR<br>AHGLEVEPSALEQGFQRAYRAQSHSFPNYGLSHGLTSRQWLDV<br>VLQTFHLAGVQDAQAVAPIAEQLYKDFSHPCWQVLDGAEDTLR<br>ECRTRGLRLAVISNFDRLLEGILGGLGLREHFDVLTSEAGWP<br>KDPDRIFQELRLAHMEPVVAHVGDNYLQDYGPRVAGMHSFL<br>VVGPOALDPVVRDSVPKEHILPSLAHLPLALDCELGSTPGL   |
| 6393       | 2017   | 730  | TGGSKMAAVATCGSVAASTGSVAATASKSNVTSFQRRGPRASVT<br>NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGT<br>LLIEEDKYNISPLLFKYFLAEGIVNGHTLLVASAKEDPANILQ<br>ELPAPLLDDKCKKEFDEVDVNHKTPESNIKMIAWRYQLLPKME<br>IGPVSSSRFGHYDASKRMPQELIASNWHGFFLPEKISSTLVK<br>EPCSLTPGYTKLLQFIQNIIEEGFDGSGNPQKQNRNLRIGIQN<br>LGSPLWGDDICCAENGNSHSLTKFLYVLRGLLRTSLACIITM<br>PTHLIQNKAIARVTTLSDDVVVGLESFIGSERETNPLYKDYHGL<br>IHIRQIPRLNNLICDESVDKDLAFKLKRLFTIERLHLPDLSD<br>TVSRSSKMDLAESAARLGPCCGMAGGKKHLD   |
| 6394       | 1418   | 511  | GAAAGGEGARRRPAAMATVMAATAAERAVLEEFWRLLHDEVHA<br>VLKQLQDILKEASLRFTLPGSGTEGPAKQENFILGSCGTQVKG<br>VLTQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLQIQDAR<br>NHVSQAIYLLTSRDQSYQFKTGAEVLLMDAVMLQLTRARNRLT<br>TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCCLTVYQ<br>LHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLEVSHVHKVEC<br>VIPWLDALVYFTVSLQQLCKDKISVFSSYWSYRPF   |
| 6395       | 13   | 658  | PSGRPTRPLCCAARRGAARHGGSVSGWPAGRTPPTETSNPGSSVM<br>ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP<br>PCKPSCVSQLGQRAEPKATERGILRATGVAVESQLKPEELPSMQ<br>DLLEEASSRDMQMGPLFLRMQLVPSIEERETPLTREDRPALQE<br>PPWSLGCTGLKAAMQIQRVVIVPPTLGHRRNPWVARDSGE  |
| 6396       | 1  | 1221   | ANILSSPSKRQKGTLLIGYSEGTPLYNFMGDAFQHSQSIPRF<br>IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI<br>SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF<br>INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGILVNL<br>IGICAFSHAHSASHGASQGSCHSSDHSNHHMHGSHDHGHGSH<br>GSAGGGMNANMRGVFLHVLADTLGSIGIVSTVLIEQFGWFIAD<br>PLCSLFIAILIFLSVVPKIDACQVLLLRPPYEKELHIALEK<br>IQKIEGLISYRDPHFWRHSASIVAGTIHQVTSVDLEQRIVQOV<br>TGILKDAGVNNLTIQVEKEAYFQHMSGSLSTGFHDVLAMTKQMES<br>MKYCKDGTIYIM  |
| 6397       | 391  | 122  | GAGGVGRFEAIRAPARMIEVVNCNDRLGKKVRVKCNTDDTIGDLK<br>KLIAAQGTGRWNKIVLKKWYTIKDHVSLGDYIEIDGMNLELYY  |

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|------------|--|--|--|
| 6398       | 353  | 1306   | HKQMGPLINRCKKILLPTTVPFATMRIWLLGGLLPFLLLSGLQ<br>RPTGSEVAIKIDPDFAPGSFDDQYQGCCKQVMEKLTQGDYFTK<br>DIEAQKNYFRMNQKAHLAWLNQGVLPQNMTHAVAILFYTLN<br>SNVHSDFTRAMASVARTPQQYERSPHFKYLHYLTSAIQLLRKD<br>SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA<br>QEFNGTLPFTFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH<br>PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIATASLSFLTS<br>VIIFSKSRV   |
| 6399       | 75   | 1245   | PNLETYFGRHCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK<br>RRGMADSLSTPLPSPEDRLAKLHPSKELLEYQKKMAECEAEN<br>EDLLKLELYKBACEGQHKLECDLQOREEIEAELQKALSMDQVC<br>LFQEREHVLRLYSENDRLRIRELEDKKIKQNLALVGTDAEVT<br>YFCKEPPHKVTILQKTIQAVGECEQSESAFKADPKISKRRPSR<br>ERKESSEHYQRDIQTLILQVEALQALQEQTKLRSREIEGLIED<br>RRIHLEEIQVQHQRNQNKI KELTSKNLHHTOELLYESTKDFLQLR<br>SENQNEKESWMLKDNLSKIKQYRVQCKKEDKIGKVLPMVHE<br>SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM  |
| 6400       | 2520   | 1053   | KTMKCEVVYEVQSAILRHNCGYAMKTKGFFHNLMERKDFETWL<br>DNISVTFSLTDLQKNETLDIILISLSGAVQLRHLSNNLETLKR<br>DFLKLPLLELSFYLLKWLDPQTLTCLVSKQWNKVISACTEVW<br>QTACKNLGWQIDDSVQDALHKKVYLKAILRMKQLEDHRAFTS<br>SLIGH SARVYALYYKDGLLCTGSDDLAKLWDVSTGQCVCYGIQT<br>HTCAAVKFDEQKLVTSFDTVACWESSGARTQHFRGHTGAVF<br>SVDYNDELILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV<br>VLQCKVKSLHSPGDYILLSADKYEIKIWPIGREINCKCLKTL<br>SVSEDRSICLQPRLHFDGKYIVCSSALGLYQWDFASYDILRVIK<br>TPEIANLALLGFGDIFALLPFDNRYLYIMDLRTESLISRWPLPEY<br>RKSKRGSSFLAGEASWNLGLDGHNDTGLVVFATSMFDHSIHLVLW<br>KEHG  |
| 6401       | 109  | 766  | PGAANSRPDLRGCTGPPALRMLVLPSPCPQPLAFSSVETMEG<br>PPRTRCSPEPGPSSSIGSPQASSPPRPNHYLLIDTQGVPTVL<br>VDEESQREPGASGAPGQKKCYSCPVCSSRVFEYMSYLQRHSITHS<br>EVKPFECDCIGKAFKRAHSLARHHSIHLAGGGRPHGCPLCPRRF<br>RDAGELAQHSRVHSGERPQCPCPRRFMEQNTLQKHTRWKHP   |
| 6402       | 1196   | 279  | TTSQCGGIRQSSAIPVASMFAATCLRNALLLPBEEQDPKQEN<br>GAKNSNQLGNTESSESSESETCSSKSHDGDKPIAPPSSPLRKQE<br>LENLKCSILACSAYVALALGDNLMALNHADKLLQOPKLSGSLKF<br>LGHLAAEALISLDRISDAITHLPENVTDVSLGISSNEQDQGS<br>DKGENEAMESSGKRAPQCYPPSSVNSARTVMLFNLGSAYCLRSEY<br>DKARKCLHQAASMIHPKEVPEAILLAVYLELQNGNTQLALQII<br>KRNQLLPAVKTHSEVRKKPVFPVHPHQIPIQMPAFTTVQRK  |
| 6403       | 2  | 1690   | RGIHTSVLQGNLQNMYSNNVIMNLLNLTQVQQRNLTITNLQ<br>RSVDDTSQAIQRIKNDFONLQVFLQAKKDTDLKEKVQSLQTL<br>AANNALAKANNDTLEDMNSQLNSFTGQMNITTSQANEQNLK<br>DLQDLHKDAENRTAIFKNQLEERFQLFETDIVNIISNISYTAHH<br>LRTLTSLNEVRTTCTDTLTHTDDLTSLNNTLANIRLDSVSLR<br>MQQDLMRSLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP<br>PGPRGPRGRGSGQPPGPTGNKQKQKGEKGEPPGPAGERGP<br>PAGPPGERGGKSGSGQPKGSRGSPGKPGQPGSGDPGPPGP<br>CKEGLPGQPGPPGFQGLQGTGVEGVPGRGLPGLPGVPGMPGP<br>KGPPGPPGPGSAGVPLALQNEPTPAPEDNSCPFWKNTDKCYF<br>FSVEKEIFEDAKLFCEDKSSHLVPINTREEQQWIKKQMVGRSH<br>WIGLTDSERENWKNLDGTSPTYKNWKAGQPDNNGHGHGPGEDC<br>AGLIYAGQWDFQCEDVNNFICEKDRETVLSSAL |
| 6404       | 1012   | 222  | AAALAMAPAPGLISVFSSQELQALQVAQRAACCLAGARA  |

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|------------|--|--|--|
|            |  |  | RFALGLSGGSLVSMILARELPAAVAPAGPASLARWTLGFCDERLV<br>PFDHAESTYGLYRTHLLSRLPIPEQVITINPELPVEEAEDYA<br>KKLRQAFQGDSPVFDLLILGVGPDGHTCSLFPDHPLLQEREXI<br>VAPISDSKPPFPQVRVTLTLPVLNAAARTVIFVATGEGKAAVLKRI<br>LEDQEBNPLPAALVQPHTKGLCNFLDEAAARLLTVPFKHSPL   |
| 6405       | 1  | 1456   | AALPRPTPRAPLGREGTGSDEMAASMFYGRVAVATLRNHRFR<br>TAQRAAAQVLGSSGLFNNHGLVQQQQQRNLSLHEYMSMELLQE<br>AGVSVPKGYVAKSPDEAYALAKLGSKDVIKAQVLAGGRGKGT<br>FESGLKGGVKIVFSPREAKAVSSQMIGKKLFTKQTGEKGRICNQ<br>VLVCERKYPREYFPAITMERSFQGPVLIGSSHGGVNIEDVNAE<br>TPEATIKEPIDIEEGIKKEQALQLAKMGFPNIVESAENMVK<br>LYSLFLKYDATMIEINPMVEDSDGAVLCMDAKINFDSNSAYRQK<br>KIPDLQDWTQEDERDKDAKANLNYIGLDGNIGCLVNGAGLAMA<br>TMDIIKLHGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL<br>VNI FGGIMRCDVIAQGI VMAVKDLEIKIPVVVRLOQTRVD DAKA<br>LIADSLGKILACDDLDEAARMVVKI SEIVTLAKQAHVDVKFQLP<br>I   |
| 6406       | 1036   | 167  | HPROMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD<br>DDDDHDDHEDNDKMNDSSEGMDPERLKA FNMFVRLFVDENLDRM<br>VPISKQPKKIQAIIESCSRQFPFQERARKRIRTYLKSCRRMK<br>KNGMEMTRPTPHLTSAMAENILAAACESETRKAARKMRLEIYO<br>SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN<br>YSYRGYALSSNLQPPASLOTGNHNSNGESGEARALASRPAPSWV<br>CRAALGSGMGRGKQRPVMERGCLTA  |
| 6407       | 492  | 150  | VGLCLAVSQTVLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGV<br>SWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNAC<br>VLTISPVOPEDDADYYCSVGYGFSF  |
| 6408       | 1458   | 903  | RGCTISSQAWRLFGGVTGRGNMREKCYFCSGPIYPGHGMFVR<br>NDCKVFRFCCKSKCHKNFKKKRNPRKVRWTKAFKAGKELTVDN<br>SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKQAKFIMNR<br>LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGQLEEKMVQQLQE<br>DVDMEDAP  |
| 6409       | 150  | 446  | NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP<br>GPACLPPTKTFRSYLPCHRTYSCVHCRAHLAKHDELISKSFQGS<br>HGRAYLFNSV   |
| 6410       | 85   | 607  | RGGTAGCVACLGCWGQSSSPKAAPFAGSACLPAADSCPCLLFQAC<br>AISGLFNCITIHPLNIAAGVWMIMNAFILLCEAPFCQFIEPA<br>NTVAEKVDRLRSWQKAVFYCGMAVVPVIVISLTTLTLLGNAIAPA<br>TGVLVGLSALGKKGDAISYARIQQORQQADEEKLAE TLBQEL  |
| 6411       | 302  | 772  | RLSIMASSLNEDPEGSRTITYVKGDLFACPKTDSLHCISEDCRM<br>GAGIAVLFKKKFGGVQELLNQKKSGEVAVLKRDRYIYYLITK<br>KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ<br>WENVSAMIEEVFEATDIKITVYTL   |
| 6412       | 61   | 1709   | RPVTSFSPLPSCGGRIGTRTMLGRSLREVSAAALKQGGITPTL<br>CQKCLSLIKKTKFLNAYITVSEVALKQAESEKRYKNGQSLGD<br>LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDQ<br>GALLMGKTNLDEFAMGSGSTDGVFPGVKNPWSYSKYREKRRQN<br>PHSENEDSDWLTIGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP<br>AAHCGLVGPKPSYGLVSRHGLIPLVNSMDVPGILTRCVDAAIV<br>LGALAGDPDRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV<br>PELSSEVQSLWSKAADLFESEGAKEVSLPHTSYSIVCYHVL<br>TSEVASNMARFDGLQYGHRCIDVSTEAMYAATRREGFNDVVRG<br>RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL<br>TPTTLEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP<br>VALSNQGLPIGLQFIGRAFCQQLLTVAKWFKEQVQFPVIQLQE<br>LMDDCSAVLENEKLASVSLKQ |

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|------------|--|--|--|
| 6413       | 2  | 885  | HEPRCAGMAASLWMDLEPYMDENFISRAFATMGETVMSVKIIR<br>NRLTGI PAGYCFVEFADLATAEKLHKINGKPLPGATPAKRFKL<br>NYATYCKQPDNSPEYSLFVGDLTPDVGMLYEFFVKVYPSCRG<br>GKVVLDQTKGVSKGYGVKFTDELEQKRALTECQGAUGLGSKPVR<br>LSVAIPKASRVKPEYSQMYSSYNQYQQYQNYAQWGYDQNT<br>GSYSYSPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTANKEF<br>MEQSEELYDALMDCNQLDTSSETPAMM   |
| 6414       | 1  | 538  | RGGRAALLPWRRFPCCRPKPPARPSSRATPGPRSPGMATSIGV<br>SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV<br>LKEELANA EYSP EEMPQLTKHLS ENIKDKLKEMGFDRYKVVQV<br>VIGEQRGEGVFMA SRCFWDADTDNYTHDVFMDNLSLFCVVAAGFC<br>FYY   |
| 6415       | 2  | 1168   | FVRQWQSSHRRACGLGCEARAGGEEPRGRASSVAGWVGAFRAP<br>FIEAAVAGLGAGSGKRRRGWKMPVHSGRDKKETNNHDEMEVDYA<br>ENEGSSSEDEDETESSSVSESDGSSSEMDDEDCERRRMECLDEMSN<br>LEKQFTDLKDQLYKERLSQVDAKLQEVIAKKAPEYLEPLATLQ<br>NMQIRTKVAGIYRELCLSVKNKYCEIQASRQHCESEKLLLYD<br>TVQSELEEKIRRLBEDRHSIDITSELWNDELQSRKKRDPFWD<br>KKKPGVVS GPYIVYMLQDL DLEDWT TIRKAMATLGPHRVKTEP<br>PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV<br>IT TINHDEVWFKRPDGSKSKLYISQLQKGYSIKHS |
| 6416       | 410  | 1519   | ETAPADLEIPACAPVLLSRATSSSTSVTGGKMAPSLTQEILSHL<br>GLASKTAAMGTLGLRTFLNFSVDKDAQRLLRAITGQCVDRSAI<br>VDVLTNRSREQRQLISRNFEQRTQDLMKSLQAALSGNLERIVM<br>ALLOPQAQFDAQELRTALKASDSA VDAIEILATRTPPQLQEC<br>AVYKHNFQVEAVDGTITSETSGILQDILLALAKGRDSYSGIIDY<br>NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS<br>TGQEELEAVQNRFRHGDAQVALLGLASVIKNTPLYFADKLHQALQ<br>ETEPNYQVILIRILISRCETDLSIRA EFRKKFGKSLYSSLODAV<br>KGDCQSALLALCRAEDM                   |
| 6417       | 1  | 845  | RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAPVIACVLS<br>LISTIYMAASIGTDFWYEYRSPVQENSSDLNKS I WDEFI SDEAD<br>EKTYNDALFRYNGTVGLWRRCTIPKNMHWYSPPERTESFDVVT<br>KCVSFTLTQFMEKFVDPGNHNSGIDLLR TYLWRCQFLLPFVSL<br>GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV<br>AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA<br>AHTNRKEYITLMKAYRVA   |
| 6418       | 2  | 662  | TRTRPRPPGLGAAGKAGARSTSTPAGASPAAYQADPPPPAH<br>TPAPPPPPPCGGIACHGEPKFGYDNLQRQPIFTTQQAELVQ<br>YFDCSSSGNIGEDPDHLNQSSSPSQMFPMRPQAAPGRRRRGRQ<br>TYSRFQTLLEKEFLFNPLYLTKRRRIEVSHALALTERQVKIWFQ<br>NRRMKWKKENNKDKPPVSRQEVKDGETKKEAQELEEDRAEGLTN  |
| 6419       | 1  | 973  | PGRPRVRNFDLNSKSILOEFFCTR SIQIPANRSKTAMSKCPIFP<br>MARSISTSGPLDKEDTGRQKLISTGSLPATLQCATDSLGLWHL<br>PSPDPVTVPYLSPLVWVWKELESLENEGDAITVADFVDHPIV<br>FWNLVWYFRRDLPSNLPLGLILSSBHCNKYSKIPRHCMSEDSKY<br>VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF<br>NQELLKSMVKS I KMNDVYGPM SQILETLNKC PHFKRQRS LYREI<br>LFLSLVALGRENIDIDAFDKEYKMAYDRLTSPQVKSTHNCRRPP<br>STGVNECRKTFGEPLY  |
| 6420       | 207  | 1187   | RKMIDKNQTCGVGQDSVPYMICLIHILEENFGVEQLEDYLNAN<br>YLLWVFTPLILLILPYFTIFLLYLTIFLHIYKRKNVLKAYSH<br>NLWDGARKTVATLWDGHA AVWHGYEVHGMKIPEDGPALIIFYH<br>GAIPIDFYFMAKIFIHKGRTCRVVADHFVKIPGFSLLLDVFC<br>ALHGPREKCEVILRSGLLAI SPGGVREALISDETYNIWVGHRR<br>GFAQVAIDAKVPIIPMFTQNI REGFRSLGGTRLFRWLYEKFRYP   |

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|------------|--|--|--|
|            |  |  | FAPMYGGFPVKLRTYLGDPIPYDPOITAEELAEKTKNAVQALID<br>KHQRIPGNIMSALLERFH   |
| 6421       | 1844   | 362  | WALSLRRQPERMSNKLSPHPSVVLRSFEMASSPAVLASRL<br>YQWSLKSSAQFLGSPQLRQVQGIIRVPMARMAATLILEPAGRCW<br>DEPVRIAVRGLAPEQPVTLRASLRDEKALFQAHARYRADTLGE<br>LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA<br>VELEVLDGHDPPDGRLLCQTRHERYFLPPGVRRPVRVGRVGT<br>LFLPPEPGPPFGIVDMFGTGGGLLEYRASLAGKGFVAMALAY<br>NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPVGLLGISKGG<br>ELCLSMASFLKGITAAVINGSVANVGGLTRYKGETLPPVGVNR<br>NRIKVTKDGYADIVDLNSPLEGPDQKSFIPVERAESTFLFLVG<br>QDDHNWKSEFYANBACKRLQAHGRRKPKIICYPETGHYIEPPFY<br>PLCRASLHALVGSPIWGGEPRAHAMAQVDAWKLQOTFFHKLHG<br>GREGTIPSKV  |
| 6422       | 181  | 2133   | EGENLSWFOEFWGDIAKEFYWKTPCPGPFLLRYNFDVTGKIFIE<br>WMKGATTNICYNVLDNRNVHEKKLGDKVAFYWEWNEPGETTQITY<br>HQLLVQVCQFSNVLKQGIHKGDRVAIYMPMIPBLVVMALACAR<br>IGALHSIVFAGFSSESCLERILDSSCSLLITDADFYRGEKLVNL<br>KELADEALQCKQEGFPVRCCLVVKHLGRAELGMGDSQSPPPI<br>KRS CPDVQISWNQIDLWWHELMQEGDECEPEWCDAEDPLFIL<br>YTSGSTGKPKGVVHTVGGYMLYVATTFKYVDFHAEDVFWCTAD<br>IGWITGHSYVTYGFLANGATSVLFEGIPTYPDVNRLWSIVDKYK<br>VTKFYTAPTAIRLLMKFGDEPVTKHSRASLQVLGTGVEPINPEA<br>WLWYHRVVGAAQRCPIDVTFWQTETGGHMLTPLPGATPMKPGSAT<br>PFFFGVAPAILNESGEELEGEAEGLVFKQWPWPGIMRTVYGNHE<br>RFETTYFKKPPGYVVTGDGQQRDQDGYWITGRIDMLNVSGHL<br>LSTAEVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT<br>FSPKLTTELKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV<br>LRKIAQNDHDLGDMSTVADPSVISHLFSHRLTIQ |
| 6423       | 614  | 1237   | ANLKEIPRDLPPETVLLYLDNSQITSIPNEIFKDLHQLRVLNLS<br>KNGIEFIDEHAFKGVATLQTLDLSDNR IQSVHKNAFNNLKARA<br>RIANNPWCDCTLOQLRSMASNHETAHNVICTSVLDEHAGRP<br>FLNAANDADLCNLPKKTDDYAMLVTMFGWFTMVISVYVYVRQN<br>QEDARRHLEYLKSPLSRQKKADEPDISTVV   |
| 6424       | 1  | 1188   | KKVSFPVAAVHCSCVLFRRKYNFIDKLRLFTRGSGGGMGPRL<br>GEGGGKGGDVVVAHNRM TLKQLKDRYPRKRFVAGVGANSKISA<br>LKSGSKGDWEIPVPVGISVTDENGKIIGELNKENDRILVAQGG<br>GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPPNAGKSSLLSC<br>VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH<br>MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII<br>LLTKELELYKEELQTKPALLAVNMKMDLPDAQDKFHELMSQLQNP<br>KDFLHLFEKNMIPERTVBFQHIIPISAVTGEIEELKNCIRKSL<br>DEQANQENDALHKKQLNLNWSIDTMSSTEPSPSKHAVTTSKMDI I   |
| 6425       | 1850   | 1144   | LAMEGGGGIPLLETLKEESQSRHVLPAFVNSLQKSNWGFLLTG<br>LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR<br>CRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLWYSRYRA<br>WREGVHGS AKFYISDLWKVTFQSQYSNVVIFGVPPQMMQLQEKLE<br>RELEDDARVIACRFPPHWTDPHVTGEGIDTVWAYDASTFRGRE<br>KREPTSMHFQLP IQA   |
| 6426       | 30   | 565  | SRGAAGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR<br>LHAEFAAERDWBQFHQPRNLLALVGEVGE LAELFQWKTDGEPG<br>PQGWSPRERAAQBELSDVLIYLAALACRVDLPLAVLSKMDI<br>NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT<br>ST   |
| 6427       | 145  | 959  | AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK<br>NIREYVRWMMYIWFALFMAAEIVTDIFISWFPPFYIEIKMAFVL   |

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|------------|--|--|---|
|            |  |  | WLLSPYTKGASLLYRKVFHPSLSRHEKEIDAYIVQAKERSYETV<br>LSFGKRGRLNIAASAAVQAATKSQAGLAGRLRSFMSQDLRSISDA<br>PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDEECWSDTEA<br>VPRAPARPREKPLRSQSLRVVKKRPPVREGTSRSLKVRTRKKT<br>VPSDVDS   |
| 6428       | 1982   | 444  | SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR<br>EKINAAIQDMPSEEEIAQLLSGSYIHYFHLRLILDLLKGTEAST<br>KNIFGRYSSQRMKDQWEIIALYBKDNTYLVELSSLLVRNVNVEI<br>PSLKKQIAKCCQLQOBYSRKEEECAQAGAEEMREQFVHSCQKQYI<br>TGENVRGELLALVKDLPSQLAEIGAAAQQSLGEAIDVYQASVGP<br>VCESPTQVLPMLRFVQKRGNSTVYEWRTGTETPSVVERPHLEEL<br>PEQVAEDAIDWGDGFGVEAVSEGTDGSGISAEAGIDWGIFPESDS<br>KDPGGDGIDWGDDAVALQITVLEAGTQAEQVARGPDALTLEY<br>TETRNQFLDELMELEIFLAQRAVELSEADVLVSQFQLAPAIL<br>QGQTKKVMVTVSVLEDLIGKLTSLQLQHLFMIASPRVYDRVT<br>EFLQKLLKQSLALAKKELMVQKQEALEEQAALEPKLDDLLEK<br>TKELQKLEADISKRYSGRPVNLGTSLS   |
| 6429       | 3413   | 3442   | EPSSWTAAPRGPLAAHPLEAAVQEDDRRLSFDRIKVFANGTL<br>VKSVDKADAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE<br>NDHKVYFGGDLKVDCAVATGLPNPEISWSLPDGLVNSFMQSDDS<br>GGRTKRYVVFNGTLYFNEVGMREEGDYTCFAENQVGDDEMVR<br>VKVVTAPATIRNKTCLAVQVPGDVVTACEAKGEMPKVTWLS<br>PTNKVIPTSSSEKYQIYQDGTLLIQAKQRSDSGNYTCLVRNSAGE<br>DRKTVMHVNVPKINGNPNPITTVREIAAGGSRKLDCKAEG<br>IPTPRVLWAFPEGVVLPAFYGNRITVHNGSLDIRSLKSDSV<br>QLVCMARNEGGEARLIVQLTVLEPMKPIFHDPISEKITAMAGH<br>TISLNCGAAGTPTPSLVVLPNGTDLQSGGQLQRFYHKADGMLH<br>ISGLSSVDAGAYRCVARNAAGHTERLVSLLKVLKPEANKQYHNL<br>VSIINGETLKLPTCPFGAGQGRFSWTLPNGMHLEGQTLGRVSL<br>LDNGTLTVREASVFDRTYVCRMETEYGPSVTSIPVIVIAYP<br>ITSEPTPIVITRPGNTVKNLNCMAMGIPKADITWELPKSHLKAG<br>VQARLYGNRFLHPQGSLLTIQHATQDAGFYKCMKNILGSDSKT<br>TYIHVF |
| 6430       | 1946   | 602  | RTRVSTGLRRRTLWSEAVGASSTRGDTGIPGSGEGGAGPGGEG<br>AMLEAMAEPSPEDPPPTLKPETQPPKEKRRTIEDFNKFCSEVLA<br>YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSPDLRTI<br>QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM<br>KLKDSLFDLDGPKVASPLSPTSLSLTHTSRPPAALTVPVLSQGDLS<br>HPPRKDKRKNRKLFGAGAGVGLRRPRPTPGDGEKRSRIKSK<br>KRKLKKAERGDRLP PPGPPQAPPSTDSBBBBBBBBBBBBBEMA<br>TVVGGEAPVPVLPPTPEAPRPPATVHPEGVPPADSESEKVGSTE<br>TSQDGDASSSEGEEMRVMDIMVESGDDSWDLITCYCRKPFAGR<br>PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQCKELRPEARLIG<br>GPPKSGEP  |
| 6431       | 3  | 605  | WNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR<br>LEEEALRRKERLALREKTGRKDKEDGEPKTKHLREEEEBGEKH<br>RELRLRNYVPEDEDLKRRVPQAKPVAVEEKVKEQLEAAKPEPV<br>IEVDLANLAPRKPDWDLKRDVAKKLEKLKKTQRAIAELIRER<br>LKGQEDSLASAVDAATEQKTCDS  |
| 6432       | 56   | 1692   | GGLGTMSGRIKQNPETTFEYVVEVAYPRTGGTSLSDPEVQROFPE<br>DYSQEVLTQLTKFCFFYVDSLTVSQVQGNFTFVLTIDISKQR<br>FGFCRLSSGAKSCFCILSYLPWFVFFYKLLNIALDYTTKRQENQ<br>WNELETLHLKLPIDPGVSVHLSVHSYFTVPDTRLELPSIPENRN<br>LTEYFVAVDVNNMLHLYASMLYERRILICSKLSTLTACHGSA<br>AMLYPMYQHVYIPVLPPLLDYCCAMPYILIGIHLSLMEKVRN<br>MALDDVVILNVDNTLTETPFDDQLSLPNDVISSLNRLKKVSTT  |

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|------------|--|--|--|
|            |  |  | TGDGVARAFLKAQAFFGSYRNALKIEPEEPITFCERAFVSHYR<br>SGAMRQFLQATQQLQFKQFIDGRLLDLSNGEGFSDFVEEINM<br>GBYAGSDKLYHQWLSTVRKSGAILNTVTKANPAMKTIVYKFDI<br>AENGCAPTPEEQLPKTAPSPLVEAKDPKLEDRRPITVHFGQVR<br>PPRPHVVKRPKSNIAVEGRRTSVSPSEQNTIATPATLHLQKSI<br>THFAAKFPTRGWTSSSH  |
| 6433       | 1524   | 484  | APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA<br>PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL<br>LPLLLLVATTGPGVALTDEEKRLMVELHNLRYRAQVSPTASDML<br>HMRWDEELAAFAKAYARQCVWGHNKERGRGENLFAITDEGMDV<br>PLAMEEWHHEREHYNLSAATCSPGQCMGHYTQVWAKTERIGCG<br>SHFCEKLQGVETNIELLVLCNYEPPGNVKGKRPYQEGTPCSQCP<br>SGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSPRATEASDSRKM<br>AEGDPKPSVVSGLNSGPGHVWGLGLLLPLVLVLAGIF  |
| 6434       | 40   | 2002   | MPQLNFGMADPTQMGGSLMLLAGEHALGTPEVFSGTCRPNVSE<br>SPELRQKSPFLQFAEISSSTSHSDASTKQCQTSALFOFAEISSN<br>TSQLGGAEPVVKRCGKSALFLQLAEMCLASEGKMMEESKLKAKES<br>DGGRIKLEKKEKEKEIKMEKXTDETRLOKEAEFEKSARENLRDS<br>KELRNFEALQIDDIMAUKMEDPKIRKEELEEDHKCSHFDPFSY<br>SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPELKKKKK<br>KSKMDRHGNDKSTPKKTCCKRQSSBESDIESVIYIEAVAKGDWG<br>IEKLQDTPRKKVTRTSSSGKGSILDAKPPKKVKRSREKKMSKEKS<br>SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS<br>LSGQAKPEDSDCHRIETCGSRKSERSCGALYKTLVSEGMLTS<br>LRANVDRGKRSSGKGNSSDHEGCWNEESWTFSSQSGTSGSKPKK<br>TKPKEDCLGSAKLDEEFKKFNSLPQYSPVTFDRKCVVPVRKK<br>KKTGNVSSEPTKTSKSGDKWSNKQLFLDAIHPTAIFSEDRNT<br>MEPVHKVKNIPSI FNTPEPTTTARTFGGQPKESKENPDYSPCQ<br>DTQRAGYHHEEVLWMTNLMNCCGVLYLQLRHTAMTNA |
| 6435       | 2227   | 657  | ALQRDAAAAYAHPEYEEERFLOEETVSQQINSIELLQTRPLALPE<br>VVKSRQLQRQVHLRGRPASQPTVIRGITYYKAKVSEENDIEE<br>QDEFFSGDNGVDLLIEDQLLRHNGMLTSVTRRPAATRQGHSTA<br>VTSDLNARTAPWSSALPQFSTSDPSIANHASVGP TLQTTSVSPD<br>PTRESVLQSPQVPATTVAHTATQQEAPAPPAVSPREALMEAM<br>HTVPVPPTTVRTDSLGDAPAGRGTTPASPTLSPEBEDDIRNVI<br>GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYY<br>GNTLVEFRNLNFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR<br>AFTRNIIKYDLKQRYVAAWAMLDHVAEEATPWRWQGHSDVDFA<br>VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRG<br>LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHNTQIVPR<br>LLFENEYFYTTQIDYNPKDRLLYAWDNGHQTYYHVIFAY   |
| 6436       | 1295   | 341  | GACRPPVRQDPDSGFDYEALPAGATVTTMVGAGAVAGILEHCV<br>YPIQDCVKTRMQSLQPDPAARYRNVLALWRIIRTEGLWRPMPRL<br>NVTATGAGPAHALYFACYELKKTLSVDIHPGONSHIANGAAGC<br>VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDVRAVWQNEGAG<br>AFYRSYTTQLTMNVFPQAIHFMTYEFLEQEHFNPQRRYNPSSHVL<br>SGACAGAVAAAATTPLDVCKTLLNTQESIALNSHITGHITGMAS<br>AFRTVYQVGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT<br>KRQEEWRACK  |
| 6437       | 1828   | 360  | PPAPAPPASPARHVTRTARGHLEGGSRAPPLQAVFLQIKNMVK<br>LIHTLADHGGDDNVCCAFSFSLLATCSLDKTIIRLYSLRDFTELP<br>SPLKFHTYAVHCCCFSPSGHILASCSTDGTTLVWNTENGQMLAV<br>MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG<br>SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKAH<br>DLGITCCDFSSQPVSDGEQGLQFFRLASCQDQCQKIVISPTH<br>ILGFELKYKSTLSGHCAPVLACAFSHDQMLVSGSVDSKIVIVD  |



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|------------|--|--|---|
|            |  |  | TNTENILHTLTQHTRYVTFCAFPNTLLLATGSMDDKTVNIWQFD<br>LETLCQARSTEHQLKQFTEDWSEEDVSTWLCQADKDLVGIFKM<br>NNIDGKELLNLTKESSLADDLKIESLGLRSKVLRIEELRTKVKS<br>LSSGIPDEFICPITRELMKDPVIASDGYSYEKAMENWDPAKRN<br>RTSPP   |
| 6438       | 109  | 901  | EVQILRAKMFQTGGLIVFYGLLAQTMAGFGGLPVPLDQTLPLNV<br>NPALPLSPTGLAGSLTNALSNGLLSGGLGILENLPLLDILKPG<br>GGTSGGLLGLLGLKVTSPVIGLNNIIDIKVTDPLLELGLVQSP<br>DGHRLVVTIPLGIKQVNTPLVGASLLRLAVKLDITAEILAVRD<br>KQRIHLVLGDCTHSPGSLQISLLDGLGLPLIQGLDLSLTGILN<br>KVLPELVQGNVCPVNEVLRGLDITLVHDIVNMLIHGLQFVIKV   |
| 6439       | 23   | 412  | SIQTASAITTEMASQSQGIQQLLQAEKRAEKVADARKRRARRL<br>KQAKEEAAQMEVEQYRREREHEFQSKQAAMSGQNLSAEVEQAT<br>RRQVQGMQSSQQRNRERVLQAQLGMVCDVRPQVHPNYRISA   |
| 6440       | 3  | 517  | RARWNSDMGDLPLGLVRLSIALRIQPNQGVFYKVDGQRFGQNR<br>IKLLTGSSYKVEVKIKPSTLQVENISIGGLVLPLELKSKEPDGD<br>RVVYTGTDTGVTPTKSGERQPIQITMPFTDGTFTVWQVKF<br>VNYHKRDHCQWGSPPFSVIEYECKPNETRSLMWVNKESFL   |
| 6441       | 234  | 1373   | KSGGLRRRQRPGRSAAVGEEELPPGMEKFAAMLLGSVGDALGY<br>RNVCKENSTVGMKIQEELQSGGLDHLVLSPGEWVPSDNTIMHI<br>ATAEALTTDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC<br>AQLKPNNYLLAWHTPFNEKSGSGFGAATKAMCIGLRYWKPERLET<br>LIEVSVECGRMTHNHTGFLGSLCTALFVSFAAQGKPLVQWGRD<br>MLRAVPLAEYCRKTIKHTAEYQEHWFYFEAKWQFYLEERKISK<br>DSENKAIFFPDNYDAEREKTYRKWSSEGRGRRGHADAPMIAYDA<br>LLAAGNSWTELCHRAMFHGGESAATGTAGCLFGLLYGLDLVFK<br>GLYQDLEDKEKLEDLGAALYRLSTEEK |
| 6442       | 34   | 796  | AEDPAGGLAGQDTMFARGLRKRCVGHEDVEGALAGLKTVSSYS<br>LQRLSLLDMSLVKLQCHMLVEPNLCRSVLANTVRQIQEEMTQ<br>DGTWRTVAPQAERAPLDRLVSTEILCRAANGQEGAHPASGLGD<br>GHTQGPVSDLCPVTSQAAPRHLQSSAWEMDGPENRGSFHKSLD<br>QIFETLETKNPSCMEELFSDVDSPPYDLDTVLTGMGGARPGPC<br>EGLEGLAPATPGPSSSSCKSDLGELDHVVEILVET   |
| 6443       | 2  | 555  | MASPAASSVRPPRPKKEPQTLVIPKNAEEOKLKERLMKNPDK<br>AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYHLRRR<br>EYQRQDYMDAMAEKQKLDAEFQKRLKKNIAAEEQTAKRRKKRQ<br>KLKCKLLAKMKLEQKQKEGPGQPKQGGSSSSAEASGTEEEEEE<br>VPSFTMGR   |
| 6444       | 390  | 899  | GSTPRGKMRAPPEPKPGDLIEIFRPFYRHNAIYVGDGYVHLLA<br>PPSEVAGAGAASVMSALTDKAIKKELLYDVAGSDKYQVNNKHD<br>DKYSPLPCKSI IQRAEELVGQEVLYKLTSENCEHFVNELRYGVA<br>RSDQVRDVI IASVAGMGLAAMS LIGVMFSRNKRQKQ   |
| 6445       | 2  | 753  | AGAAGAAGAARSPPQAHTKGVRLPSRRSPDCGRMELAGSF<br>SEEQWEACAEELQPALAGADWQLLVETSGISIRLLDKKTGLY<br>EYKVGVLDCSPTLLADIYMSDYSRKQWDQYVKELYEQECNGE<br>TVVYVEVKYPPFMSNRDYVYLRQRRLDMEGRKIHVILARSTSM<br>PQLGERSGVIRVKYKQSLAIESDGKKGSKVFMYYFDNPGGQIP<br>SWLINWAAKNGVFNFLKDMARACQNYLKKT  |
| 6446       | 1  | 1651   | RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS<br>DSGDEAAWEDEDDADLPHGKQQT PCLFCNRLFTSAEETFHCKS<br>EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV<br>PWEKEEYLRPVLEDDLLLQFVEDLYEPVSVFPFSYPNGLENTS<br>VVEKLKHEARALSAAALARAREDLQKMKQFAQDFVMHTDVRT<br>CSSSTSVIADLQEDDGVYFSSYGHYGIHEEMLDKIRTESYRD<br>FIYQNPFIKDKVVLVDVGCCTGILSMFAAKAGAKKVLGVDQSEI   |

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|------------|--|--|---|
|            |  |  | LYQAMDIIIRLNKLEDITITLYKGIIEVHLPVEKVDVUISEWMMGY<br>FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA<br>DRIAFWDDVYGFKMSCKKAVIPEAVVEVLDPKTLISEPCGKH<br>IDCHTTSISDLEFSSDFTLKITRTSMCTAAGYFDIYFEKNCHN<br>RVVFSTGPQSTKTHWKQTVFLEKPPSVKAGEALKGVTVHKNK<br>KDPRLSTVTLTLNNSQTQYGLQ   |
| 6447       | 1554   | 1068   | RLGPABWHLSGPCHATLGAANRGRALGVRAAWRGAPLCQRVMP<br>SRTNLATGIPSSKVYSRLSSDDGYIDLQFKKTPPKIPYKAIA<br>LATVLPPLIGAFLLIIGSLLSGYISKGGADRAVPVLIIGILVFL<br>PGFYHLRIAYASKGYRGYSYDDIPDFDD   |
| 6448       | 74   | 559  | GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLQK<br>FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAIVLSTYLEMG<br>AVELRGSRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER<br>QFIVRKVHYDPEKDVHIEAQKRNQKEDL  |
| 6449       | 597  | 1876   | EYGVCCENLRKLEITGVSCRDVAKLHRYRHILGLWQPDIGPYG<br>GLLNVVVDGLFIIGWMLPPHDPHVDPMRFKPLFRILHMERKA<br>ATVECMYGHKGPHGHGHIQIVKKEDEFSTKCNQTDHHRMSGGRQEE<br>FRTWLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI<br>YLPSPRPDDLKPGLFKGTGSHGLEIVMLSFHRRARGTKITG<br>DPNIPAGQQTVEIDLRRHIQLPDLENQRNFNELSRIVLEVRERV<br>RQEQQEGGHEAGEGRGROGPRESQPSAPQAPRAEAPSKGPDGTGP<br>EDGGEFGDAVAAAEQPAQCGQGQPFVLPVGVSSRNEDYPRCTRM<br>CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY<br>SRVQATFRNADAPSPQAFDEMLKNIQSLTS |
| 6450       | 848  | 269  | FVPAPRTVSGKRSLPGWEERGEQEQRTGREFSGNGGRAVEAAR<br>MRLLCGLWLWLSLLKVLQAQTPTPLPLPPMQSFQGNQFGGEWF<br>VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGQHC<br>DTWSYVLIIPAAQPGQFTVDHRVWTHEQAGRPODQPAQQLVAAS<br>RDAGPVHLPGQSSGPIG   |
| 6451       | 232  | 939  | HSPTPTSPRATMEDVKLEFPSPLOCKEDAEWYTPMRREMQUE<br>ILPGLFLGPYSSAMSKLPVLQKHGITHICIRQNEANFIKPN<br>FQQLFRYLVDIADNPVENIRFPMTKEPIDGSLQMGKVLVH<br>GNAGISRSAAAFVIAYIMETFGMKYRDAFAYVQERRFCINPAGF<br>VHQLQEYEAIIYLAKLTIQMSPLQIERSLSVHSGTGSCLKRTHE<br>EEDDFGTMOVATAQNG   |
| 6452       | 1  | 652  | RTRGESSNMEPLAAYPLKCSGPRAKVFVAVLLSIVLCTVTLFLLQ<br>LKFLKPKINSFYAFEVKDAKGRVTSLEKYKGKSVLVNVASDCQ<br>LTDNRNVLGLKELHKEFGPSHPSVLAFFPCNQFGESEPRPSKEVES<br>FARKNYGVTFPIPHKIKILGSEGEPAFRFLVDSSKKEPRWNFWK<br>YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIKKKEDL  |
| 6453       | 827  | 223  | HRRWLPGLSMSPPRRTLPRPLSLCLSLCLCLLAAALGSAQSGSC<br>RDKKNCKVVSQQLRKRLTPQYHVTOEKGTESAFEGEYTHHK<br>DPGIYKCVVCGTPLFKSETKFDGSGGWPSFHDVINSEAITFTDD<br>FSYGMHRVETSCSQCAHLGHI FDDGPRPTGKRYCINSAAALSFT<br>PADSSGTAEGSGVASPAQADKAEL  |
| 6454       | 827  | 223  | HRRWLPGLSMSPPRRTLPRPLSLCLSLCLCLLAAALGSAQSGSC<br>RDKKNCKVVSQQLRKRLTPQYHVTOEKGTESAFEGEYTHHK<br>DPGIYKCVVCGTPLFKSETKFDGSGGWPSFHDVINSEAITFTDD<br>FSYGMHRVETSCSQCAHLGHI FDDGPRPTGKRYCINSAAALSFT<br>PADSSGTAEGSGVASPAQADKAEL  |
| 6455       | 1042   | 173  | RVHLATVSASAAWDAIGLFPVRSHMQGSTRRMGMVMTDVHRRFLQL<br>LMTGVLLEWVDKRLQTHCYKVHORNATVDKLEDFINNINSVLE<br>SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF<br>RKALELIIDSETGFASSTNINLVDQLKGKMRKKEAEQVLQKP<br>VQNKWLEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL  |

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|------------|--|--|---|
|            |  |  | LIQGQSCETCGIRMHLPCVAKYFQSNAPRCPHCNDYWPHEIYK VFDPEKERESGVLSNKKSLRSRQH  |
| 6456       | 2  | 555  | RPQSRISIMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA TVEAEALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR RPAPFEVVFVSADGSSQEMLDPMRELHGAWLALPFHDPYRHELR KRYNVTAI PKLVIVKQNGEVITNKGKQIRERGLACFQDWWVEAA DIFQNFVS  |
| 6457       | 23   | 892  | PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLLET IILGKQYSLNIIISVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQATEFNQWKNVVFILQFLLSCLFGLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTSSQLKPKPVGEENICLDLKS  |
| 6458       | 23   | 892  | PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLLET IILGKQYSLNIIISVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQATEFNQWKNVVFILQFLLSCLFGLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTSSQLKPKPVGEENICLDLKS  |
| 6459       | 23   | 892  | PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLLET IILGKQYSLNIIISVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQATEFNQWKNVVFILQFLLSCLFGLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTSSQLKPKPVGEENICLDLKS  |
| 6460       | 23   | 892  | PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLLET IILGKQYSLNIIISVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQATEFNQWKNVVFILQFLLSCLFGLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTSSQLKPKPVGEENICLDLKS  |
| 6461       | 1653   | 360  | LQRTLRITAVGQTHPIAWMAWEPFSLGAFYGPASFITFVNCMYF LSIFIQLKRHPERKYEKTEEQQLAANENGEINHQDSMSLS LISTSALENEHTFHSQQLGASLTLLLYVALWMFGALAVSLYYPL DLVFSFVFGATSLSFSAFFVHHCVNREDVRLAWIMTCCPGRSS YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ GCKLTNLQAAAAQCHANSPLNSTFQLDNSLTEHSMNDIKMHV APLEVQVFRTNVHSSRHHKNRSKGRASRLTVLREYAYDVPTSVE GSVQNGLPKSRGLGNNEGHSRRRAYLAYRERQYNPPQDSSDAC STLKSSRNFEKPVSTTSKKDALRKPAVVELENQKQSYGLNLAI QNGPIKSNQEGPPLGTDSTGNVRTGLWKHETTV |
| 6462       | 3  | 773  | SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH PDSQSMBESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSIIQ YLHAYPYPQMYDPSHPAYRAVSPVLMHSPGAYLSPGFHYPVYG KMSGRETEKVNTPSVNTKTTTESKALDLLQHANQYRSKSPA PVEKATAEREREAEERERDRHS PFQQRHLHHTHHHTHVGMGYPLIP GQYDPFQGLTSAALVASQVAAQASASGMFPQQRRE   |
| 6463       | 2  | 350  | VILCILGGWIFKNADRSMEKKKGEPRTAEARFPWVDEDLKSSD LHQAEDADEWQSEENVEHI PFSSHNYPEKEMVKRSQEFYELL NKRRSVRFISNEQVPMVIDNVIRTAGL   |
| 6464       | 12   | 1154   | GILROKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVQTVLG  |

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|------------|--|--|---|
|            |  |  | LVEPSKLGRTLTTHLMTFDCCYCPFPQCEAISKEPIVMKNL<br>YWIQKNAYSHKENLQNLQETEAKEELLYFKANGGGALVENTTT<br>GISRDTQTLKRLAEETGVHIIISGAGFYVDATHSSETRAMSVEQL<br>TDVLMNEILHGADGTSIKCGIIEIGCSWPLTESERKVLQATAH<br>AQAQLGCPVIIHPGRSSRAFFQIIRILQEAGADISKTVMSHLDR<br>TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR<br>IRRVRLVVEEGCEDRILVAHDINTKTRLMKYGGHGYSHILTNNV<br>PKMLLRGITENVLDKILIENTPKQWLTFK   |
| 6465       | 126  | 1396   | KMTVFFKTLRNHWKKTAGLCLLTWGGHWLYGKHCDNLLRRAAC<br>QSAQVFGNQLIPPAQVVKATVFLNPAACKGKARTLFEKNAAPI<br>LHLSGMDVTIVKTDYEGQAKKLELMENTDVIIVAGGDGTLQEV<br>VTGVLRRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVQHI<br>TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV<br>KVSKEYWLEPLKIKAAHFFSTLKKEWPQTHQASISYTGPTERFPN<br>EPEETPVQRPSPSLYRRLRLASYWAQPDALSOEVSPEVWKDVQ<br>LSTIELSITTRNNOLDPTSKEDFLNICIEPDTISKGDFITIGSR<br>KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFISIDSEYEAMPV<br>EVKLLPRKLQFFCDPRKREQMLTSPQ  |
| 6466       | 1134   | 828  | VARGTELSQLEKAHPADMGRRKSKRKPPPKKMTGTLETQFTC<br>PFCNHEKSCDVKMDRARNTGVISCTVCLLEEFQTPITYLSEPV<br>YSDWIDACEAANQ  |
| 6467       | 301  | 2571   | GELRVLALAHGELACHAVLTASLLSLRSRLMDSMDMYERNVET<br>IKCVVVDGNAVGTRLICARACNATLTQVQLLATHVFTVWAIQ<br>YRVCEVLEERSRDVDDVSLSRLWDTFGDHHKDRRFAYGRSDV<br>VVLCSIANPNLSLHVKTWYPEIKHFCPRAPVILVGCQLDLRY<br>ADLEAVNRARRPLARPIKNEILPPEKGREVAKELGIPYYETSV<br>VAQFGIKDVFDAIRALISRRHLQFWKSHLRNVQRPLQAPFL<br>PFKPPPPPIIVVDPSPSSSECPAHLLEDPLCADVILVLQERVRI<br>FAHKIYLSSTSSSKFYDLFLMDLSEGLGGPSEPGGTHPEDHQGH<br>SDQHSHHHHHHGRDFLLRAASFVCEVDEAGGSGPAGLRST<br>SDGILRGNGTGYLPGRGRVLSWSRAFVSIQEMAEDPLTYKSR<br>LMVVVKMDSSIQPGPFRAVLKYLTYGELDENRDLMHIAHIAEL<br>LEVFDLRMMVANILNNEAFMNQETKAFHVRRTNRVKECLAKGT<br>FSDVTFLDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV<br>FPYTSKSCMRVLELYLTGMFTSSPDLDMDKLIILANRLCLPHL<br>VALTEQYTVTGLMEATQMMVDIDGDVLVFLAQLFHCAYQLADW<br>CLHHICTNYYNVCRRKFRPMKAMSPENQYFEKHRWPPVWYLKE<br>EDHYQRARKEREKEDYLHLKQPKRRWLFWNSSPSSSAASSS<br>SPSSSSAVV |
| 6468       | 3  | 1374   | DAWAGTNMAALAPVGPSPASRGPRLAAGLRLPLMLGLLQLLAEFG<br>LGRVHHLAKDDVRHKVHLNTFGFFKDGVMVNVSSLSLNEPED<br>KDVITIGFSLDRTKNDGFSSYLDEVDVNYCILKKQSVSVTLILDI<br>SRSEVRVKSPPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN<br>QTQKTQDGGKSKRSTVDSKAMGEKSFVHNNGGAVSFQFFPNIS<br>TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA<br>GEIPLPKLYISMAFFFLSGTIWIHLRKRNDVFKIHWLMAAL<br>PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYITHLLKGALLF<br>ITALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES<br>TEEGTTEYGLWKDSLFLVDLLCCGAILFPVWWSIRHLQEASATD<br>GKGKFSRAHFVLLSL  |
| 6469       | 3  | 1374   | DAWAGTNMAALAPVGPSPASRGPRLAAGLRLPLMLGLLQLLAEFG<br>LGRVHHLAKDDVRHKVHLNTFGFFKDGVMVNVSSLSLNEPED<br>KDVITIGFSLDRTKNDGFSSYLDEVDVNYCILKKQSVSVTLILDI<br>SRSEVRVKSPPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN<br>QTQKTQDGGKSKRSTVDSKAMGEKSFVHNNGGAVSFQFFPNIS<br>TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA  |

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|------------|--|--|---|
|            |  |  | GEIPLPKLYISMAFFFFLSGTIWIHILRKRNDVFKIHWLMAAL<br>PFTKSLSLVPHADYHYISSQGFPIEGWAVVYIYTHLLKGALLF<br>ITIALIGTGNWAFIKHILSDKDKKIFMIVIPRRVLNAVYIIIES<br>TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD<br>GKGKFSRAHFVLLSL   |
| 6470       | 2726   | 1437   | AAASGVSSRAADAPVLAQSPASAGNGRPSTFRVPGSRHRHPSAPRS<br>GPLPREDGCRTPGPQLPLPGALLRPRTLLSSAAETGRSRHPT<br>QHPSSGRCRGGTSPSSAAGRPASMAEAEEDCHSDTVRADDE<br>ENESPAETDLQAQLQMFRAQWFMELAPGVSSSNLENRPCCRAARG<br>SLQKTSADTKGQEQAKEEKARELFLKAVEEEQNGALYEAIKFY<br>RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDSKMADLLS<br>YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIPRWVS<br>SDLDLRSLEQLSLVCRGFYICARDPEIWRACLKVGWGRSCIKLV<br>PYTSWREMPLEPRVRFDGVYISKTTYIRQGEQSLDGFYRAWHQ<br>VEYYRYIRFPDGHVMMLTTPPEPQSIVPRLRTR   |
| 6471       | 1750   | 299  | FFFDKMAAGSGVGGKRSSKSDADSGFLGRPTSVDPALRRRRR<br>GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLSEAPN<br>EKLFPVDTGSKKEGLTKKRTKVQKSLLLKKPLRVDLILENTSK<br>VPAPKDVLAHQVPNAKKLRKEQLWEKLAKQGELEPREVRAQAR<br>LLNPSATRAKPGPDTPVERPFYDLWASDNPLDRPLVGQDEFFLE<br>QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLSS<br>AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE<br>ESDGEPEGQGEQGEAGDAEVCPTPARLATTEKKTEQQRREKA<br>VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR<br>RQARREAEADKPRRLGRLYQAPDIDVQLSSELTDSLRTLKPEG<br>NILRDRFKSFQRRNMIEPRERAKFKRYKVKLVKEKRAFREIQ |
| 6472       | 3  | 897  | SCGSDRAQWAMEFFPDVDALFPERITVLDQHLRPPARRPGTTT<br>ARVDLQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY<br>ILKDSSARPAGKGAIGFIKVGYKKLVLDREAHNEVEPLCIL<br>DFYIHESVQRHGHGRELQYMLQKERVEPHQLAIDRPSQKLLKF<br>LNKHYNLETTVPQVNNFVIFEGPFAHQHPPAPSLRATRHSRAA<br>AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN<br>RAPRRATPPAHPPPSSSLGNSPERGLRPFVP  |
| 6473       | 22   | 912  | SSAVEFVWEKMAAEPNRTEIQTFLKRLRAVPTNKACFDGAK<br>NPSWASITYGVFLCIDCSGVHRS LGVHLSFIRSTELDSNNWFQ<br>LRMCQVGGNANATAFFRQHGCTANDANTKYSRAAQMYREKIRQ<br>LGSAAALRHGTDLWIDNMSSAVPNHSPKKDSDFTEHTOPPAW<br>DAFATEPSGTQQPAPSTESSGLAOPHGPNTDLLGTS PKASLEL<br>KSSIIGKKKPAAKKGLGAKKGLGAQKVSSQSFEIERQAQVAE<br>KLREQQAADAKKQAEESMVASMLAYQELQIDR  |
| 6474       | 3  | 462  | LQRQRQHPAAAPAVPVRCTFCFTDIVIMPKRKSPEENTEGKDG<br>KVTQKEPTRRSARLSAKPAPPKPEPKRKTSAKKEPGAKISRG<br>KGGKKEEKQEGAGKEGTAPSENGETKAEIHSRSTVNVSTSRGTP<br>PSTLSVKQIETVRVKGTEN  |
| 6475       | 3  | 462  | LQRQRQHPAAAPAVPVRCTFCFTDIVIMPKRKSPEENTEGKDG<br>KVTQKEPTRRSARLSAKPAPPKPEPKRKTSAKKEPGAKISRG<br>KGGKKEEKQEGAGKEGTAPSENGETKAEIHSRSTVNVSTSRGTP<br>PSTLSVKQIETVRVKGTEN  |
| 6476       | 106  | 1090   | ARAMAQYKGTMRREAGRAMHLLKKRERQREQMEVLKORIAEETIL<br>KSQVDKRFSAHYDAVEALKSSTVGLVTLNDMKARQEALVRE<br>RQLAKRQHLQEQRLQEQRRRQEQRRERKRKISCLSFALDDLDD<br>QADAAEARRAGNLGKNPDVDTSLPDRDREEEENRLREELRQEW<br>EAQREKVKDEEMVTFSYWDGSGHRRTRVRKGNVTQVQFLKKAL<br>QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIARARGK<br>SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF<br>PASRWEAYDPEKKWDKYTIR  |

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|------------|--|--|--|
| 6477       | 227  | 915  | LQGHLMGIMAASRPLSRFWGKNIVCVGRNYADHVREMRSAVL<br>SEPVLFKLPSTAYAPEGSPILMPAYTRNLHHELELGVVMGKRCR<br>AVPEAAAMDYVGGYALCLDMTARDVQDECKKGLPWTILAKSFTA<br>SCPVSASFVPKEKIPDPHKLKLWLKVNGLRQGETSSMIFSIPIY<br>IISYVSKIITLEEGDIILTGTGPKGVGPVKENDEIEAGIHGLVSM<br>TFKVEKPEY   |
| 6478       | 2  | 1495   | FVSSRILPESLASSEASTLEAMGRKEEDDCSSWKKQTNTIRKTF<br>IMEVLGSGAFSEVFLVKORLTGKLFALKCIKKSAPFRDSSLEN<br>EIAVLKKIKHENIVTLEDIYESTTHYYLVMLVSGGELFDRILE<br>RGVYTEKDASLVIQOVL SAVKYLHENGIVHRDLKPENLLYLTP<br>ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA<br>VDCWSIGVITYILLCGYPPFYETESKLFKEIKQGYEFESPFW<br>DDISESAKDPICHLEKDPNERYTCEKALSHPWIDGNTALHRDI<br>YPSVSLQIQKNFAKSKWRQAFNAAVVHMRKLHMLHSPGVPR<br>EVENRPPETQASETSRPSSPEITITEAPVLDHVALPALTLQPC<br>QHGRRTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC<br>SSCLNIGSKGKSSYCEPTLLKKANKKQNFKSEVMVPVKASGSS<br>HCRAGQTGVCILM   |
| 6479       | 3  | 949  | SCRGPQWHPAGGQAGAMELLSALSGLGELALSFSRVLPFPVFDLS<br>YFIVSILYLKYEPAVELSRRIPIASWLCAMLHCFQSYILADLL<br>LGEPLIDYFSNNSSILLASAVWYLIFCPLDLFYKCVCFPLPVKL<br>IFVAMKEVVRVKIAVGIIHHAHHYHHGWFVMIATGWVKGSGVA<br>LMSNFEQLLRGVWKPETNEILHMSFPTKASLYGAILFTLQQTRW<br>LPVSKASLIFITFLFMVSCVKVFLTATHSHSSPFDALGYICPVL<br>FGSACGGDHHDNHGSGSHGPGQAQHSAMPAKSKEELSEGRK<br>KKAKKAD  |
| 6480       | 192  | 514  | DFMSIYFPIHCPDYLRS AKMTEVMNTQPMEEIGLSPRKDGLSY<br>QIFDPDSDFDRCKLKDRLPISIVVEPTEGEVESGELRNWPFEEFL<br>VQDEQDNCEETAKENKEQ  |
| 6481       | 110  | 1131   | KSRMDLDVVMFVIAGGT LAIPILAFVASFLLWPSALIRIYYWY<br>WRRITLGMQVRVYHHEDYQFCYSFRGRPGHKPSILMLHGFSAHKD<br>MWLSVVKFLPKNLHLVCVDMPGHEGTRSSLDLSDIGQVKRIH<br>QFVECLKLNKPPFHLVGTSMGGQVAGVYAAAYPSDVSSLWLVCP<br>AGLQYSTDNQVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC<br>SYVRFKVPQQILQGLVDVRI PHNNFYRKLFL EIVSEKSRYSLHQ<br>NMDKIKVPTQIIWKGQDQVLDVSGADMLAKSIANCQVELLENCG<br>HSVVMERPRKTAKLIIDFLASVHNTDNNKKLD   |
| 6482       | 2517   | 568  | EPVSKVSQSRKAGVPTANIEESQAVEAAMANVPWAEVCEKFA<br>ALALSVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDDE<br>RPEAEDGPGAGDHALGLPAEVEPEGPVAQRAVRLAVIEFHLGV<br>NHIDTEELSAGEEHLVKCLRLRLRRYRLSHDCISLCIQAQNNLGI<br>LWSEREEIETAQAYLESSEALYNQYMKVGSPPLDPTERFLPEE<br>EKLTEQERSKRFEKVYTHNLYLAQVYQHLEMFKAHYCHSTL<br>KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI<br>FGOTGKISATEDTPEAEGEVPELYHQKGEIARCWIKYCLTLMQ<br>NAQLSMQDNIGELDLQKSELRALRKKEDEESIRKKAQVFGT<br>GELCDAISAVEEKVSYLRPLDFEEARELFLGQHYVFEAKEFFQ<br>IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE<br>PLTVDLNPQYYLLVNRQIQFEIAHAYYDMDLKVATADRLRDPD<br>SHIVKKINNLNKSALKYYQLFLDSL RDPNKVFPFEHIGEDVLRPA<br>MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP<br>EAAQETIEVELELSKEMVSLPTKMERFRTKMALT |
| 6483       | 3  | 623  | NSHLLCGLRARAPLSANGREARAMEQRLAEFRAARKRAGLAAQP<br>PAASQGAQTPGEKAEAAATLKAAPGWLKRFLVWKPRPASARAQP<br>GLVQEAAPQGSTSETPWNTAIPLPSCWDQSFLNTITFLKVLW<br>LVLLGLFVELEFGLAYFVLSLFYWMYVGTGRGPEEKKEGEKSAYS  |

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|------------|--|--|--|
| 6484       | 201  | 965  | VFNPGCBAIQGTLTAEQLERBLQLRPLAGR<br>QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPCQQLF<br>MILWLKGVKFNVTVDMTKPEELKDLAPGTNPFFLVYNKELKT<br>DFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFKFSAYIK<br>N <sup>*</sup> QKEANKNFEKSLLEPKRLDDYLTN <sup>*</sup> PLLEIDPDSAEPEPVS<br>RRLFLDGDQLTLADCSLLPKLNI <sup>*</sup> IKVAAKRYRDFDIPAEFSGW<br>RYLHNAYAREEFTHTCPEDKEIENTYANVAKQKS   |
| 6485       | 6  | 1091   | FVDLVRAVEFLPCPDSQKLEKQSSSEESNGSNSMRSILEDEE<br>DEEPPRVLLYHEPRSFEVGLVWHKHKKYFPWPAVVKSVQRDK<br>KASVLYIEGHMNPMMKGF <sup>*</sup> TVSLKSLKHFDCKEKQTLNQAEDF<br>NQDIGWCVSLITDYRVRLGCGSFAGSFLYYAADISYPVRKSIQ<br>QDVLGTKLPLQSKGSPPEPVVGCPLGQRPCKRMLPDRSRAARD<br>RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTLSSSQYVT<br>CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD<br>VLLPEAII <sup>*</sup> CAISAGDEV <sup>*</sup> DKTAEK <sup>*</sup> YIKGPSLSYREKEIFDNQL<br>LEERNRRRR                         |
| 6486       | 10   | 581  | LVLQAGGAHLSPSRVTQGIYMLAFSEMPPDPYSELSDSLTLA<br>GGTGRFSGPLHRAWRMNFRQRMGWI <sup>*</sup> GVGLYLLASAAAFYVVE<br>ISETYNRLALEHIQHPPEELEGTTWTHSLKAQLLSLFFVWVTV<br>IFLVPYLMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV<br>KASNQISRLQLIDT   |
| 6487       | 352  | 863  | SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLCASN<br>YYNGCIFHRNIGKFMVQTGDPGTGRGGNSIWGKKFEDEYSEYL<br>KHNRVGVSMANNGPNTNGSQFFITYGQPHLDMKYTVFGKVID<br>GLETDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ   |
| 6488       | 878  | 241  | TALQEFGTSGPPLSLRPFALPSGTGRFKPLFGARGSPSPRPV<br>MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH<br>KDEFFFGSGGISSCPGGTLLGPPDSVVDVGSTEVTEEIFLEYL<br>SSLGESLFRGEAYNLFHHCNTTFSNEVAQFLTGRKIPSYITDLP<br>SEVLSTPFGQALRPLLDLSIQIQQPGSSSVGRPNQGS   |
| 6489       | 1457   | 375  | KVAKMATALSEEELDNEDYSLNVRREASSEELKAAVRRCLML<br>YHPDKHRDPELKSQAERL <sup>*</sup> PNLVHQAYEVLSDPQTRAIYDIYGR<br>GLEMEGNEVVERRRTPAEIREEFERLQREERRLQORTNPKG<br>ISVGVDATDLFDYDEEYEDVSGSSFPQIEINKMHISQSIAPL<br>TATDTAILSGSLSTQNGNGGGSINFALRRVTSAGWGELEFGAG<br>DLQGPLFGLKLFRLNLT <sup>*</sup> PRCFVTTCALQFSSRGIRPGLTTVLAR<br>NLDKNTVGYLQWHCSSLQVQRPHNRTRACAPSPSPRFLHVP<br>TWDACECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLTTPR<br>SKRRTGGG  |
| 6490       | 3  | 1183   | HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH<br>KDLIHVVSFDFHGRMATCSSDQSVKVDKSESGDNHCTASWKT<br>HSGSVVRVTWAHPEFGQVLASCSFDR <sup>*</sup> TAAVWEEIVGESNDKLRG<br>QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE<br>APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGS<br>DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTD <sup>*</sup> PVHDIAFAPNL<br>GRSFHILAIATKDVRI <sup>*</sup> FTLKPVRKELTSSGGPTKFEIHIVAQFD<br>NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL<br>KNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS |
| 6491       | 3  | 1183   | HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH<br>KDLIHVVSFDFHGRMATCSSDQSVKVDKSESGDNHCTASWKT<br>HSGSVVRVTWAHPEFGQVLASCSFDR <sup>*</sup> TAAVWEEIVGESNDKLRG<br>QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE<br>APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGS<br>DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTD <sup>*</sup> PVHDIAFAPNL<br>GRSFHILAIATKDVRI <sup>*</sup> FTLKPVRKELTSSGGPTKFEIHIVAQFD<br>NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL   |

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|------------|--|--|---|
| 6492       | 34   | 2573   | <p>KGNGSPVNGSSQOGTSNPSLGSNIPSLQNSLNGSSAGRKHS</p> <p>IPFLKSCCCCLFDFPPPPLDQVQEECEVERVTEHGTPKPFRRK<br/> FDSVAFGESQSEDEQFENDLETDPPNWQQLVSRVLLGLKPCBI<br/> KRQEVINELFYTERAHVRTLKVLDQVFYQVRSREGILSPSELRK<br/> IFSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTNFSG<br/> PGEEKLKHAATAFCSNQPFALMIKSRQKDSRFQTFVQDAESN<br/> PLCRRLLQKDI IPTQMORLT KYPLLLDNIAITYTEWPTEREKVKK<br/> AADHCRQILNYVQAVKEAENKORLEDYQRRLLDTSSLKLEYPN<br/> VEELRNLDLTKKKMIHEGPLVWKVNRDKTIDLYTLLEDILVLL<br/> QKQDDRLLVLRCHSKILASTADSKHTFSPVIKLTSTVLVRQVATDN<br/> KALFVISMDSNGAQIYELVAQTVSEKTVWQDLICRMAASVKEQS<br/> TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG<br/> LESTLISSKQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLLK<br/> EVGEDYQIAIPDShLPVSEERWALDALRNGLLKQLLVQQLGLT<br/> EKSQOEDWQHFPYRTASQGPQTD SVIQNSENIKAYHSGEGHMP<br/> FRGTGDIATCYSPTSTESFAPRDSVGLAPDSQASNILVMDH<br/> MIMTPEMPTMEPEGGLDSDGEHFFDAREAHSDENPSEGDAVNK<br/> EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSITLQPMGTGIP<br/> AVESTHQQHSPOPTHSDGAISPTPEFLVQQRWGAMEYSCFEI<br/> QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYITLCQRLAGS<br/> ALTDKHSKDS</p> |
| 6493       | 557  | 1147   | <p>TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAVPSPSRSEVA<br/> KEQNTGHNINGVQPSGTSKTLYSTNMALSSSPGISAVQLVRT<br/> VGHTTTNHLIPALCTSSPQTLPMNNSCLTNAVHLNNVSVVSPVN<br/> VHINTRTSAPSPALKLATVAASMDRVPKVTSSAIISSIARENH<br/> EPERLGLNGIAETTVAMEVT</p>   |
| 6494       | 2425   | 1052   | <p>AVAGGARPCSTPSSPHRRCRHRPRPLPRPPAAINSASAVYVLD<br/> LKGKVLICRNYRGDVMSEVEHFMPILMEKEEEGMLSPILAHGG<br/> VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVQVFSEYFKEL<br/> EEESIRDNFVYIYELLDELMDFGYPQTTDSKILQEYITQEGHKL<br/> ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLVLSAN<br/> GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS<br/> VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK<br/> PLIWIESVIEKHSHSRIEYMIKAKSQPKRRSTANNVEIHIPVFN<br/> DADSPKFKTTVGSVKWVPENSEIVWSIKSPGGKEYLMRAHFGL<br/> PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL<br/> PWVRYITQNGDYQLRTQ</p>  |
| 6495       | 2425   | 1052   | <p>AVAGGARPCSTPSSPHRRCRHRPRPLPRPPAAINSASAVYVLD<br/> LKGKVLICRNYRGDVMSEVEHFMPILMEKEEEGMLSPILAHGG<br/> VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVQVFSEYFKEL<br/> EEESIRDNFVYIYELLDELMDFGYPQTTDSKILQEYITQEGHKL<br/> ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLVLSAN<br/> GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS<br/> VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK<br/> PLIWIESVIEKHSHSRIEYMIKAKSQPKRRSTANNVEIHIPVFN<br/> DADSPKFKTTVGSVKWVPENSEIVWSIKSPGGKEYLMRAHFGL<br/> PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL<br/> PWVRYITQNGDYQLRTQ</p>  |
| 6496       | 247  | 559  | <p>LRAVSLPLQLVLPYYSIHSIFCIMFLCAQEWLTLGLNVPLLFY<br/> HFWRYPHCPADSSelayDPPVVMNADTISYQKEAWCKLAFYLL<br/> SFFYYLYCMIYTLVSS</p>   |
| 6497       | 1053   | 352  | <p>ANTQICRLCPRRHLHPFCGAKMGNGTEEDYNFVKVVLIGESGV<br/> GKTNLLSRFTNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD<br/> TAGLERYRAITSAYYRGAVGALLVFDLTKHQTAYAVVERWLKELY<br/> DHAEATIVVMLVGNKSDLSQAREVPTTEARMFAENNGLLFLETS<br/> ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGSQAQAGQ</p>   |



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|------------|--|--|--|
| 6498       | 2636   | 272  | <p>BPGPGKKRACISL</p> <p>SLRLCPWGTHTLAGPTTMRLLSSLLALLRPALPLILGLSLGCSLSL<br/> LRVSNIQGEGEDPCVEAVGERGGQNPDSRRRLDQSDDFKPRI<br/> VPPYRDPNKPYPKVLRTYIQTGLSRRERLLVAVLTSRATLSTL<br/> AVAVNRTVAHHFPRLLYFTGQRGARAPAGMVVSHGDERPAWLM<br/> SETLRHLHTHFGADYDWPFIQDDTYVQAPRLAALAGHLSINQD<br/> LYLGRAEEFIGAGEQARYCHGGFYLLSRSLLLRLRPHLDGCRG<br/> DILSARPDDEWLGRCLIDSLGVGCVSQHQCCQYRSFELAKNRDPE<br/> KEGSSAFLSAFAVHPVSEGLMYRLHKRFSALELERAYSEIEQL<br/> QAQIRNLTVLTPEGEAGLSNPVGLPAPFTFHSRFEVLGWDYFTE<br/> OHTFSCADGAPKCPQGASRADVGDALETALEQLNRRYQPRLRP<br/> QKQRLNGYRRFDARGMEYTLDDLLECVTQRGHRRALARRVSL<br/> LRPLSRVEILPMYPVTEATRVQLVPLLVAAEAAAAPAFLEAFAA<br/> NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAEELERRY<br/> PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTITVWTRPG<br/> PEVLNRCRMNAISGWQAFPPVHFQEFNPALSPORSPPGPGGAP<br/> DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAG<br/> ELAGQEEEEELEGLEVMDFLRPSGLHLFRAVEPGLVQKFSLRD<br/> CSRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAOKST</p> |
| 6499       | 3  | 2040   | <p>SCSADTRPSGQANPTVGLRAAAGAFRTGSPLAIGPETPQVACL<br/> GHPPVRPQVSGGPGAMPDPAHLFPFFYGSISRAEAEHLKLKLAGM<br/> ADGLFLLRQCLRLSGGYVLSLVHDVRFHHPFIERQLNGTYAIG<br/> GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPFGLEPOPGVFD<br/> LRDAMVRDYVRQTKLEGEALAEQAIISOAPQVEKLIATTAHERM<br/> PWYHSSLTREBAERKLYSGAQTGKFLLRPRKEQCTYALSIIYG<br/> KTVYHYLISQDKAGKYCIEGTFKFDTLWQLVBYLKLKADGLIYC<br/> LKEACPNSASNASGAAAPTLPAPHSTLTHPQRRIDTLNSDGYT<br/> PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKFLKRDNL<br/> LIADIELGCGNFGSVRQGVYMRKKQIDVAIKVLKQGTEDKADTE<br/> EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGQPLHKF<br/> LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL<br/> VNRHYAKISDFGLSKALGADDSYTTARSAGKWLKMYAPECINF<br/> RKFSRSRSDVWSYGVMTWEALSYGQKPYKKMKGPVMAFIEQGR<br/> MECPPECPPELYALMSDCWIYKWEDRPDFTLVEQMRACYYSLA<br/> SKVEGPPGSTQKAEAAACA</p>   |
| 6500       | 1773   | 726  | <p>TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK<br/> MLSESSSFLKGVMLSIFCALITMLGHIRIGHGNRMHHHHHHL<br/> QAPNKEDILKISEDERMELSKSFRVYCIILVVKPDVSLWAAVKE<br/> TWTKHCDKAEFFSSENVKFESINMDTNDMMLMRKAYKYAFDK<br/> YRDQYNWFLLARPTTFALLENLKYFLLLKDPSPQPFYLGHTIKSG<br/> DLEYVGMEGGIVLSVESMKRLNLSLNIPEKCPQEGGMIWKISED<br/> KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN<br/> QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ</p>   |
| 6501       | 1  | 570  | <p>LVGMSGGGTETPVGCEAAPGGGSKKRDLSLGTAGSAHLIIKDLGE<br/> IHSRLLDHRPVIQGETRYFVKEFEERKGLREMRVLENLKNMIHE<br/> TNEHTLPKCRDTMRDLSQVLQRLQAANDSVCRLLQOREQERKKI<br/> HSDHLVASEKQHMLQWDFNMKEQPNKRAEVDEEHRKAMERLKEQ<br/> YAEKEDLAKFSTF</p>  |
| 6502       | 213  | 1650   | <p>AGNKPDPWAGRNRTAVLPDVSVFHREDVGNWRSWLQSSYQAVKE<br/> KSSEALEFMKRDLTFTQVQVQHD TACTIAATASVVKEKLATEGS<br/> SGATEKMKKGLSDFLGVISDTFAPS PDKTIDCDVITLMGTPSGT<br/> AEPYDGTKARLYSLQSDPATYCNEPDGPPFLDAWLQSFCLCEK<br/> KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHOLEQ<br/> EQARRDALKQRAEQSISEEPGWEEEEELMGISPISPKEAKVPV<br/> AKISTFPEGEPGPQSPCBENLVTSVEPPAEVTPSESSESISLVT<br/> QIANPATAPPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP</p>   |

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|------------|--|--|---|
|            |  |  | IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG<br>KSTPSNNGKGSSTDISDWEKDFDLDMTEEEVQMALSKVDASG<br>EVSQGGSGSEGSEPNPGCESSPQPAQLSPQEGPCSCLR  |
| 6503       | 213  | 1650   | AGNKPDPWAGNRRTAVLPDVSVFHREDVGVWRSWLQQSYQAVKE<br>KSSEALEFMKRDLEFTQVVOHDTACTIAATASVVKEKLATEGS<br>SGATEKMKKGLSDPLGVISDTFAPSPDKTIDCDVITLMGTPSGT<br>AEPYDGTAKRLYSLOSDPATYCNEPDGPELFDWLWSQFCLEEK<br>KGEISELLVGSPIRALYTKMVPAAVSHSEFWHRYFYKVHOLEQ<br>EQARRDALKQRAEQSISEEPGWEEEEELMGISPISPKEAKVPV<br>AKISTFEGEPGQSPCFENLVTSVEPPAEVTPSESSSISLVT<br>QIANPATAPPEARVLPKDLSQLLEASLEEQGLAVDVGETGSPSP<br>IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG<br>KSTPSNNGKGSSTDISDWEKDFDLDMTEEEVQMALSKVDASG<br>EVSQGGSGSEGSEPNPGCESSPQPAQLSPQEGPCSCLR |
| 6504       | 2131   | 1294   | GKVCVLAHVWCLSLSPPPAGMKTPNAQEAEGQOTRAAAGRATG<br>SANMTKKKVSQKKQGRPPSSQPCRNIVGCRISHGWKEGDEPITQ<br>WKGTVLDQVPINPSLYLVKYDGDICVYGLELHRDERVLSLKILS<br>DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA<br>PIMKAWFYITYEKDPVLYMYQLDDYKEGDLRIMPESSESPPTE<br>REPQGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF<br>DDDFHIYVYDLVKKS   |
| 6505       | 2131   | 1294   | GKVCVLAHVWCLSLSPPPAGMKTPNAQEAEGQOTRAAAGRATG<br>SANMTKKKVSQKKQGRPPSSQPCRNIVGCRISHGWKEGDEPITQ<br>WKGTVLDQVPINPSLYLVKYDGDICVYGLELHRDERVLSLKILS<br>DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA<br>PIMKAWFYITYEKDPVLYMYQLDDYKEGDLRIMPESSESPPTE<br>REPQGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF<br>DDDFHIYVYDLVKKS   |
| 6506       | 1  | 1350   | EVSPTSCCLTVAVADPGVSEGFGRGAGCEMPGRGRCPDCGST<br>ELVEDSHYSQSQLVCSDCGCVVTEGVLTTFSDENLREVITYSR<br>STGENEQVRSRQGRLLRRVRLCRVLQLPPTFEDTAVAYYQAY<br>RHSGIRAAARLQKKEVLVGCCLVITCRQHNWPLTMGAICTLLYAD<br>LDVPSSTYMQIVKLLGLDVPSLCLAEVLKTYCSSFKLFQASPSV<br>PAKYVEDKEKMLSRMTQLVELANETWLVTRHPLPVITAATPLA<br>WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA<br>EQLAWLRVRLDKRSVVKHIGDLLQHRQSLVRSFRDGTAEVET<br>REKEPPQWGGQGEVGNNSLGLPQGRPASPALLLPPCMLKS<br>PKRICPVPPVSTVTGDENISDSEIEQYLRTPOEVRDFQRAQAAR<br>QAATSVPNPP                               |
| 6507       | 1878   | 929  | RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA<br>ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD<br>IAWIAADEEETIARVRSRTRPLRHTWKPSPLIVMQRNASVPNLR<br>GSEERLLALKKPPALPALSRTTELQDELSHLRSQIAKIVAADAAS<br>ASLTDFLSPGSSNVSSPLPCFGSSFHSTTSFVSDITEETEVE<br>VPELPSVPLLCSASPECKPEHKAACSSSEEDDCVSLSKASSFA<br>DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRKFKALKE<br>EDISRKGN  |
| 6508       | 862  | 342  | WEARKRPQRNPSEERREVRVPPPHLQGRSGLEPGTFRKMAAAR<br>SLGRVLPFGSSVFLCDMQEKFHNIAYFPQIVSVAARMLKNTTL<br>DLLDRGLQVHVVDACSSRSQVDRVALARMRQSGAFLSTSEGL<br>ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGGNSLLH   |
| 6509       | 2  | 1053   | FVINPRGGRKRRRQAQAVTQAATRASGTPSPRDGTMTQGLSVAN<br>KAPGTEGQQQVHGEKKEAPAVPSAPPSYEATSGEGMKAGAFPP<br>APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHDLFTTFSWDQKV<br>RRVFRVKVYTIILLIQLLVTLAVVALFTFCDPVKDYVQANPGWY<br>ASYAVFPATYTLTACSGPRRHFPWNLLLTFTLSMAYLTGML   |

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|------------|--|--|---|
|            |  |  | SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFSTSCQGVLFVL<br>LMTLFFPSGLILAILLPFQYVPWLHAYVAALGAGVFTLPLALDTQ<br>LLMGNRRHSLSPEEYIFGALNIYLDIIYIPTPLQLFGTNR  |
| 6510       | 37   | 1156   | PCALDGCPCQRAVHPLSSAMGLLAPLKTQFVLHLLVGFVFFVS<br>GLVINVFQCLCTALWPVSKQLYRRRLNCRLAYSLWSQLVMLLEWV<br>SCTECTLFTDQATVERFGKBHAVIILNHNFEIDFLCGWTMCERF<br>GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV<br>EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMVEAAKGLPVV<br>KYHLLPRTKGFTTAVKCLRGTVAAVVDVTLNFRGNKNPSLLGIL<br>YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY<br>NQKGMFPGEQFKPARRPWTLNLFSLWATILLSPLFSFVLGVFAS<br>GSPLLILTFILGFVAGNGHCR  |
| 6511       | 2541   | 1425   | GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGKK<br>TNATNFSDIVKQGYVMKSRKLGIIYRRCLVFRKSSSKGPORLE<br>KYPDEKSVCLRGCPKVTETISNVKCVTRLPKETKRQAVAIIFTDD<br>SARTFTCDSELEAEWYKTLVSVECLGSRLNDISLGEPLDLAGPV<br>QCEQTDRFNVFLPCPNLDVYGECKLQITHENIYLDIHNPRVK<br>LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFQTQGEQEI<br>YQRVHSATLAI AEQKRVVLEMEKNVRLNKGTEHYSYPCPTPT<br>MLPRSAWYHHITGSONIAEASSYAGEGYGAAQASSETDLLNRFI<br>LLKPKPSQDSDSEAKTPSQ  |
| 6512       | 159  | 807  | FGKSTWFPFLSRSLRVASGRSCKLGHGGYTGSFGFGEPRDSGA<br>EVPSGSGRATGCGRGVGRARQGRAPGSSIWKEPRMVCTRKT<br>TLVSTCVILSGMTNIIICLLYVGWVTNYIASVYVRGQEPADKKL<br>EEDKGDTLKIIERLDHLENVIKQHQEAPAKPEEAEAPFTDSS<br>LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRPLDRP  |
| 6513       | 2  | 756  | FVSPGPGFSLAQLNLIWQLTDTKQLVHVSFAEGQDQGSAYANRTA<br>LFPDLAQNASLRLQVRVVADEGSFTCFVSIIRDFGSAVSLQV<br>AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGO<br>GVPLTGNVITTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV<br>LQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF<br>SPEPGFSLAQLNLIWQLTDTKQLVHVSFAEGQDQGSAYANRTALF<br>PDLAQNASLRLQVRVVADEGSFTCFVSIIRDFGSAVSLQVAA<br>PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGOV<br>PLTGNVITTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV<br>QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP<br>EPGFSLAQLNLIWQLTDTKQLVHVSFTTEGR  |
| 6514       | 985  | 302  | VGIPGPTISSAAEMDLDLDEELRYSLATSRKMGRRRAQQESA<br>QAENHLNGKNSSLTGTETSSAKLPRCRQGGWAGDSVKASKFRR<br>KASEEIEDFRLRPQSLNGSDYGGDIPIIPDLEEVQEEDFVLQVA<br>APPSIQIKRVMTYRDLNDLMKYSIAIQTLDGEIDLKLLTKVLAP<br>EHEVRERNPSWQDDVGDWDHDLFTVSSVLTWDPLQTEKEDP<br>AGQARHT   |
| 6515       | 1345   | 305  | GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIV<br>VHGGGAGPISKDRKERVHQMVRATVGYGILREGGSAVDAVEG<br>AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKLSAGAVSA<br>VQCIANPIKLARLVMEKTPHCFITDQGAQFAAAMGVPEIPGEK<br>LVTERNKKRLEKEKHEKGAQKTDQCNLGTGVAVALDCKGNVAY<br>ATSTGGIIVNMVGRVGDSPCLGAGGYADNDIGAVSTTGHEGIL<br>KVNLRALTLEFHIEQGXVBEAADLSLGYMKSRVKGLGGLIVVSK<br>TGQWVAKWTSTSPWAAAKDGKLFHFGIDPDDTTITDLP<br>FRRLRYLGQDATAARDLRTRGQGYCPSATARQQVLVSALQQL<br>KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR<br>KPGIAMKLEPFLSLGNTFNSITLQDEIHDDQGTTFVIFQERQLQI<br>LEKLNELLTNMEBLKEEIRFLKEAIPKLEEYIQDBLGKKITVHK<br>ISPQHRARKRLPTIQSSATSNSEAESEGGYITANTDTERQS |

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|------------|--|--|--|
|            |  |  | FPVPKAFNTRVEELNLDVLLQKVDHLRMSSESGKSESFELLRDHK<br>EXFRDEIEFMWRFRARAYGDMYELSTNTQEKHYANIGKTLSERA<br>INRAPMNGHCHLWYAVLCGYVSEFEGIQNKINYGHLFKEHLDIA<br>IKLLPEEPFLYLKGRYCYTVSKLSWIEKKMAATLFGKIPSSSTV<br>QEALHNFLEKAEELCPGYSNPNMYLAKCYTDLEENQNALKFCNL<br>ALLLPTVTTKEDKEAQKEMQKIMTSLKR  |
| 6517       | 3  | 1414   | GRVWGGSSSLNAMVYVRGHAEDYERWQRGARGWDYAHCLPYFR<br>KAQGHGELGASRYRGADGPLRVSRGKTNHPLHCAFLATQQAGYP<br>LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA<br>EAEITLVSRLVEGTRAVGVEYVKNQSHRAYASKEVILSGGAIN<br>SPQLMLLSGIGNADDLKKLGIPVVCNLPVGVQNLQDHLIEYIQ<br>ACTRPITLHSAQKPLRKVCIGLEWLWKTGEGATAHLETGGFIR<br>SQPGVPHPDIQFHELPSQVIDHGRVPTQOEAYQVHVGPMTGTSV<br>GWLKLRANPDHPVQPNYLSTETDIEDFRLCVKLTREIFAQE<br>ALAPFRGKELQPGSHIQSDKEIDAFVRKADSAYHPSCTCKMGQ<br>PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGLNAPTIMIA<br>EKAADIIKGQPALWDKDVVYKPRTLATQR   |
| 6518       | 242  | 1098   | PAWNPGSEPRTRVRPRARSFPLPPPRAPRRRRHRLRAVPGPSR<br>RHRERRRAPPSTMGDAGSERSKAPSLPPRCPCGFWGSSKTN<br>LCSKCFADFKKQPDSDSAPSTNSQSDLFSEETSDNNNTSIT<br>TPTLSPSQPLPTELNVTSPSKECGPCTDTAHVSLITPTKRSC<br>GTDSQSENEASPVKRPRLLENTSESTSRSKOKSRRRCFCQCT<br>KLELVQQLGSCRCGYVFCMLHRLPEQHDCTFDHMGGRGEEAM<br>KMKVLDKRVGRSCQRIGEGCS   |
| 6519       | 3  | 1113   | ERKMAEPPSPVHCVAAPATATVSEKEPFGKLQLSSRDPPGSL<br>AKKVRTEKKAPRRVNGEGSGGNSRQLQPPAAPSPQSYGSPAS<br>WSFAPLSAAPSPSSSRSSFSFAGTAVPSSASASLSQPGPRKLL<br>VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEREKERRRHGL<br>GGAREAGGASREENGVEKPLPRDKIKDKIKERDKEREKKKKHK<br>VMNEIKKENGVEKILLKSGKEPKTNIEDLQIKKVKKKKKKKHK<br>ENEKRRPKMYSKSIQTICSGLLTDVEDQAAGILNDNIKDYVG<br>KNLDTKNYDSKIPENSEPFPVSLKEPRVQNNLKRDLTLEFKQLI<br>HIEHQPNGGASVHCLQ   |
| 6520       | 3  | 1113   | ERKMAEPPSPVHCVAAPATATVSEKEPFGKLQLSSRDPPGSL<br>AKKVRTEKKAPRRVNGEGSGGNSRQLQPPAAPSPQSYGSPAS<br>WSFAPLSAAPSPSSSRSSFSFAGTAVPSSASASLSQPGPRKLL<br>VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEREKERRRHGL<br>GGAREAGGASREENGVEKPLPRDKIKDKIKERDKEREKKKKHK<br>VMNEIKKENGVEKILLKSGKEPKTNIEDLQIKKVKKKKKKKHK<br>ENEKRRPKMYSKSIQTICSGLLTDVEDQAAGILNDNIKDYVG<br>KNLDTKNYDSKIPENSEPFPVSLKEPRVQNNLKRDLTLEFKQLI<br>HIEHQPNGGASVHCLQ   |
| 6521       | 184  | 1798   | KLFKATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP<br>IRRTVNSTRETTPPKSLAEGEEKPEPDISSEESVSTVEQENE<br>TPPATSSAEQPKGEPENEEKEENKSSEETKKDEKQSKKEKK<br>VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC<br>FOKSGASVVAIRKYIHKYPSLELERRGYLLKQALKRELNRGVI<br>KQVKGKASGSFVVVQXSRKTPQKSRNRNRSSAVDPEPQVKLE<br>DVLPLAFTRLCEPKEASYSIRKYVSQYYPKLRVDIRPQLLKNA<br>LQRAVERGQLEQITGKGASGTQFKKSGEKPLLGSLMEYAILLS<br>AIAAMNEPKTCSTTALKKYVLENHPTNSNYQMHLKKTLQKCB<br>KNGWMEQISGKGSFTQLCFPYYPSPGVLPFKKEPDDSRDEDE<br>DEDESSEEDSEDEPPPKRRLQKKTAKSPGKAASVKQRGSKPA<br>PKVSAQRGKARPLPKKAPKAKTPAKTRPSSVVIKPSGGSS<br>KKPAT SARKE |
| 6522       | 1042   | 392  | NKWLRLPSRSHRTPESGRVLSLFRLLPPPGMALSGSTPAPCWEED  |

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|------------|--|--|---|
|            |  |  | ECLDYVGMISLHRMFEVVGQQLTECELELLAFLLDEAPGAAGGL<br>SRARSGKLKLLLELERRGQCDESNLRLLGQLLRVLARHDLPLHLA<br>RKRRRPVSPERYSYGTSSSSSKRTGECRRRRQSSSSANSQQGSP<br>PTRQRRRSRGRPSGGARRRRRGPPHPSSSSQSPDPLPKAK   |
| 6523       | 2  | 1097   | ASCQTRRRRTAALDSGERIAGRRSPIALAMASNFNFDIVKQGYVKI<br>RSRKLGI FRRCLVFKKASSKGPRLLEKFPDEKAAFRNFHKVT<br>ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEWC<br>KHLCECLGTRLNDISLGEFDLLAAGVQREONERFNVYLMPTPN<br>LDIYGECTMQITHENIYLWDIHNKVKLVMPWPLSSLLRRYGRDST<br>WFTFESGRMCDTGEGLFTFQTREGEIMYQKVHSATLAI AEQHER<br>LMLEMEQKARLQTSLTEPMTLSKSI SLPRSAWWHHITRQNSVGE<br>IYSLQGNHENRHSDLTGKSKCTSENRFLEENAPLVMYGITHHLF<br>MDTSTCKVVDHLE   |
| 6524       | 2  | 1097   | ASCQTRRRRTAALDSGERIAGRRSPIALAMASNFNFDIVKQGYVKI<br>RSRKLGI FRRCLVFKKASSKGPRLLEKFPDEKAAFRNFHKVT<br>ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEWC<br>KHLCECLGTRLNDISLGEFDLLAAGVQREONERFNVYLMPTPN<br>LDIYGECTMQITHENIYLWDIHNKVKLVMPWPLSSLLRRYGRDST<br>WFTFESGRMCDTGEGLFTFQTREGEIMYQKVHSATLAI AEQHER<br>LMLEMEQKARLQTSLTEPMTLSKSI SLPRSAWWHHITRQNSVGE<br>IYSLQGNHENRHSDLTGKSKCTSENRFLEENAPLVMYGITHHLF<br>MDTSTCKVVDHLE   |
| 6525       | 1  | 1859   | GESPFSEBESIEFNPSSSGRSARTVSSNSFCSDDTGWPSQSQSV<br>PVKTPSDAGNSPIGFCPSDEGFTKKCTIGMVGEISIQSSRYK<br>KESKSGLVKPGSEADFSSSSSTGSI SAPEVHMSTAGSKRSSSSR<br>NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP<br>SYAPSSPSSSSSGSYKSGDCSPIMRRSGRYMSCGENHGVPPNP<br>EQYLTPLQKEVTVRHLKTKLESERRLHERESEIVELKSQLAR<br>MREDWIEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD<br>KGIQKYFVDINIQNKLESLLQSMEMAHSGSLRDELCLDFPCDS<br>PEKSLTLNPPPLDTMADGLSLEEQTGEGADRELLVGDSTIANST<br>LFDEIVTATTESGDLELVHSTPGANVLELLPIVMGOEESVUV<br>ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPD<br>MESFPPELSALVVDLTPRNPNSAII LSPVETPYANVDAEVHANR<br>LMRELDFAACVEERLDGVIPLARGGVVRQYWSSFLVDLLAVAA<br>PVVPTVLWAFSTQRGCTDPVYNIGALLRGCCVVALHSLRRTAFR<br>IKT  |
| 6526       | 2  | 2034   | SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQOLEEAYSSGKGCN<br>GRVVP TDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGD<br>NKYVPYSESFSQVLEETYMLAVTLDEWKKLESNREIIILHNP<br>KLMVHYQPVAGSDWGSTPMEQGRPRTVKRGVENISVDIHCGEP<br>LQIDHLV FVVGIGPACDLRFRSIVQVNDFRSVSLNLLQTHFK<br>KAQENQIGRVEFLPVNWHSPHSTGVDVLDQRITLPSINRLRH<br>FTNDTILDVFPYNSPTYCQITVDTVASEMNRIYTLFLQRNPDFK<br>GGVSIAGHSLGSLILFDILTNRQDSLGDIDSEKGSINIVMQGD<br>TPTLEEDLKKLQLEFFDI FEKEKVDKEALALCTDRDLQEIGIP<br>LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN<br>TRNGDYLDVGIGQSVSKYPRLIYKPEIFFAFGSPIGMFLTVRGL<br>KRIDPNYRFPTCKGFFNIYHPDPVAYRIEPMVVGVEFEPMLI<br>PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTTRAPY<br>PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPIV<br>GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV<br>LKEIYQTQGIFLDQPLQ |
| 6527       | 1  | 922  | GNVPLLSRILPSACKIYKQGINIRLDTTLIDFTDMKCQRGDL<br>FIFNGDAAPSESFVVLONEQKVYQRIHHEESEMETEEVDILMS<br>SDIYSATLSTKSI SFTRAQTGWLFREDKTERVGNFLADFYLVNG  |

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|------------|--|--|--|
|            |  |  | LVLESRRKREHLSEEDILRNKAIMESLSKGGNIMEQNFEPIRRO<br>SLTPPPQNTITWSEYISAENGKAPHLGRELVCCKESKTKPKATIA<br>MSQEFPLGIELLLNVLEVVAPFKHFNKLREPVQMKLPPGFPVKL<br>DIPVFTTITATVTFQEFYRDEFDGSIPTIPDDYKEPDSRFDDL   |
| 6528       | 1  | 1073   | LTGPAAAEPRCAADAGMKRALGRRKGWVLRRLKILFCVLGLYIA<br>IPFLIKLCPGIQAKLIPLNFVRVPYFIDLKKPQDQGLNHTCNYY<br>LQPEEDVTIGVWHTVPAVWVKNAQGGKQDMWYEDALASSHPILY<br>LHGNAGTRGODHRVELYKVLSSLGYPVVTFDYRGWGDVSGTPSE<br>RGMTYDALHVFDMIKARSGDNVPYIWGHSLGTGVATNLVRRLC<br>RETPPDALILESFTNIREEAKSHPFVVIYRYPGDFWFFLDPI<br>TSSGIKFANDENVKHISCPILLHAEDDPVVPFQLGRKLYSIAA<br>PARSRFDKVKVQFVPHSDLGVRHKYIYKSPELPRILREPLGKSE<br>PEHQH  |
| 6529       | 363  | 2215   | THIRYNKIGVVKTMSCGNEFVETLKKIGYPRADNLNGEDFDWLF<br>EGVEDESLKWFQGNVNEQNVLSERELEAFSILQKSGKPILEGA<br>ALDEALKTKCTSDLKTPRLDDKELEKLEDEVQTLKLNKLIQR<br>RNKQQLMASVTSKSLRLNAKEEATKLLKQSQGILNAMITKIS<br>NELQALTDEVQQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSE<br>EQSTAALTLYTKQFFQGIHEVVESSNESQFFNFKIQTSPSICD<br>NQEILEERLEMARLQLAYICAOHLIHLKASNSSMKSSIKWAE<br>ESLSHLSLTKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA<br>VVRENAQLLNMPPVVGDFDLQIAKQDYTTARQELVNLQIKQKA<br>SFELLQLSYETELRKHRDIYRQLENLVQELSQSNMMLYKQLEML<br>TDPSPVQQINPRNTIDTKDYSTRHLYQVLEGENKKLEFLTHGN<br>LEEVAEKLKQNISLVQDQLAVSAQEHFFLSKRNKDVDMLCDTL<br>YQGGNQLLLSDQELTEQPHKVESQLNKLNLHLLTDILADVKTTRK<br>TLANNKLHQMEREFVYFLKDEYLDKDIVENLETQSKIKAWSLE<br>D   |
| 6530       | 128  | 2986   | GAHHKGAIVQVHPLLPSSSTIMIHDLCLVFPAPAKAVVYVSDIQ<br>ELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA<br>ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAQR<br>INSAPQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPOSNIL<br>FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVI<br>SQDLVQVEVLLLRVIRIRAPIMRMRTGTQMPIYVTGITNHQNP<br>FSGNAVPGLTFFHWSVTKRUVLDLGRHHEASIRLPSQYNFAMNV<br>LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKIQ<br>LLNPEIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDPGEKVPV<br>VHDEKGFSLAGSMIGTSTIEVIAQEPFGANQTIIVAVKVPVS<br>YLRVMSFVLHTQNKALVAVPLGMTVTFTVHPHDNSGDPVFAH<br>SSVLNFATNRDDFVQIGKPTNNTCVVTVSVGLTLRLRVWDAKH<br>PGLSDFMPLPVLAISPELSGAMVVGDLCLATVLTSLGLESGT<br>WSSSANSILHIDPKTGAVARAVGSVTYVEVAGHLRTYKEVVV<br>SVPQIRIMARHLPIQTSFORATASKVIVAVGDRSSNLRGECTPT<br>QREVIQALHPETLISCQSQFPAVDFPSPQDVFTVEPQFDTALG<br>QYFCSITMHLRTDKQRKHLNKKKTALVVSASLSSSHFSTEQVGA<br>EVPFSPGLFADQAEILLNHYTSSEIRVFGAPEVLENLEVKSGS<br>PAVLAFAKEKSPGWPSFITTYTVGLDPAAGSQGPLSTTLTFSSP<br>VTNQAIAPVTVAFFVDRRGPGPYGASLFQHFLLDSYQVMFFTLF<br>ALLACTAVMIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS<br>SPTSPNALPPARKASPPSGLWSPAYASH |
| 6531       | 845  | 1425   | PSASTPPASDPDPDIRTCHFLVEDPSVGCISGSEKCTISS<br>SLCMVITYYDVKVRFIVRGCGQYISYRCQEKNTYFAEYWYQA<br>QCCQYDYCNSSWSSPQLQSSLEPHDRPLALPLSDSQIQWYQAL<br>NLSLPLPNFHAGTEPDGLDPMVTLNLNLGLSFAELRRMYLFLNS<br>SGLLVLPQAGLLTPHPS   |
| 6532       | 2  | 954  | AAGPPSEVVNQDSLFPPEPEGPAPQVLLGPGGGLIKGVAPPTL  |

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|------------|--|--|---|
|            |  |  | ITDSTGTHLVLTVTNKNHSPGLSRGSPQPFSSQPGSPAPAPSA<br>QMDLEHPLQPLFGTPTSLKKKEPPGYEAMSQQPKQENGSSSQ<br>QMDDLFDILIQSGEISADFKEPPSLPGKEKPSKTVCSPLAAQ<br>PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP<br>EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL<br>DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD<br>LQLHWDSC   |
| 6533       | 1798   | 373  | STISWILARVEPPRRSSGVGAARLRFPGGSRLRARACVLALAVL<br>ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGIEG<br>GAKLCSKLKAEKFLQKVEAGKVAIKESHQSTNLTHLRAIVES<br>AENLEEVSVLHVFGYDTLGEKQTLVVDVWANGGHTWVKAIGR<br>KAEALHNIWLRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII<br>FAFYNSVSSPMAEKLKENGISVRGDIVAVNALLDHPEELQPS<br>ESDDEGPPELLQVTRVDRENILASVAFPEIKVDVCKRVNLDITT<br>LITYVSALSYGGCHFIKFKVLTEQAEQERKEQVLPQLEAFMKD<br>KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS<br>ERARLVAASSKINSRSLTIFGTGDTLKAITMTANSFVRAANNO<br>GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH |
| 6534       | 47   | 596  | KATRFISAFFVLNKGVSFAKLPHTSWSWSLQTLSEFLFSGDLA<br>EKSQCFFPCSMLELIPLLGIHFVLRRTARAQSVTPDIHITVS<br>EGASLELRNYSYGATPYLFWMERTVEEAFILLVCLKFWRVASS<br>LEKKEKEDESQQLLLGSRYNVLKAHCLLPLIRWLTSGDLSLSAQ<br>PHCPQGL   |
| 6535       | 250  | 964  | LIKTFFRDVAIQRDLLPKBNLETLLTAFLEIDKAFSSSHARLS<br>ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL<br>TIDHTPERKDEKERIKKCGGFVAVNSLGQPHVNGRLAMTRSIGD<br>LDLKTSGVIAEPETKRIKLHADDSEFLVLTDTGIFMVNSQEIW<br>DFVNQCHDPNEAAHVAVEQAIQYGTEDNSTAVVVPFGANGKYKN<br>SEINFSSRSFASSGRWA   |
| 6536       | 242  | 1174   | SLVKEMTNQYGLIFKQEQAHDDAIWSVAGTNNKENSETVVTGS<br>LDDLKVKWKRDERLDLQWSLEGHQLGVVSDISHTLPAASS<br>LDAHRLWDLNGKQIKSIDAGPVDATLAFSPDSQYLATGTHV<br>GKVNIFGVESGKKEYSLDTRGKFILSIAYS PDGKYLAGAIDGI<br>INIFDIATGKLLHTLEGHAMPIRSLTSPSPDSQLLVTASDDGIK<br>IYDVQHANLAGTSLGHASWVLNVAFCPDDTHFVSSSSDKSVKVV<br>DVGTRTCVHTFFDHDQDVGVNGVNGSKIVSVGDDQEIHIYDC<br>PI  |
| 6537       | 1638   | 921  | NRFNPPPTQGPDPFSLVYRPDVPDEVAKD KASFRNYTSGPLLD<br>FTTYKLMHTHTQTVDFVRSKHAQFGGFSYKKMTVMEAVDLDGLV<br>DESDDPVDVFPNSFHAFTAEGRKAHPDKDWFHLVGLLHDLGKV<br>LALFGEPPQWAVVGDTFPVGCRCQASVVFCDSTFDQNDPLQDPRY<br>STELGMYQPHCGLDRLVMSWGHGDEARGGQWGGGGRWGTVGGGG<br>AEAVPAGDTLSPQSTCTR  |
| 6538       | 3345   | 2412   | PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRRLTKQVQ<br>ARHNRDDEAIKKA VNEYDETMKXIIPVMAQAKIYWNLENYPMV<br>EKIFRKSVEFCNDHDVWKLNVAVLFLMQENKYKEAIGFYEPIVK<br>KHYDNI LNVAI V L N L C V S Y I M T S Q N E K A E E L M R K I E K E E E Q L<br>SYDDPNRKMVHL CIVNLVIGTLYCAKGN Y E F G I S R V I K S L E P Y N<br>KKLGTD TWYAKRCFLSLENNMSKHMIVIHDSV IQECVQPLGHC<br>ELYGTNIPAVIEQPLEEERMHVGNVTVDSE RQLKAL IYEIIGW<br>NK   |
| 6539       | 218  | 339  | FLGAASPHPHFSSSLAPHPDQPEFTPVQDELEAMELWGPV  |
| 6540       | 3  | 391  | LERLWLLLRPPEDAMAECP TLGEAVTDHPDRLWANEKFVYLDE<br>KQAWLPLTIEIKDRQLQRLVLLRREDVVLGRPMPTPTQIGPSLLP<br>IMWQLYPDGRYRSSDSSFRLVYHIKIDGVEDMLLELLPDD   |

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|------------|--|--|---|
| 6541       | 1165   | 536  | RTLVRRIILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP<br>RFEGRKPDSDWGNREPFGPGEHFRTDPRPDHPPHDGHSASRE<br>RSSSLQGMMDASLPKRKPWHDGPGTSBHREMEAPGGPSEDGGRG<br>KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEFPGGPPGSGTP<br>SRGGRSGSNWGRGSMNMSGPPRRGASRGGRGR  |
| 6542       | 3  | 3775   | SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFARKEGT<br>KRGFLSKKTAESRWHEKWFALYQNVLFYFEGEQSCRPAGMYLL<br>EGCSERTPAPPRAGAGGGVRDALDKQYYFTVLFHGEQKPLE<br>LRCEEEQDGKENMEAIHQASYADILIEREVLQKYLHLVQIVET<br>EKIAANQLRHQLEDQDTEIERLKSEI IALNKT KERM RPQSNQE<br>DEDPDIKKIKKVQSFMRGWLCCRKWKTIQDYICSPHAESMRKR<br>NQIVFTMVEAESEYVHQYLYLVNGFLRPLRMAASSKKPPISHDD<br>VSSIPLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM<br>LNIYQEFVRNHQYSLQVLNCKQNRDQDKLLKQYEANPACEGRM<br>LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE<br>ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILDDTSQTFIROG<br>SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLTKHFLICTRS<br>SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKSGSQVFGHLD<br>KIVVEPPDRAAFTVLLAPSRQEKAAWMSDISQCVDNIRCNGLM<br>TIVFEENSKVTVPHEMIKSDARLHKDDTDICFSLTNSCKVPQIR<br>YASVERLLERLTLRLFLSIDPINTFLHTYRIFTAAVVLGKLS<br>IYKRFPPTSIPVRSLELFFATSONNRGEHLVDGKSPRLCRKFSSP<br>PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTSSSPPTTTQS<br>PAASPPPHGTQIPLDLRGLSSPEQSPGTVEENVDMNPRVLCNK<br>LKRSIQKAVLESAPADRAGVESSPAADTELSPCRSPSTPRHLR<br>YRQPGGQTADNAHCSVSPASAFIATAAAGHGSPPGFNNTERTC<br>DKEFIIRRTATNRVLNVRHVVSKHAQDFELNNEKMNVLNLE<br>EVLDPDPLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC<br>MKAECFESLSAMELAEQITLLDHVIFRSIPYBEFLGQGMKLDK<br>NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKQWAV<br>ADICRCLHNYNGVLEITSALNRSATYRLKKTWAKVSKQTKALMD<br>KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMVLTDLAFIEEGT<br>PNFTEGLVNFVSKMRMISHIIREIRQFQTSYRIDHQPQVAYL<br>LDKDLIIDEDTLYELSLKIEPRPLA |
| 6543       | 1857   | 950  | FVSGCGRAGIGLSWAMAAEARVSRWYFGLASCGAACCTHPLDL<br>LKVHLQTQEVKLRTGMALRVVRTDGILALYSGLSASLCRQMT<br>YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLGVSGLAGGFVG<br>TPADLVNVRMNDVKLPQGGRRNYAHALDGLYRVAREEGLRLRF<br>SGATMASSRGALVTGQLSCYDQAKQLVLTGYLSDNIFTHFVA<br>SFIAGGCATFLCQPLDVLTRLMNSKGEYQGVFHC AVETAKLGP<br>LAFYKGLVPAGIRLIPHTVLTFFVLEQLRKNFGIKVPS  |
| 6544       | 630  | 79   | PSPCFIRSRLDGQPMWAGLEAWLSQNFSLHQPSRVVRRAST<br>EPSDTPPEPRTLNPSFAGWVQQHPELELMSSFRERFGRNWLQY<br>RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQBEAR<br>GPQESPQKMSSEVRAEPQEBEEKEGKEEKEGEMAPLPEAHLG<br>EGKQKECP  |
| 6545       | 176  | 560  | PPHSHALLPAAMTPLLTLILVVLMLPLAQLDCHVCAYNGDN<br>CFNPMRCAMVAYCMTTRTYTPTRMKVS KSCVPRCFETVYDGY<br>SKHASTTSCCQYDLNCGTGLATPATLALAPILLATLWGLL  |
| 6546       | 1657   | 364  | HLNLGLDEVAFFVADLGAIVRKHFCLKCLPRVRPFYAVKCN<br>SPGVLVLAQLGLGFSKANKAEMELVQHIGIPASKIIICANPCKQ<br>IAIKYAAKHGIGQLSFDNEMELAKVVKSHPSAKMVLCIATDDS<br>HSLSCLSLKFGVSLKSCRHLENAKHHVEVVGVSFHIGSGCPD<br>POAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTGAKVRF<br>EEIASVINSALDLYFPEGCGVDIFAELEGYYVTSAPTAVASIIA<br>KKEVLDDQPGREEENGSTSKTIVYHLDEGVYGFNSVLFDNICP  |



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|------------|--|--|---|
|            |  |  | TPILQKKFSTEOPLYSSSLWGPVVDGDCVAGLWLPQLHVGDWLVFDNMGAYTVGMGSPFWGTQACHITYAMSRVWAEALRRQLMAAEQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM   |
| 6547       | 1  | 541  | LHSKYLAPALCSQPGMMRCCRRRCCCRQPFPALRPLLLPLVLLPPLAAAAAGPNRCDTIYQGFACELIRLGDSMGRGGELETICRSWNDFHACASQVLGSGCPPEAAAVWESLQEQARQAPRPNLHTLCGA PVHVRERGTGSETNQETLRATAPALPMAPPLLAALALAYLLRPLA   |
| 6548       | 2  | 219  | FVSRLSVRDVRFPFTFLGGHGADAMHTDPDYSAAVPIETDAEDG IKCGGITFTLGKGTVEVGELKILSRFQNA  |
| 6549       | 73   | 1490   | ETGRVCEADARPACGSRSSRRRRKEAAPGIPTPSPSSSSPTSSRPAARAFSKAPARLSRPRAREEPPDPGRRYIQBEIIQARKHKLIKMCSSVAALKWFLTDRIREDYPOKEILRALKAKCCEELDFRAVVMDEVVLTIEQGNIGLRINGELITAYPQVVVVVPTPWVQSDSODITVLRHLEKMGCRIMNRPQAILNCVNKFWTQELAGHVLPDFTFSYGGHENFAKMIDEAEVLEFFPMVVKNTRGHRGKAVFLARDKHHLADLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCSTDGRMQSNCSLGGVGMCSLSEQKQLAIQVSNILGMDVCGIDLLMKDDGSFCVCEANANVGPIAFDKACNLVDAGIADYAAASLLPSGRLTRRMSLLSVVSTASETSEPELGPFASTAVDNMSASSSSVSDSPBSTERELLTKLPGGLFMNQLLANEIKLLVD  |
| 6550       | 2293   | 922  | FRVSRDGPDCGIEQMG LAMEHGGSYARAGGSSRGCWYLLRYFFLFVSLIQFLIILGLVLFMVYGNVHVSTESNLQATERAEGLYSQLLGLTASQSNLTKEINFTRAKDAIMQMWLNARRDLDRINASFRCQCGDRVIYTNQRYMAAILSEKQCRDQFKDMNKS CDALLFMLNQKVKTLEVEIAKEKTICTDKESVLLNKRVAEEQLVECVKTRELQHQRQLAKEQLQKVQALCLPLDKDKFEMDLRNLRDSSIIPRSLDNLGYNLYHPLGSELASIRACDHMPSLMSSKVEELARSLRADIERVARENSDLQROKLEAQQLRASQEAQKQVEKEAQAREAKLQAECSROTQALAEKAVIRKERDNLAKELEKKREAEQLRMELAIRNSALDTCIKTKSQPMMPVSRMPGPVNPQPIDPASLEEFKRKILESQRPPAGIPVAPSSG   |
| 6551       | 157  | 748  | IQPPDPRNMTLAAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYEADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFNASLPRRRDPSLEEIOKKLEAAEERRKYQEAELLKHLAEKREHEREVIQKAIENNNFIKMAKEKLAQKMESENKENREAHLAAMLERLQEKDKHAEVVRKNKELKEEASR  |
| 6552       | 157  | 748  | IQPPDPRNMTLAAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYEADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFNASLPRRRDPSLEEIOKKLEAAEERRKYQEAELLKHLAEKREHEREVIQKAIENNNFIKMAKEKLAQKMESENKENREAHLAAMLERLQEKDKHAEVVRKNKELKEEASR  |
| 6553       | 2  | 1807   | FVWSKMAAHLISYGRVNLNVLREAVRRELREFLDKAGSKAIVWD EYLTGPFGLIAQYSLKKEHEVEKMF TLKGNRLPAADVKNIIFFVRPRLELMDIIAENVLSEDRRGPTTRDPHILFVPRRSLCEQRLKD LGVLGSFIHREBYSLDLPFDGDLSESEGAFFKCYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLDNRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGKDLPTAKKLQNLNSAEELYAEIRDKN FNAVGSVLSKKAKIIISAAFEERHNAKTVEIKQFVSQPLPHMQAARGSLANHTSIAELIKDVTTSDFDKLTVEQEFMSGIDTDKVN YIEDCIAQKHSLIKVLRVCLQSVCSGLKQKVLDDYYKREILQTYGYEHILTLEHLEKAGLLKQPTGGRRNYP TIRKTLRLWMDDVNEQNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRLPGPHFBERQPLPTGLQKKRQPGENRVTLIFFLGVTFAEIAALRFLSQL EDGGETEYVIATTKLMNGTSWIEALMEKPF |

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|------------|--|--|--|
| 6554       | 119  | 1244   | FEMGSQVSVEGALHVVIVGGGFGGIAAASQLOALNVFMLVDM<br>KDSFHHNVAALRASVETGFAKKTFFISYSVTFKDNFRQGLVVGID<br>LKNQMVLQGGGEALPFSHLILATGSTGPPGKFNEVSSQQAIIQ<br>AYEDMVRQVQRSRFIVVVGGSAGVEMAABIKTEYPEKEVTLLH<br>SQVALADKELLPSVRQEVKEILLRKGVLILLSESVNLEELPLN<br>EYREYIKVQTDKGTVEATNLVILCTGIKINSSAYRKAFESRLAS<br>SGALRVNEHLQVEGHSNVYATGDCADVTPKMAVLAGLHANIAV<br>ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRIM<br>VRLTKSRDLFVSTSWKTMRSPP                                  |
| 6555       | 1552   | 498  | IMALLRKINQVLLFLLITVTLCVILYKKVHKGTVPKNDADDESE<br>TPEELEEEI PVVICAAGRMGATMAAINSISNTDANILFYVVG<br>LRNTLTRIRKWIHESKLREINFKIVEFNPMGLKGKIRPDSSRPE<br>LLQPLNFVRFYLLPLIHQHEKVIYLDLDDVIVQGGDIQELYDTTLA<br>LGHAAPFSDDDCLFSAQDINRLVGLQNTYMGYLDYRKKAIDKLG<br>ISPSTCSFNPGVIVANMTEWKHORITKOLEKWMQKNVEENLYSS<br>SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL<br>QEAKLLHWNHGRHKPWPDPFSVHNDLWESWFPDPAGIFKLNHHS  |
| 6556       | 241  | 1449   | ASLCKGCFVTHVLVILPSSLQSPPTFGFLDDIGVLVRGRHVI<br>PAALKAFFRLVNSQGGQLRVVVFVNTAGNILQHSKAQELSAALLG<br>CEVDADQVILSHSPMKLFSEYHEKRMVLVSGQGPVMEQAQGLGFR<br>NVVTVDELRAFPPLDMVDLERRLKTTPLRNDFPRIEGVLLLG<br>EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL<br>WMAEAKMPREFGHTFLLCLETIYQKVTGKSLRYEGLMGKPSILT<br>YOYAEGLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY<br>LOKATHDGAPELGAAGTRQQQPSASQSCISILVCTGVYNPRNPQ<br>STEPVLGGGEPFFHGHRLCFSPLMEASHVNDVNEAVQLVFR<br>KEGWALE |
| 6557       | 2598   | 1534   | RMCGRTSCHLPRDVLTRACAYQDRRGQQLPEWRDPDKYCPSYN<br>KSPQSNPVLRLHFEKDADSSERI IAPMRWGLVPSWFKESDP<br>SKLQFNTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC<br>QGTNRQPYFYIYFPQIKTEKSGSIGAADSPENWEKVDNWRLLT<br>MAGIFDCWEPPPEGGDVLYSYTIIITVDSCKGLSDIHRMPAILDG<br>EEAVSKWLDGFEVSTQEALKLIHPTENITFHAVSSVVNNSRNT<br>PECLAPVDLVVKKELRASGSSQRMQLWLATKSPKKEDSKTPQKE<br>ESDVPQWSSQFLQKSPLTPKRGTAGLLEQWLKREKEEFPVAKRP<br>YSQ   |
| 6558       | 21   | 1138   | FHGRRRGGRKMELGSCLEGGREAAEEGEPEVKRRLLCVEFAS<br>VASCDAAVAQCFLAENDWEMERALNSYFEPVVEESALERRPETI<br>SEPKTYVDLTNEETDSTTSKISPSEDTQENGSMFSLITWNID<br>GLDLNNLSERARGVCSYLALYSPDVI FLQEVIPPYYSYLKKRSS<br>NYEII TGHEEGYFTAIMLKSRVKLSQBEI IPPFSTKMRNLLC<br>VHVNVSGNELCLMTSHLESTRGHAARMNQLKMVLKKMQEAPES<br>ATVIFAGDTNLRDREVTRCGGLPNNIVDVVEFLGKPKHCQYTD<br>TQMNSNLGITAAACKLRFDRIFFRAAAEHGHIIPRSLDLLGLEKL<br>DCGRFPSDHWGLLCNLDIIL                                   |
| 6559       | 3  | 364  | GPESGLPTRPKKLANQTPIAMDCASRSCSVPTGPATTICSS<br>DKSCRCGVCLPSTCPHTVWLLIPTCCDNCPPCHIPQPCVPTCF<br>LLNSCQPTPGLETNLTTFTQPCCEPCLPRGC  |
| 6560       | 3  | 1435   | TATSGGIWLRKKRCHWRPLPQSCVGTGEGGLQVRDTSRIAAG<br>GVDHTKMSLHGASGGHERSRDRRSSDRSDSSHERTESQLTPC<br>IRNVTSPTRQHHVEREKDHSSSRPSSPRPKASPNGISAGNS<br>SRNSSQSSSDGCKTAGEMVFVYENAKEGARNIRTSEVTLIVD<br>NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAE<br>GIGSTVFRALDYKGTGIRCPDGISIPELREACDYLCISFEYS<br>TIKCRDLSALMHLSNDGARRQFEBFYLEEMILPLMVASQSGER<br>ECHIVVLTDDDVVDWDEEYPPQMGEYSQIIYSTKLYRFFKYIE  |

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|------------|--|--|---|
|            |  |  | NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKRPFGRPEBVIYN YVQRPFFIRMSWEKEEGKSRHVDQCCKSKSITNLAAAAADIPQD QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAGQNPML  |
| 6561       | 3  | 1086   | PGRRFRKRESSSRWFADCLLGLRGFPASSLLSPSPSPSWPSHS PCPMAALTDLSEFMYNFKNCNLVGNLSEKYVFTIGCDSPGPNLL AKQLVDRGMQVLAACFTEEGSQKLQDRTSYRLQTTLLDVTKSES IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNWLTKDDFVKV INVNLVGLIEVTLHMLPMVKRARGRVNMSSSGGRVAVIGGGYC VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES RMRKLWERLPQETRDSYGEDYFRIYTDKLNIMQVAFPRVRDVI NSMEHAIVSRSPRIRYNPGDLAKLLYIPLAKLPTPTDFILSRY LPRPADSV   |
| 6562       | 1  | 1562   | MSTLYDIRAHKAQLRRFFASSDSNKALEQRRRLHTPKLEHLDRV LVEWFLGKRSEGVFVSGPMLIEKAKDFYEQMLTBPVFSGGWL WRFKARHGIKKLDASSEKQSAHQAAEQFCAPFRSLAAEHGLSA EQVYNADETGLFWRCLPNPTPEGGAVPKPKQKDRLTVLMCANA TGSHRLKPLAIGKCSGPRAFGIOHLPVAYKAQGNWVDKEIFS DWFHHIFVPSVREHFRITIGLPEDSKAVLLDSSRAHPQEAELVS SNVFTIFLPASVASLVQPMQGIIRDFMRNFINPPVPLQGPBAR YMNDAIFSVACAWNAPVSHVFRARWKLWPSVAFAGSSSEEE LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQQAASWGVAG REAEGGRPPAATSPAENVVSSSEKTPKADQDGRDPEGEVAVE QAQAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSQQQVRRRR GALGAVVKEALQEGPGGCGATAQSPLPCCSSTAGDN |
| 6563       | 1319   | 2694   | LARPAQPVLLREPEGAGPPVPAHGLVHHLQGGHLRERAHDPLEA HEHPLPCDQMFWRQMGHRLRMVEANSRGVWVIGYDHTAWVYTG GYGGGCFQGLASSTNIYTSQSDVKCVHIYENQRWNPVTGYTSRG LPTDRYMNSDASGLQECTKAGTKPPSLQWAWVSDWVDFSVVGG TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL EVPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS ELNPAGSSWLHVGTQDPFASISIGACYQVWAVARDGSFAFYRGSV YPSQAPGDCWYHIPSPPRQLKQVSAGQTSVYALDENGNLWYRQ GITPSYPQGSSEHVSNNVCRVSVGPLDQVWVIANKVQGSLSLS RGTVCHRTGVQPHPEKPGHGWYDYGIGGWDHISVRANATRAPRSS SEQEPPSAPPEAHGPVCC   |
| 6564       | 1  | 975  | APGSCALWSYCCRGWSRAMRGCCQLLGLRSSWPGDLLSARLLSQE KRAETHFGPETVSEEEKGGKVYQVFESVAKKYDVMNDMMSLGI HRVWKDLLLWKMHLPLPGTQLLDVAGGTGDIARFNLNYVQSQHQR KQKRLRAQQNLSWEEIAKEYQNEEDSLGGSRVVCDINKEMLK VGRQKALAQGYRAGLAWVLGDAEELPFDDDKFDITYIAFGIRNV THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV IPVLGEVIAGDWKSYQYLVESIRRFPSQEEDKMIEDAGFHKVT YESLTSGIVAIHSGFKL  |
| 6565       | 1464   | 999  | RSVAVGLTKRRMGLKLNTRYISLILAVQIAYLVQAVRAAGKCD AVFKGFSDDLKLGDSMANYPQGLDDKTNIKTVCTYWEDPHSCT VTALDCQEGAKDMWDKLRKESKNLNIQGSLELCGSGNGAAGS LLPAFPVLLVSLSAALATWLSF   |
| 6566       | 3  | 1385   | KYESAQPGGTQPEPGLCARMATHKALVMCLGLPLFLFPGAWAQG HVPFGCSQGLNPLYNLCDSGAWGIVLEAVAGAGIVTTFVLT IILVASLFFVQDTKKRSLGTQVFFLLGLTGLFCLVFACVEKPDF STCASRRFLFGLVFAICFSCLAHVFAFNFLARKNHGPRGWVIF TVALLLTVEVIINTEWLIITLVRSSEGGPQGNSSAGWVASP CAIANMDFVMALIYVMLLLGAFLGAWPALCGRYKRWRKHGVFV LLTTATSVAIWVWVIMYTYGNKQHNSTWDDPTLAIALAANAW AFVLFYVIVEVSQVTKSSPEQSYQGDMPYTRGVGYETILKEQKG QSMFVENKAFSMDPEVAAKRPVSPSYSGYNGQLTSVYQPTMAL   |

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|------------|--|--|--|
|            |  |  | MHKVPSEGAIDIIILPRATANSQVMSANSTLRAEDMYSAQSHQA ATPPKDGKNSQVFRNPYVWD  |
| 6567       | 125  | 863  | TKRSNLKAYACSIHIRTMSYVFNVDSSQTNVPLQACIDGDFN YSKRLLESQFDPNIRDSRGRTGLHLAAARGNVNDICQLLHKFGAD LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMTAESESA MESHSLLNPNLQOQEGVLSSFRRTTWQEFVEDLGFWRVLLLIFVI ALLSLGIAYVSGVLPFVENQPBVLVH   |
| 6568       | 3  | 1183   | HASDRLLVLPDNYSHPSQASANLQGPSRTTELPHPTLASISSPM LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL KIHLLQTTDYGFLANHTNPLTVSKIDTEMKRKLCGEFEYFRNHS LEPLSTFLTMTCSYIMIDNVILLMNGALQKKSVKELGKCHPLG RPTMEAVNIAETPSDLFNAILIETPLAFFQDCMSEVALDELN IELLRNKLYKSYLEAFYKFCRNHGDVTAEVMCPILEFEADRRAF IITLNSFGTELSEKEDRETLYPTFGKLYPEGLRLLAQAEFDQMK NVADHYGVYKPLFEAVGGSGGKLTEDVYEREVQMNVLAFNRQF HYGVFYAYVKLKEQEI RNIVNIAECISQRHRTKINSYIPIIL  |
| 6569       | 205  | 1532   | RRRGFQRLGHGRPTPLLCRNRTAGPSHNEKQARAFQGLRPVDP RRMWLFPLTKSASSAAGSPGGLTSLQQKQRLIESLRNSHSSI AEIQKDVEYRLPFTINNLINILPQQFQPKVISVYPPIR HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLEDFWKNPPVLA PTSTAFPYLYSNPSGMSPYASQGFPPPPYPPQEANRSITSLSV ADTVSSSTTSHTTAKPAAPSGVLSNLPLPIPTVDASIPTSONG FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLLEQFTLPLQLK QIITDKDDLVSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM KSTPEKKMQROHELSESCASALQARLKVAHAHEEESDNIAED FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLOQAIAMHSQFHA PL  |
| 6570       | 330  | 1304   | ARLPRLTFLREGFLYVLLSHWVFGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQGL YGLSAVQTMHMHNTLGYPNVHEITRSTITEMAAAGLVDARF PFPALPFTTHLFHPKQGAIAHVLPAHKKDRPRDFANLAVAATQ EDPPKMGDLSKLSPLGSPISGLSKLTPDRKPSRGRLPSTKKE FICKFCGRHFTKSYNLLIHERHTHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKQCEGKGFQCSRTLAVHKTLMQTSSPTAA SSAKCSGETVICGGT  |
| 6571       | 169  | 656  | APDMNRKKLQKLTDTLTKNCKHLFRGFDKNDGCVNVLEWIGHL SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHLKNSLLKQP SEEDPDEGIKDLVEITLKKMDHDHDKLSFADYELAVREETLLL EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM   |
| 6572       | 49   | 1646   | TPERAQPGALLGAAGCCVCGGRWWPRSHERGYSFSAKMGSKRRN LSCSERHQKLVDENYCKKLHVQALKNVNSQIRNQMVQENENDNRV QRKQFLRLQNEQFELDMEEAIQKAEENKRLKELQKQEEKLAM ELAKLKHESLKDEKMRQVRENSIELRELEKKLKAAYMNERAA QIAEKDAIKYEQMKRDAEIAKTMMEBEHKRIIKEENAAEDKRNKA KAYYLDELKQLEBEQEKKKQRAYEQLLKEKLMIDEIVRKIYEED QLEKQKLEKMNAMRRIIEEFQKEQALWRKKKREBEMEENRKII EFANMQQREEDRMAKVQENBEKRLQLQNALTKLEMLRQRED LEQVRQELYQEEQAEIYKSKLEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEENFRKTMFAEDDRIELMNAQKORMKQLE HRRAVEKLEERRQQFLADKQRELEEWLQQRROGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLGEFRKVVYQQRSEI CEEK |
| 6573       | 767  | 275  | GGGGGESQSFRAQDGTTRTPATDCLMYLQGPRLMTQGGYDMVQK LFLDFRRRLSQRPTEBLEQRNLIKPRNEQEEQEEKREIKRRL TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR   |

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|------------|--|--|---|
| 6574       | 204  | 1159   | <p>LTAAADKVSRGECWRVGGRTVCWVSLGSPGSGV</p> <p>LESSVPVSVGVFWACGVSWTGAAGLQDGLSDTMARNAEKAMTALARFQAQLEEGKVKEKRRPFLASECTBLPKAKWRRQIIGEISKKVAQIQNAGLGEFRIRDLNDEINKLLREKXGHWVRIKELGGPDYKVGPKMLDHEGKEVPGNRYKYFGAAKDLPGVRELFEKEPLPPRKTAEMLKAIIDFEYYGYLDEDDGVIVPLEQEYKELRLAEVLVEKWAEREARLARGEKEEEEEEEINIYAVTEESDEEGSQEKG GDDSQQKFIHVPVPSQOEIEALVRRKKMELLQKYASETLQAQ SEEARLLGY</p>   |
| 6575       | 117  | 820  | <p>SPALASQSGGITTEKMLEFQENGVIDLPDYEHVEDETFFPPFPF ASPERQDGEGETEPDEESGNGAPVPPPKRTVKRNIPKLDARLI SERGLPALRHVFDKAKFKGKGHEADLKMLIRHMEHWAHRLFPK LQFEDPIDRVEYLGSKKEVQTCCLKRIRLDLPILHEDFVSNNDDEV AENNEHDVTSTELDPFLTNLSESEMFASLSISLTTEEQQORIER NKQLALERRQAKLP</p>  |
| 6576       | 1  | 1060   | <p>PEPQALVGQKRGALRLVARLVLTVSAPAEVRRRVLRLPVLSWMD RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPFDFHLLRTYGDV VVPVANGVQYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL YLKDWHLCDRDFPVEDVFTLPVYFSSDWLNEFDALDVEDDYRFVY AGPAGSWS PFHADIPRSFSSWVNVCGRRKMLLFPFGQEEALDRR HGNLPHYDVTSPALCDTHLHPRNQLAGPPLITQEAGEMVFPVPSG WHHGVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH G</p>   |
| 6577       | 2271   | 987  | <p>SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS TNSNGNETSGSSTIGETSNRSRDRDRYRRNRSSRSRSGRQCRHR SRSWDRRHGSESRSRDRHREDRVHYRSPLATGYRYGHSKSPHF REKSPVREPDVNLSPEDARTVFCMQLAARIRPRDLEDFFSVAV GKVRDVRIISDRNSRRSGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQXGNGGPMRLYVGLHFNITED MLRGI FEPFGKIDNIVLMKDSDTGRSGYGFITFSDSECARRAL EQLNGFELAGRPVRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQIMAKLAEGAGIQLPSTAAAAAQAALQLNGAVPLGA LNPAALTALSPALNLSQCLQLSSLFTPTM</p> |
| 6578       | 377  | 1489   | <p>PSSSATMNRAPLKRATILHMLTGAADPSAEAEANGKEPFLRLA LQIALVVSLSYVWTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTLLCKGLSALAACCPGAVDFPSLRDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTFVFNVLISYLLKQTTSFYA LLTCGIIIGGFVLGVDQEGAETLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLGELQALRDF AQLGSAHFWMMLTGLGFGAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTNNMVLGGSSAYTWVRGWEMK KTPPEPSPKDSEKSAMGV</p>  |
| 6579       | 2  | 711  | <p>RPPRVVYPELRELSAAAPRWSHRTAPGIMVIFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRHLKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVEKKVNEILNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEMKKREMDLRSYSSLMKV ENMSSNQDGNDSDEFM</p>  |
| 6580       | 62   | 1571   | <p>LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEGKYLPSLEMFQRFRQFGYHDTPG PREALSQRLVLCCEWLRLPEINTKEQILELLVLEQFLTILPQELQ ANVQEHCPESAEEAVTLLEDLELDEPHQVSTPNEQKPVWE KISSSGTAKESPSSMQPOPLETSHKYESWGPLYIQESGEEQEPF QDPRKVRDCRLSTQHEESADEQKGEAEGLKGDIIISVIANKPE ASLERQCVNLENEKGTKPPLEAGSKKGRESVPTKPTPGERRYI</p>  |

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|------------|--|--|---|
|            |  |  | CAECGKAFSSNNLTGKRRTHTEGKPYVCTKCGKAFSSNNLT<br>HYRTHLVDRPYDCKCGKAFGQSSDLLKHORMHTEBAPYQCKDCG<br>KAFSGKGLIRHYRIHTGEKPYQCNECGKSFQAGLSSHQRLH<br>TGKPKYKCKCGKAFNHSSNFNKHRIHTGEKPYWCHHCCKTFC<br>SKSNLSKHQVHTGEGEAP  |
| 6581       | 228  | 476  | RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVS<br>AADLMAYCEAHAKEDPLLTPVPAENPFREKKFFCAIL   |
| 6582       | 1428   | 718  | CFTTKTHCSPVSPYLSPLVLRKELESLENEGDQVHTSSFIN<br>QHPPIIWTLLVWFRRDLPSNLPGLILTSEHCNEGVQLPLSSLS<br>QDSKLVYIQLWDNINLHQEPREPLVSWRNFNSEKSSLSSEE<br>QQETSTLVETIRQSIQHNNVLKPINLLSQMKPGMKRQRSLYRE<br>ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP<br>PSASVEWCRKCFGAPLI   |
| 6583       | 487  | 41   | RIFSMTSGRLRWCTWRPATALWSASLRGTSSMHPSPRSISLP<br>LSMMLSPLPNTRGLSPALFRSPDSEHATSCPRHLWRCRAPL<br>RSPSPILGRQLVLRPSPLVHTHNSGKEVLGLQVQSRSGTGAPAC<br>SQAGSGAVQGGNWCIF   |
| 6584       | 189  | 1750   | PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVN<br>FATWQARLERDLNKKIYQEEEMPESGAGSEFNRLREBARCKY<br>IVLKEFRPEDQPWLLRVNGKSGRKPKGIKGGVTEENTSYYIFTQ<br>CPDGAFAFPVHNWYNFTPLARHRTLTAEBAEWEWERRNKVLNH<br>FSIMQORRLKDQODEDEEKEKRRKASELRINDLEDDLEMS<br>SDASDASGEEGRVPAKAKKAPLAKGGKKKKKGSDEAFEDS<br>DDGDFEGQEVDMYSDGSSSSQEEPEKAKAPQOEEGPKGVDEQS<br>DSSESEEEKPPEDEKEEEKKAAPTQEKRRKDDSEESDSSE<br>ESDIDSEASSAFFMAKKTTPKRRKPSGGSSRGNSRPGTPSAE<br>GGSTSSTLRAAASKLEQGGKRVSEMPAAKRLRLDTGPQSLGKST<br>PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMITKDLKKFKQTKK<br>TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE   |
| 6585       | 3  | 1678   | GPINRSRIDDFVGGDPRAEASCSVLHSPHAMADSRDPASDQ<br>MQHWKEQRAAQKADVI.TTGAGNPVGDNLNVITVGRGPLLVQDVVF<br>TDEMAHFDRBRIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE<br>HIGKKTPIAVRFSTVAGESGSADTVRDPGRPAVKFYTEDGNWDL<br>VGNNTPIPIFIRDPIFPSPFIHSQKRNPQTHLKDPMVWDFWSLR<br>PESLHQVSFLFSDRGIPDGHHRMNGYGSHTFKLVNANGEAVYCK<br>PHYKTDQGIKNLSVEDAARLSQEDPDYGIKDLFNAIATGKYPSW<br>TFYIQVMTFNQAFETFFNFDFDLTKVWPHKDYPLIPVGLVLNRRN<br>PVNYFAVEQIAFDPSNMPPGIEASPKMLQGRFLFAYPDTHRRH<br>LGPNYLHIPVNCYPYRVRVANYQRDGPMDQDNQGGAPNYYPNSF<br>GAPEQPSALEHSIQYSGEVRRENTANDDNVTQVRAFYVNVLE<br>EQRRLCENIAGHLKDAQIFIQKAVKNFTEVHPDYGSHIQALL<br>DKYNAEKPKNAIHTFVQSGSHLAAREKANL |
| 6586       | 32   | 804  | PLPEQPAESTSTMPVSGTPAPNKKRKSCLIMELTGGGQESSGL<br>NLGKKISVPRDVMLEELSLLTNRGSKMFKLRMRVEKFIYENHP<br>DVFSDDSMDFQKFLPTVGGQLGTAGQGFYSKSNRGGSSQAGG<br>SGSAGQYGSQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE<br>TSGGDQAGGEGKHITVFKTYISPWERAMGVDPOQKMELGIDLLA<br>YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV  |
| 6587       | 75   | 1117   | RRVPSLGKMPCEWDGEHDIETPYGLLHVIRGSPKGNRPAILTY<br>HDVGLNHKLCFNTFFNFEDMQEITKHFFVCHVDAPGQOVGASQP<br>PQGYQFPMEQLAAMLPSVVQHFGFKYVIGIGVAGAYVLAKFA<br>LIFPDVLEGLVLVNIIDPNGKGWIDWAATKLSGLTSTLPDVTLSH<br>LFSQEBLVNNTLVQSYRQQIGNVVUNQANLQLFWNMYNSRRDL<br>DINRPGTVPNAKTLRCVMLVVGDNAPAEAGVVECNKLDPTTTT<br>FLKMADSGGLPQVTQPGKLEAFKYPLQGMGYMPSASMTLARS<br>RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTEVSC  |

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|------------|--|--|--|
| 6588       | 137  | 501  | LGLQAQLLELRNNYQLSDELKXNGVELTSLRQKRAYLQKEFSK<br>AQKALSKSKKAQEVEVLLSENEMLQAKLHSEEDFRLQNSTLMA<br>EFSKLCSQMEQLEQENQQLKEGAAGAGVAQAGP  |
| 6589       | 2  | 1405   | RPWGSAMATFSRQEFFQQLQGLLPTAQQGLDQIWLILAICLA<br>CRLWLRLGLPSYLKHAHVAGGFFSLYHFFQLHMVWVLLSLC<br>YLVLFLCRHSSHRGVFLSVTILYLLMGEMHMDTVTHKMRGA<br>QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW<br>ISFHSYLQAVQGRPLSCRNLQKVARSLALALLCLVLSTCVGPYL<br>FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSPHFSNYFV<br>GFLSEATATLAGAGFTEEKDHLWDLTVSKPLNVELPRSMVEVV<br>TSWNLPMYSWLNNNYVFNALRLGTFSAVLVTYAASALLHGFSFH<br>LAAVLLSLAFITYVEHVLKRLARILSACVLSKRCPPDCSHQHR<br>LGLGVRALNLLFGALAIHFLAYLGSFLFDVDDTTEEGYGMAY<br>TVHKWSELSWASHWVTFGCWIFYRLIG  |
| 6590       | 2177   | 656  | VRAYEHVLSLENVFTPMFCHRDYFRQLLRGAESPTRNSKLN<br>GSLSDDDFRNTQKRGSFGISRIGSKIKGVFKSTMEGAMLPNY<br>GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY<br>VDFFEDPSSERKEKKEKRIPVFCIDVERNDRAVGHPEHWSVYR<br>RYLEFYVLESKLTEFHGAPDAQLPSKRIIGPKNYEFLKSKREE<br>FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG<br>KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL<br>SPTSENNKKLFNDLFKNANRAENTERKQNYFMEVMTVEGVY<br>DYLMYVGRVVFQVPDNLHLLMGTRILPKNTLEMYTDYYLQCKL<br>EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKAKQTFEEM<br>MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI<br>VIQELFPELNKVQKEVTSVTSWM  |
| 6591       | 2177   | 656  | VRAYEHVLSLENVFTPMFCHRDYFRQLLRGAESPTRNSKLN<br>GSLSDDDFRNTQKRGSFGISRIGSKIKGVFKSTMEGAMLPNY<br>GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY<br>VDFFEDPSSERKEKKEKRIPVFCIDVERNDRAVGHPEHWSVYR<br>RYLEFYVLESKLTEFHGAPDAQLPSKRIIGPKNYEFLKSKREE<br>FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG<br>KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL<br>SPTSENNKKLFNDLFKNANRAENTERKQNYFMEVMTVEGVY<br>DYLMYVGRVVFQVPDNLHLLMGTRILPKNTLEMYTDYYLQCKL<br>EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKAKQTFEEM<br>MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI<br>VIQELFPELNKVQKEVTSVTSWM  |
| 6592       | 3  | 1861   | APEFLGSTISSGSMIDANLKLQAEQRLKAIVAEKFAIATKEG<br>DLPQVERFFKIFPLGLHEEGLRKFSEYLCKQVASKAEENLLMV<br>LGTDMSDRRAAVIFADTLTLFEGIARIVETHQPIVETYYGPR<br>LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQFRHVQNNLMRNS<br>TTEKIEPRELDPILTEVTLMNARSELVLRFLKKRISSDFEVDGS<br>MASEEVKQEHQKCLDKLLNNCLSLCTMQELIGLYVTMEEFMRE<br>TVNKAVALDTYEKGQLTSSMVDVFIKVCIGRALSSSSIDCL<br>CAMINLATTELESDFRDVLCNKLRMGFPATTQDIQRGVTSVN<br>IMHSSLQGGKFDTKGISTEAKMSFLVTLNNVEVCSENI STLK<br>KTLES DCTKLFSQIGGEQAQAKFDSCLSDLAASVSNKFRDLLQE<br>GLTELNSTAIKPQVQPWINSFFSVSHNIEEEFPNDYEANDPWVQ<br>QFILLNEQQMAEFKASLSPVIYDSLTLGMLTSLVAVELEKVVLS<br>TFNRLGGLQFDKELRSLIAYLTTVTWTIRDKFARLSQMATILN<br>LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR<br>LRL |
| 6593       | 3  | 1837   | EAFSAGSRRRGLALQRGVILGGLGGYCPCCRRRGRLLVLLLLVR<br>RGGEQGGGRGRGDKRRRRQARRQRRRPEPAEARGGKMADVLSVL<br>RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNVYVWGTEGKEQPR   |

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|------------|--|--|---|
|            |  |  | EYITLDSILFLLNNVHLSHPVYVRRRAATENIPVVRPDRKDLLG<br>YLNGEASTSASIDRSAPLEIGLQSRSTQVKRADEVLAEEKPRI<br>EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA<br>IKAKIMAKKRSTIKTDLDDITALKQRSFVDAEVDVTRDIVSRE<br>RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAPN<br>AAPVDPTLRKTQPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH<br>GMTLKSVTGASARKTQTPAAQPVPRPVSQARPPPNQKKSRTPT<br>IIIIPAAATSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETH<br>IQRRKDOMQPGGTAISVTVPYRVVDQPLKMPQDWDRVVAVFVQ<br>GPAWQPKGWPLLDPGSPVDIFAKIKAFHLKYDEVRLDPNVQKW<br>DVTVLELSYHKRHLDRPVFLRVWETLDRYMKHKSHLRF |
| 6594       | 1  | 1096   | EFPGRFRGSGASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA<br>DILSTIGYDNIQIHLNNGRKNCKEFEDFLKRAAIEERYGKDLL<br>NLSRKKPCQSEINTLKRALEVFKQQVDNVAQCHIQLAQLSREE<br>ARKMEEPREKQKLQRKKTELIMDAIHKQSLQFKKTMDAKNYE<br>QCRDKDEAEQAVSRANLVNPKQKEKLFVKLATSKTAVEDSDK<br>AYMLHIGTLDKVVREEWQSEHIKACEAFAEQECERINFFRNALWL<br>HVNQLSQQCVTSDMEYEQVRKSLMCSIQRDIEYFVNQRKTGQI<br>PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP<br>NYSLVDDYSLLYQ  |
| 6595       | 57   | 781  | PLGTMSDSDLGDEGLLSLAGKRKRGRNLPKESVKILRDWLYLH<br>RYNAYPSEQEKLISLGGQTNLSVLQICNWF INARRLLPDMLRKD<br>GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS<br>VCSMPLHSGQGEKPAAPFPGELESFKPLVTPGSTLTLLTRAEA<br>GSPSTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAEMELQK<br>QDPSPLPLHTPIPLVSENPO   |
| 6596       | 2  | 1026   | PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAIY<br>GEWCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYPGTAP<br>PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD<br>VLIQKSQMTPEGPDVKKKTEEDVECEDDLILACQPESSVKALD<br>FDISETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVVCVKQV<br>KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLODCEDDGETA<br>AGGRLLHLMELILNVKNVMVVSRWYGGILLGPDRFKHINNCARN<br>ILVEKNYTNPSPESSKALGKNKKVRKDKKRNEH   |
| 6597       | 2  | 1026   | PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAIY<br>GEWCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYPGTAP<br>PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD<br>VLIQKSQMTPEGPDVKKKTEEDVECEDDLILACQPESSVKALD<br>FDISETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVVCVKQV<br>KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLODCEDDGETA<br>AGGRLLHLMELILNVKNVMVVSRWYGGILLGPDRFKHINNCARN<br>ILVEKNYTNPSPESSKALGKNKKVRKDKKRNEH   |
| 6598       | 1099   | 419  | PRVRWATTMAMSFEPWQYRFPFPFTLQPNVDTRQKQLAAWCSL<br>VLSEFCRLHKQSMTVMEAQESPLFNNVKLQKLPVESIQIVLEE<br>LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRGQNNVS<br>FTLYELTNGEDTEDEEFHGLDEATLLRALQALQEHKAEIITVS<br>DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPFKTGSVTPPD<br>SKGLQS  |
| 6599       | 164  | 1593   | KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR<br>MMEVAAADVQKLGGSVELVDIGKQKLPDGSEIPLPPIILGLRGS<br>DPQKTKVCIYGHLDVQPAALDEGWSEPTLVERDGLHGRGST<br>DDKGPVAGWINALEAYQKTGQEI PVNVRFCLGMEESGSEGLDE<br>LIFARKDTFFKDVYVCISDNYWLGKKKFCITYGLRGICYFFIE<br>VECSNKLHSGVYGGSVHEAMTDLILLMGSVLVDKRGNLIIPGIN<br>EAVAAVTFEEHKLYDDIDFIDIEFARKDVGAQILLHSHKKDILMH<br>RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE   |



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|------------|--|--|--|
|            |  |  | VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPPWVSDFSHPHYL<br>AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVNLPPVGS<br>ADGAHSQNEKLNRYNIEGTMMLAAYLYEVSQLKD  |
| 6600       | 2  | 934  | PGRLFRVAAMESAGLEQLLRELLLPETERIRRATEQLQIVLRAP<br>AALSALCDLLASADPQIRQFAAVLTRRLNTRWRRLAAEQRES<br>LKSLLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLLQLL<br>QHSTHSPHS PEREMGLLLSVVTSRPEAFQPHHRELLRLNET<br>LGEVGSFGLLFYSLRTLTTMAPYLSTEDVPLARMLVPLIMAMQ<br>TLIPIDEAKACEALEALDELESEVPVITPYLSEVLTFCLEVAR<br>NVALGNAIRIRILCCLTFLVKVKS KALLKNRLLATLAHPFPHC<br>GC  |
| 6601       | 529  | 1420   | PRAAARAPPPAVLRDRRAATAPGAGEMTLHGPLAQRYFLNHIE<br>KITTWQDPRKAMNQLNHNMLHPAVSSTPVQSRMAVSQPNLVM<br>NHQHQQCMAFSTLSQQNHPTQNP FAGLSMSPNALTTQQQQQKL<br>RLQRIQMERERIRMRQELMRQRAALCQRLPMEATLAPVQAAV<br>NPPTMTFDMRSITNNSDDPFLNGGPHYHSREQSTDGSLGLGCYV<br>PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFDCLPGT<br>NVDLGTLESEDLIPLFNDVESALNKSEPLTWL   |
| 6602       | 127  | 617  | LLDFPALPKFVLAQSPKAGKPTNTSMQSLREVIKAMTKARNF<br>BRVLGKITLVSAAPGVKVICEMKVEEHTNAIGTLHGGLTATLVD<br>NISTMALLCTERGAPGVSDMNITYMSPAKLGEDIVITAHVLKQ<br>GKTLAFTSVDLTNKGKLIAGGRHTRKHLGN  |
| 6603       | 79   | 660  | PVGPSLSAARTGLGHLFFLHRLASSRGLDMDLLQFLAFLFVLLL<br>SGMGATGLTLRTSLDPSLEIYKMFEBVKRREQLLALKNLAQLNDI<br>HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGFPPQDEKLD<br>AFSHVVENTAFFGDVVLRFPRIVHYFFDHNSNWNLLIRWGISFC<br>NQTGVFNQGPSPILSLM  |
| 6604       | 3  | 688  | TSTAQRQGGGRMSFRGGGRGGFNRGGGGGFRNGSSNHFRGGG<br>GGGGGGRFRGGGRGGFGRGGGRGGFNGQDQGPPERVLLGEFL<br>HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLR<br>DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFPLPRPPGEK<br>GPPRRGGGRGGGRGGGRGGGRGGGRGGFRGGGRGGGGFRGGRG<br>GGFRGRGH   |
| 6605       | 7  | 848  | SGSRRAVRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV<br>ALVAVAEHSGBFKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR<br>SVTLKDLVALPIIENYKDRLLAIGEVGLDFSPRFAGTGEQKEE<br>QRQVLIRQIQALAKRLNLPVNVHSRSAGRPTINLLQEQAQAEKVL<br>HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQLVKQLPLTSIC<br>LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEVIEVTT<br>QNALKLFPKLRHLLQK   |
| 6606       | 2  | 1682   | FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS<br>KSLGLIEGYGGRGKGLPATLSPAEBEKAGPHEKYGYNSYLSE<br>KISLDRSIPDYRPTCKELKYSKDLQISIIFFVNEALSIVLR<br>SVHSAVNHTPTHLLKEIILVDDNSDEBELKVPLEEYVHKRYPGL<br>VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP<br>VLSRIQENRKRVLPSIDNIQDNFEVQRYENSAHGYSWELWCM<br>YISPPKDWWDAGDPSLPRTIPAMIGCSFVVRNKFGEIGLLDPG<br>MDVYGGENIELGIKVLGCGSMEVLPCSRVAHIERKKKPYNSNI<br>GPYTKRNALRVAEVMDDYKSHVYIAWNLPLENPGIDIGDVSR<br>RALRKSLSKCKNFQWYLDHVYPEMRRYNNIVAYGELRNKAKDVC<br>LDQGPLLENHTAILYPCHGWGPQLARYTKEGFLHIGALGTTLLP<br>DTRCLVDNSKSRLPQLLDCDKVKSLSLYKRWNFIONGAIMNKGTC<br>RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK |
| 6607       | 137  | 986  | VPACAGLKKKARSLLASPPRLNLTQLQASCRAFLSPFIQSRQTT<br>GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFFSSLQTKQRPSKD<br>KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP   |

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|------------|--|--|---|
|            |  |  | SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSKVKE<br>DPVTALSILLRGTVHEKLRWTFNLVDINKGQYINQEEMMDIVKA<br>IYDMMKQYTPVLKEDTPRQHVDFVFQKMDKNKDQIVTLDEFLE<br>SCQEDDNIMRSLQLFQNVN  |
| 6608       | 224  | 1140   | RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPPSPMSVATRS<br>TGTLLQPPQKPFQGEASLPLAGEEELSKEGQDCALEELCKPLY<br>CKLCNVTLNSAQQAQAHYQGNHKKLRNYAANSCTPPPARMSN<br>VVEPAATPVVPVPPQMGSKFPGGRVILATENDYCKLCDASFSSP<br>AVAQAHYQGNHAKRLRLAEAQSNFSSESSELGQRRARKEGNEF<br>KMMPNRRNMYTVQNNSCPYFNPRSRQRIPRDLAMCVTFSGQFYC<br>SMCNVAGAGEMEFRCHLESQHKSKVSEQRVRENEMENLGYV   |
| 6609       | 1  | 443  | FLRCRRFRVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT<br>PAAEPGNFQLSPAEPGRGLASPVRAAPRAPCPAAEMSELNKTTS<br>PATNQAGQEEKGKAGNVKKAEEEEIDIDLTAPETEKAALAIQ<br>GKFRRFQKRKKDPSS  |
| 6610       | 319  | 881  | GRKSLCNLHIFIRFPLTYPDYMGMMCTAKKCGIRFQPPAILLI<br>YESEIKGKIRQIRMPVRNFSKFSCTRAAEQLKNNPRHKSYLEQ<br>VSLRQLEKLFSLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL<br>DDKELAKRKSIMDELFEKNQKKDDPNFVYDIEVEFPQDDQLQS<br>CGWDTESADEF   |
| 6611       | 978  | 212  | PGCSGAGSRVWVLPALRHLAMGSTESSEGRVSVFGVDEEERVV<br>LQGVRLSENVNRMKEPSSPPAPTSTSTFGLQDGNLRAPHKEST<br>LPRSGSSGGQPPSGMKEGVKRYEQEHAAIQDKLFQVAKREREA<br>TKHKSASLPTGEGSISHBEQKSVRLARELESREAELELRRTD<br>EQLEBRIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL<br>QAQILHCHYRDRPHEVILLCSDLVKAQRCVSAHKG   |
| 6612       | 1724   | 992  | VSTHASALSRTQGPQRPRAAASGAGAGTAGGGGSGGAEGSKM<br>STEAQRVDDSPSTSGSSSDGDQRESVQOEPEREQVQPKKKEGKI<br>SSKTAALKSTSAKRIQKELAEITLDPNCSAGPKGDNIEWRS<br>TILGPPGSVYEGGVFFLDITFS PDYPPKPKVTFRTRIVHCIN<br>SQVICLDILKDNWSPALTISKVLSICSLTDCNPADPLVGS I<br>ATQYMTNRAEHDRMARQWTKRYAT  |
| 6613       | 130  | 748  | ELELSSNMPEQSNDRVAVFGAGGVGKSSLVLRVFKGTFRSEYI<br>PTVEDTYRQVISCDKSICTLQITDITGSHQFPAMQRLSISKGHA<br>FILVYSITSRQSLEELKPIYEQICEIKGDVSEIPIMLVGNKCDE<br>SPSREVQSSEAEALARTWKCAFMTSAKLNHNKELFQELNLE<br>KRRTVSLQIDGKKSQQRKEKLKGCVM  |
| 6614       | 3  | 1191   | SSAAEAMRVLVRRCWGPPLAHGARRGRFSPQWRALRLGWEDCR<br>DSRVREKPPWRVLPFGTDQFAEALRALHAARENKEBELIDKLE<br>VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF<br>GRLLNEALILKFPYGIILNVHPSCLPRWRGPAPVIHTVLHGDVT<br>GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN<br>MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS<br>EQIFRLYRAIGNIIPLOTLWMANTIKLLDLVEVNSSVLADPKLT<br>GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSILTATDFY<br>NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVMQQCIE |
| 6615       | 832  | 35   | GRVGAGASAMSELPGDVRAFLREHPSRLQTDARKVRCILTGHE<br>LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPIHVPSTKNPH<br>QLFCKLTLRHINKCPEHVLRLHTQGRRYQALCKYEECQKQVEY<br>VPACLVHRRRRRBDQMDGGRPREAFWEPTSDEGGAASDDSM<br>TDLYPPELFTRKDLGSTEDGDTDDFLTKDEKAKKPPREKATD<br>EGRRETTVYRGLVQKRGKKQLGSLKKKPKSHHRKPKSFSSCKQS<br>G  |
| 6616       | 347  | 1886   | LLPFCQCARPLSSPPHASEDNLFWFNCLCAPPHSPQPLQYP<br>VWPLELLVITQIPAPRHLNRPFSSRGGLDSFSGSLSTPSICRS  |

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|------------|--|--|--|
|            |  |  | PAWVKMAPHPKGLVPAVLWGLSLFLNLPGPFWLQPSPPPPQSSP<br>PPQHPCHTCRGLVDSFNKGLERTIRDNPGGNTAWEEENLSKY<br>KDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQEA<br>PDLFQWLCSDSLKCCPAGTFPGSCLPCPGGTERPCGGYVQCEG<br>EGTRGGSGHCDQAGYGGEACGQCGLYPEAERNASHLVCSACF<br>GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD<br>QFCVNTGSEYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC<br>LDVDECETEVCFGENKQCENEGGYRCICAEGYQMEGICVKEQ<br>IPESAGFFSEMTDELVVQLQMFPGIIICALATLAAKGLDLVFTA<br>IFGAVAAMTYWLSERSDRVLEGFIKGR  |
| 6617       | 118  | 673  | VMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS<br>LSYHLDTKVRCPMCWQAVDGSLSLPNVSLAWVIEALRLPGDPEP<br>KVCVHRNPLSLFCEKDQELICGLCGLLGSHQHHEVTPITVCS<br>RMKEELALFSELKQEQKKVDELIAKLKVNTRIDGSAPSLCPC<br>LGPATFTFL   |
| 6618       | 548  | 136  | DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR<br>NVPKMTSERSRIPCLSAAAAGTGKKQEGRAMATLDRKVPSPPE<br>AFLGKPWSSWIDAALKHCSNDVLEAGKEGGSREVMRLNKEA<br>WKYGT  |
| 6619       | 246  | 842  | PASSEVLTAAMVFLLLNCIVAVSQNMGIGKNGDLFRPPLRNEFR<br>YFQMTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKURINLVLS<br>RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV<br>YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG<br>ILSDVQEGKHICYKFEVCEKDD   |
| 6620       | 3  | 1879   | NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE<br>DEPAPAAPLRGRKDEDAFLGDPDTPDPSFLKSARLQRLPSSSSS<br>MGSQDGSPLRETRKDPFSAAAAECSRCRQDGLTVIVTACLTATG<br>VTVALVMQIYFGDPQIFQCGAVVTDAARCTSLGIEVLKQGSVS<br>DAAVAAALCLGIVAPHSSGLGGGVMLVHDIRNESHLDIFRES<br>APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS<br>QVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFPSG<br>RPPLGSLHRLPDLAEVLDVLGTSGPAFYAGGNLTLEMVAEQ<br>HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI<br>SALNILEGFNLTSLSVREQALHWAETLKIALALASRLGDPVYD<br>STITESMDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT<br>AAQVLIMGPDDFIVAMVSSLNQPFSGSLITPSGILLNSQMLDFS<br>WPNRTANHSAPSLNSVQPGKRPLSFLPTVVRPAEGLCGTYLA<br>LGANGAARGLSGLTQVRFTPWLAFFSREPSCLDCRCLSYLWL<br>SIPHAANMG |
| 6621       | 1  | 662  | VQGITSYQRLQALRKEKSRDAARSRRKENFEFYELAKLLPLP<br>AAITSQLDKASIIRLTISYLMRDFANQGDPPWNLRMGPPNPNT<br>SVKVIGAQRRRSPSALAIEVFEHLGSHILOSLDGYVFALNQEG<br>KFLYISETVSIYLGSLQVELTGSSVFDYVHPGDHVEAEQLGMK<br>LPPGRGLLSQGTAEQGASSASSSSQSETPEPVVCFPPASDQFLL  |
| 6622       | 2  | 319  | GRASGAQEBETEAGGPERARAMEANMPKRKEPGRSLRIKVISMG<br>AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN<br>IFDMAGHPFFYEVRRPF  |
| 6623       | 1886   | 189  | KALFEKVKKFRHLHVEEGDILYAMYVROTVLKVKFLIITAYNSA<br>LVSKVQFTVDCNVDIQDMTGYNFSCNHTMAHLFSKLSFCYLCF<br>VSIYGLTCLYTLWLFYRSLREYSFEYVROETGDDIDPVKNDF<br>AFMLHMDQYDPLYSKRFAVFLSEVSENKQLQNLNNEWTPDKL<br>RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIKNMV<br>IPATIAQLDNLQELSLHQCSVKIHSALSLKENLKVLSVKFDD<br>MRELPPWMYGLRNLELYLVGSLSHDISRNVTTLESRLDKSLKI<br>LSIKSNVSKIQAQVVDVSSHQKMCIHNDGTKLVMLNKLKMTN<br>LTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEIVSFO   |

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|------------|--|--|---|
|            |  |  | HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH<br>LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP<br>DELYFCKKLTKLIGKNSLSVLSPKIGNLLPLSYLDGKGNHFEI<br>LPPELGDRCALKRAGLVVEDALFETLPSDVREQMKE   |
| 6624       | 218  | 1766   | GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRLSVKALGGC<br>RGRPSGLAHLSEQETSHWRAKRSGRACLDGPFGEILRSFIMKCTA<br>REWLVRVTTVLFMARAI PAMVVPNATLLEKLEKYMDEDEGENWIA<br>KQRKRAITDNDMQSILDLHNKLRISQVYPTASNMEYMTWDVELE<br>RSAESWAESCLWEHGPAALLPSIGQNLGAHWGRYRPPTFHVQSW<br>YDEVKDFSYPYEHCNPYCPFRCSGPVCTHYTQVWVWATSNRIGC<br>AINLCHNMNIWQIWPKAVYLVLCNYSPPKGNWGHAPYKHGRPCS<br>ACPPSFGGCGRENLCYKEGSDRYPPREETNEIERQQSQVHDT<br>HVRTSDSSRNEVISAOQMSQIVSCEVRLRDQCKGTTCNRYEC<br>PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR<br>QGRKHYPFKSNRNGIQITIGKYQSANSFTVSKVTQAVTCETTVE<br>QLCPFHKPASHCPRVYCPKLYASKSTLCSNWNSSLF   |
| 6625       | 1124   | 543  | PQPRGGGSGLLSTKALGRSRGLGMHGPSSGGTEGGVPTALRPP<br>GPLVPSTSDNLLKNIELFDKLALRFHGRLLFLKDLVLDGDEICCW<br>SFYGGGRKIAEVCCTSIYVATEKKQTKVEFPEARIPBETLNILI<br>YETPRGPDALLEATGGAAGAGGAGRGEDEENREHRVRRIRHVR<br>HITHDERPHGQIVFKD   |
| 6626       | 3  | 1498   | SAVEFVYTDTRFHLITLIGISVEFLCSLRSDATMESITACLHALQAL<br>LDVPWPRSKIGSDQDSGIELNLVLRVILTRESPSIQLASLEV<br>RQIIICAAQEHVKEKRRSAEVDGAAEKETLPEFGGKDTGGGLVP<br>GKSLVFATLELCVCILVRQPELNPKLGTSPGVKATKPKIILED<br>GSRLVSAALVILSELPAVCSPGSGSISILPTILYLTIGVLRATAV<br>KLPGGQLSSTVAASLQALKGILSSPMARABKSRTAWTDLLRSAL<br>TTILDWDPVDETHQELDEVSLLTAITVFILSTSPVTTIIPCLQ<br>KRCIDKFATLEIKDFVQIKTYQLLHSIFQYPNPAVSYPYIYS<br>LASCIMEKLQEI DKKRPENTAELEIFQEGIKVLETLVTVAEEHH<br>RAQLVACLLPILISFLDENSLSGATSIMRNLDHDFALQNLMOIG<br>PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS<br>PGKNSSIQLKTSFL   |
| 6627       | 1  | 697  | GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMML<br>GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV<br>KLQIWDTAGQERFRSVTHAYYRDAQALLLYDITNKSSFDNIRA<br>WLTEIHEYAQRDVIMLLGNKADMSSEVRSEDGETLAREYGV<br>PFLETSAGTMNVELAFALAIKELKYRAGHQADEPSFQIRDYVE<br>SQKKRSSCCSFM   |
| 6628       | 1  | 1861   | QCAEFGGGSGGGGGSGGGSGGGGAGGGEENKENERPSAGSKAN<br>KEPGDSLSEILQIIKESQQQHGLRHGDFORYRGYCSRRQRRLR<br>KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM<br>QLKQEAANTEPRKRFHLSRLRKAVKHAEELERLCESNRVDAKTK<br>LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE<br>EQAVLYNQRVVEISPNIRYCAYNIGDQSAINELMQMLRSGGTE<br>GLLAEKLEALITQTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL<br>GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVRLEELKPDQ<br>KORDYILEGEPGKVSNLQYLHSYLTIIKLSTAIKRNNEMAKGLQ<br>RALLQQQPEDDSKRSRPRQDLIRLYDIIILQNLVELLQLPGLLED<br>KAFQKEIGLKTLLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK<br>YANEVNSDAGAFKNSLKDLPDVOELITQVRSEKCSLQAAAILDA<br>NDAHQTETSSSQVDNKLVERFETFCLDPSLVTKQANLVHFPF<br>GFQPIPCPLFFDLALNHVAFPPLEDKLEQKTKSLGTGYIKGIF<br>GFRS |
| 6629       | 5653   | 4549   | GATFLGSVGGRTGKMDAATLTDTLRFAEFEDFPETSEPVWILG<br>RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC   |

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|------------|--|--|--|
|            |  |  | MLRCGQMIFAQALVCRHLGRDWRWTORRQPDSPSVLNAFIDR<br>KDSYYSIHQIAQMGVGEKSGIQWYGPNTVAQVLKKLAVFDTWS<br>SLAVHIAMDNTVMERIRRLCRTSVPCAGATAFPADSDRHCNGF<br>PAGAEVTNRPSRWRPLVLLIPLRLGLTDINAYVETLKHCFMMP<br>QSLGVIGGKPNASAHYFIGYVGEELIYLDPHTTQPAVEPTDGCPI<br>PDSEFHCQHPPCRMSIAELDPSIAVVRGGHLSQAFGAECCLGM<br>TRKTFGFLRFFFSMLG  |
| 6630       | 2  | 423  | LVQCGGIRRRSANGAMPGRHVSRRVRLYKRVLQHLRVLPDDLKS<br>LGDQYVKDEFRRHKTGVSDEAQRFLQEWVYATALLQANENRQ<br>NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI<br>SESMKPKF   |
| 6631       | 2  | 423  | LVQCGGIRRRSANGAMPGRHVSRRVRLYKRVLQHLRVLPDDLKS<br>LGDQYVKDEFRRHKTGVSDEAQRFLQEWVYATALLQANENRQ<br>NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI<br>SESMKPKF   |
| 6632       | 1273   | 588  | WNSRGRTQRGAAPLAPAAAMKAVVQVRVTRASVTVGGEQISAIGR<br>GICVLLGISLEDTQKELEHMRKILNLRVFEDESGKHSKSVMD<br>KQYEILCVSQFTLQCVLKGKPKDFHLAMPTEQAEFYNSFLEQL<br>RKTYPPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP<br>KQLSKLEKQQQRKEKTRAKGPSSESSKERNTPRKEDRSASSGAEG<br>DVSSEREP  |
| 6633       | 1145   | 617  | ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPGVGLHSNPMY<br>ANGANGLDAIITQLNQFENTGPPPADKEKIQAALPTVPVTEEHV<br>GSGLECPVKDDYALGERVRLPCNHLFHDGCIVPWLEQHDSCP<br>VCRKSLTGQNTATNPGLTGVSFSSSSSSSSSSSPSENATSNS  |
| 6634       | 1  | 1134   | CGGIPRKGSGPRRLPMARLRLDCLPRLMLTLRSLEFWSLVVYC<br>GLCASIHLLKLLWSLKGPAQTFRPAREHPPACLSDPSLGTHC<br>YVRIKDSGLRPHYVAAGERGKPLMLLLHGFPEFWYSWRYLREF<br>KSEYRVVALDLRGYGETDAP IHRQNYKLDCLITDIKDILDSLG<br>SKCVLIGHDNGGMIAWLIACYPFEMVMKLLVINPPHNPVTFEYI<br>LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG<br>IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCPLKH<br>HMVTPTLLWGENDAFMEVEMAETRFYVKNYFRLTILSEASH<br>WLQDQDPDIVNKLINTFLKEETRKKD   |
| 6635       | 1420   | 470  | EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAFSSSSG<br>GRGGAEPRLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK<br>ILAQTGRRLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPOLG<br>LVPCVVGHSMGGKTAMLLALQRPVELVERLIAVDISPVESTGVS<br>HFATYVAAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL<br>LTNLVEVDGRFVWRVNLDAITQHLDKILAFPQRQESYLGPTLFL<br>LGNSQFVHPSHHPEIMRLFPRAQMOTVPNAGHWIHADRPQDFI<br>AAIRGFLV  |
| 6636       | 1514   | 1801   | SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQFQRLKHPAE<br>QPIVRQCLQRPLCGVLGPVQQQLPPSLGVPVLSPHSDPGWCRVD<br>DGGDGVF  |
| 6637       | 2  | 1501   | CSSSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEAGKSKI<br>KASEDSLVLERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT<br>VVSFFCNNSYVLSGNEKRTCQQNGEWSGKOPICIKACREPKISD<br>LVRRRVLPQVQSRREPLHQLYSAAFSKQKLQSAPTCKKPPALPFG<br>DLPMGYQHLHTQLQYECISPFYRRLGSSRRRTCLRTGKWSGRAPS<br>CIPICGKIENITAPKTQGLRWQAAIYRRTSGVHDGSLHKGAN<br>FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVVLGKFYR<br>DDRDEKTIQSLQISAILHPNYDPIILLADIAILKLDKARIS<br>TRVQPICLAASRLSTSFQESHITVAGWNLADVRSPGPKNDTL<br>RSGVSVVDSLLCEEQEDHGIPVSVTDNMFCASWEPTAPSDIC<br>TAETGGIAAVSFPGRASPEPRWHLMLGVSWSYDKTCSHRLSTAF |

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|------------|--|--|---|
| 6638       | 1391   | 224  | TKVLPPFKDWIERNMK<br>GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPLGPM<br>PNSDIDLNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG<br>EKTDPPKEKIDIGLPPPKVSRITQQLLERKQAIQELRANVEERAA<br>RLRTASVPLDAVRAEWERTCGPYHKQRLAEVYGLYRDLFHGATF<br>VPRVPLHVAYAVGEDDLMPVYCGNEVTPTAAQAPEVTTYEAEEG<br>SLWTLTLLTSLDGHLLLEPDAEYLHWLLTNI PGNRVARGQVTCPYL<br>PPFPARGSGIHRALFLFKQDQPIDFSEARPSPCYQLAORTFR<br>TFDFYKKHQETMTAGLSPFQCRWDDSVTYIFHQLLDMREPVE<br>FVRPPPYHPKQKRFPHRQPLRYLDTRYRDSHEPTYGIY                  |
| 6639       | 2046   | 1268   | IGCFIMDGGDDNLIKKRFVSEALDERRRRRQEWEKVRKPE<br>DPEECPEEVDPRSLYERLQEQDKRKQEQEYEQFKFKNMVRGLD<br>EDETNFLDEVSRQELIEKQRREBELKELKEYRNNLKKVGISQE<br>NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSSESGNSVKRL<br>KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPAAVCIGILPGL<br>GAYSGSSDSESSDSEGTINATGKIVSSI FRNTTFLEAP   |
| 6640       | 117  | 1043   | VLEPPDVSMASEDRSLRIVLVGKTGSGKSATANTILGEITFDS<br>RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE<br>ISRCIISSCPGPHAIVLVLLGRYTEEBQKTVALIKAVFGKSAM<br>KHMVILFTRKEBLEGQSFHDFIADADVGLKSIKCEGNCRCASF<br>NSKKTSKAEKESQVQELVELIEKMQVCNEGAYFSDDIYKDTEER<br>LKQREEVLRKIYTDQLNNEIKLVEEDKHKSEKKEKEIKLLKLK<br>YDEKIKNIREEAERNIFKDFVFNRIWKMLSEIWHRFLSKCKFYSS   |
| 6641       | 1  | 894  | SAVGRRESEVRGCAPRRLRRSARRMDPVPGTDSAPLAGLAWSS<br>ASAPPPRGFSAISCTVEGAPASFCKSFAQKSGYFLCLSSLSGLS<br>NPQENVVADIQIVVDKSLPLGFSFVCDPMDSKASVSKKRMVC<br>KLLPLGATDTAVFVRLSGKTKTVPGYLRIQDMGGFAIWCKKAK<br>APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS<br>TLRRNDIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF<br>GDLTIKSLADIEEYNYGFVVEKTAARLPSPVS   |
| 6642       | 22   | 1296   | PLEERMMTKMDPNDQARDIIFELRRIAFDAESDPSNAPSGTE<br>KRKAMYTKOYKMLGFTNHINPAMDTFTQPPGMLALDNMLYLAKV<br>HQPTYIRIVLENSREDKHECPFRSAIELTKMLCEILQVGLP<br>NEGRNDYIHPMFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN<br>KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER<br>MSQDDFQSPPIVELREKIQPEILELIKQRLNRLCEGSSFRKIG<br>NRRRQERFWYCRALNKHVLHYGDLDDNPQGEVTFESLQEKIPV<br>ADIKAIVTGKDCPHMKEKSALKQNKVELELAPSI LYDPDETINF<br>IAPNKYEVCIWIDGLSALLGKDMSSSELTKSDDLTLMSMEMKLRL<br>LDLENIQIPEAPPPPIKPEPSSYDFVYHYG |
| 6643       | 3049   | 2265   | SLHAPAEGRTRGRLEAKPKMLTRKIKLWDINAHITCRLCSGYLI<br>DATTVTECLHTFCRSLVKYLEENNTCPTCRIVIHQSHPLQYIG<br>HRTMQDIVYKLVPLQEAEMRKQREFYHKLGMVPGDIKGETC<br>SAKQHLDSHRNGETKADDSNKEAAEEKPEEDNDYHRSDEQVSI<br>CLECNSSKLRGLKRWIRCSAQATVHLKFKFIKKLNLSSFNEL<br>DILCNEEILGKDHTLKFFVVTRWRFFKAPLLHYRPKMDLL   |
| 6644       | 1489   | 290  | FRPLATEPRGSSPVQLVSSMTSVRTLPLFLNLGGEMLYILDQR<br>LRAQNI PGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR<br>TVYERLAHASIMKLNQASMDKLYDLMTAPKYQVLLCPRPKDVL<br>LVTFNHLDTIKGFIRDSPITLQVDETLRQLTEIYGGLSAGEFQ<br>LIRQTLILFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVWGT<br>EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL<br>KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF<br>LARLMGMEIKKPSGPEPGFRLNLTDEEBEEQAALTRPELSY<br>EVINIQTQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM<br>DEL                              |

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|------------|--|--|---|
| 6645       | 6530   | 4646   | FVEGLAGYVYKAASEGKVLTLAALLNRSSESDIRYLLGYVSQQG<br>GQRSTPLIIAARNGHAKVVRLLLEHYRVQTOQTGTVRFDGYVID<br>GATALWCAAGAGHFEVVLLVSHGANVNHTTVNSTPLRAACFD<br>GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE<br>QRADPNKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG<br>MTPLKVAEESCKADVVELLSHADCDRRSRIEAELELLGASFPAND<br>RENYDIIKTYHYLYLAMLERFQDGDNIKEVLPPIHAYGNRTE<br>CRNPQELERQDRDALHMEGLIVRERILGADNIDVSHPIIYRG<br>AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM<br>IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN<br>YECNLYTFLYLVCISTKTQCSEEDQCKINKQIYNLIHLDPRTRE<br>GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLDCGAEVNA<br>VDNEGNSALHIIVQYNRPISDFLTLSHIIISLVEAGAHDTMTNK<br>QNKTPLDKSTTGVSSEILKTKQMKSLKCLAAARAVRANDINYQDQ<br>IPRTLEEFVGFH                            |
| 6646       | 176  | 890  | PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY<br>EGREKKGISDVRRTFCLFVTFDLLFVTLWIIELNVNGGIENL<br>EKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL<br>TTAVTSAFLAKVILSKLFSQAGFYVLPPIISFILAWIETWFLD<br>FKVLPQEAEEENRLIIVQDASERAALIPGGLSDGQFYSPPESEA<br>GSEEAEEKQDSEKPLLEL  |
| 6647       | 176  | 890  | PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY<br>EGREKKGISDVRRTFCLFVTFDLLFVTLWIIELNVNGGIENL<br>EKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL<br>TTAVTSAFLAKVILSKLFSQAGFYVLPPIISFILAWIETWFLD<br>FKVLPQEAEEENRLIIVQDASERAALIPGGLSDGQFYSPPESEA<br>GSEEAEEKQDSEKPLLEL  |
| 6648       | 413  | 897  | RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL<br>IRPQKLINPVKTSRNHQDLHRELIMNQKGLAPQNKPELQKVM<br>KRKRQVQIKQKEEAQKKKSDLEIELLKRQKLEQLELEKQKQKQ<br>EEQENAPFVKVGNLRRGTQVEVAQAQES   |
| 6649       | 1357   | 832  | WIPRAAGIRHEVKWDVKEIMSQHNIIYVDALLKEFEQFNRRLENEV<br>SKRVRIPLPVSNIWEHCIRLANRTIVEGYANVKKCSNEGRALM<br>QLDFQQFLMKLEKLTDIRPIPKKEFVETIYIKAYLTENDMERWI<br>KEHREYSTKQLTNLVNVCGLSHINKKARQKLLAAIDDIRPKR   |
| 6650       | 32   | 765  | LVPLVFSLLVQSCQVYRSIAMKFVPCLLVTLSCGLTLGOAPR<br>QKQGSTGBEFHFTQGGSDCTMRPSSLGQGAGEVWLVRVDCRNTD<br>QTYWCEYRGQPSMCQAFADPKSYWNQALQELRLHHAQCGAPV<br>LRPSVCREAGPOAHMQQVTSLLKGSPEPNQQPEAGTPSLRPKAT<br>VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGNEEAK<br>KKAWEHCWKPFQALCAFLISFFRG   |
| 6651       | 3425   | 1353   | AKELLKVGDFSLCAGFYQNTADTMENLSKEPLASFVSESFDISA<br>CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG<br>DSDDLGLGDCRNPRLDLEDSTYLRGSYTRKKDVPTDGYESSLNF<br>HNNNQEDWGCSSWVPGMETSLLPGHWTAAVKKEKCVPPYVQIR<br>DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW<br>TSTWQVADDLTQNTLDLBYLRFHAKLKQTIKNGDSQHSASSANV<br>FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP<br>RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL<br>NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQIFQDKELN<br>DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA<br>CKSTFLFLVETEDKSFVVRTKNLLRKGGHTEIEPQHFCQAFHR<br>ENDTLIIIRNEDISSHLHQIPSLKLKHFPSVIFAGVDSPGDV<br>LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIKILEKLNNG<br>RNKWLHYRENKCLKEDERVSTAHKKNIMLKSFSANIELLH<br>YHQCDSRSSTKAEILKCLLNLIQIHIDARFAVLLTDKPTIPREV |

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|------------|--|--|---|
| 6652       | 2  | 1343   | FENNIGILVTDVNNFIENTEKIAAPFRSSYW<br>IPGSTISCSCHSRRLRGGSAPRLSLGAASFRPRPPSLPLPLPL<br>PFPLFLPTRPAERAWIRRRASEWVGKMEVPRLDHALNSPTSPC<br>EEVIKNLSLEAIQLCDRDGNKSKQDSGIAEMEELPVPHNIKISNI<br>TCDSFKISWEMDSKSKDRITHYFIDLNNKENKNSKFKHKDVPT<br>KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVE<br>WSEIEFCTADYSKVHLTQLLEKAEVIAGRMKFSVFYRNQKKE<br>YFDYVREHHGNAMQPSVKDNGSHGSPISGKLEGIFPSCSTEFN<br>TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFPYCMYTAYHYV<br>ILVIAPVSGPGDEFCKQRLPQLNSKDNKPLTCTEEDGVLVYHHA<br>QDVILEVIYTDPPVDSLGLTVAEITGHQLMSLSTANAKKDPSCKT<br>CNISVGR  |
| 6653       | 170  | 1910   | FFLEPRLRPFPPASRARFVPARTRPSPLHPCCFEGGGSMLSPO<br>RVAAAASRGADDAMESKPGPVQVVLVOKDOHSFELDEKALASI<br>LQDHIRDLDDVVVSAGAFKRGKSFILDFMLRYLSQKESGHS<br>NWLGDPEEPLTGFSWRGSDPETTGIIQWSEVFTVEKPGGKKVA<br>VVLMDTQGAQDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED<br>DLQQLQLFTEYGRLAMDEIFQKPPQTLMPLVRDWSFPYEYSYGL<br>QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLPLPHG<br>LQVATSPDFDGKLDIAGEFKEQLQALIPYVLNPSKLMKEKEING<br>SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAAA<br>SAKDIYNNMEEVCGGEKPYLSPDILEEKHCEFKQALDHFCKT<br>KKMGKKDFSFRYQOELEEEIKELYENFCKHNGSKNVFSTFRTPA<br>VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY<br>IRYSGQYRELGGAIIDFGAAYVLEQASSHIGNSTQATVRDAVVGR<br>PSMDKKAQ |
| 6654       | 1  | 705  | RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNLVSCALPM<br>WKVTAFIGNSIVVAQVWEGWMSCVVQSTGQMCKVYDSLLAL<br>PQLQAARALCVIALLVLFGLLVYLAGAKCTTCVEEKDSKARL<br>VLTSGIVFVIGSVLTLPVCWTAHAVIRDFYNPLVAEQKREL<br>ASLYLGWAASGLLLLGGLLCCTCPSGGSGQPSHYMARYSTSAP<br>AISRGPESEYPTKNYV  |
| 6655       | 341  | 16   | KDAYMPKKGLLALALVFSLPVFAAEHWIDVRVPEQYQOEHVQGA<br>INIPLEKVKER IATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG<br>YTHVENAGGLKDIAPEKVKG   |
| 6656       | 2  | 1212   | TELPFRPANLAIQPPLSPLRALAPLPEKPGAVPPQKRMKAVAK<br>DLNPGVKKMSLQQLQSARGVACLGCKGTCSGFEPHSWRKICKSC<br>KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY<br>KRNRMIMTNPIATGKDPFTDTITYEWAPPGVTQKLGQYMEIIP<br>KEKQPVGTGEGAFYRRRQLMHQLPIYDQDPSRCRGLLENELKLM<br>EEFVKQYKSEALGVGEVALPGQGLPKEEGKQOEKPEGAETAA<br>TTNGSLSDPSKEVEYVCBLCKGAAPPDSPVYSDRAGYNQWHP<br>TCFVCAKCEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI<br>IFAEDYQORVEDLAHRRKHFVCEGCEQLLSGRAYIVTKGQLLCPT<br>CSKSKRS   |
| 6657       | 830  | 2120   | LLTQERAGDCLLSASTMKEVVYWSFKKADVLLLENAMPEYCEP<br>LEHFTGQDLINLTQEDFKKPLCRVSSDNGQRLLDMIETLMEH<br>HLEAHKNGHANGHLNIGVDIPTPDGSSFSIKIPNGMPNGYRKEM<br>IKIPMEPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVHER<br>VPPKEVQPPPLPDTFFDHFNVRVQWAFSICEINGMILVGLWLIQWL<br>LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLFVPGMHFNCSPK<br>LFGDWEAQLRRIMKLIAGGGLSITGSHNMGCDYLYSGHTVMTL<br>TYLFIKEYSPRRLWYWHICWLLSVVGIFCILLAHDHYTVDVVV<br>AYIITRLFWYHTMANQQVLKEASQMNLLARVWYRFPQYFEK<br>NVQGIIVPRSYHWPFPWPVHLRQVKYSRLVNDT   |
| 6658       | 35   | 855  | HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQTLEGLTKRMLM   |



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|------------|--|--|--|
|            |  |  | FDPVPVKQEAAMDVSVSYPSNYMESMKPNKYGVYISTPLPEKFF<br>QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSSLKFPSSHRRRA<br>SPGLSMPSSSPPIKKYSPSPGVQPFVPLSMPPVMAAALSRRHG<br>IRSPGILPVIQPVVQPVFMYTSHLQQLMVLSEEMENSSSS<br>MQVPVIESYEKPISQKKIKIEPGIEPORTDYYPEEMSPPLMNSV<br>SPPQALLQE   |
| 6659       | 18   | 523  | EPQRGDCETWFQNCSLPKFVCFCCWGFWLWRAHSMNSNLHSLPGL<br>RGLTSISRNLQCTNAMRVINNYORRWKQNTFLLATFANVNVN<br>CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY<br>AQTPANMFYIVACDNRDQRRDPPQYVVPVHLHTII   |
| 6660       | 514  | 1707   | CAASLDCRRHLCEDPMKLVWPSAKILLQAAAGASARACDSVTSNV<br>LPLLEQFHKHSQSSQRRRTILEMLLGLKLLQKKWSYEDKQDRPL<br>NGFKDQLCSLVFMALDTPSTQLQLVGIRTITVLGAQPDLLSYED<br>LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL<br>VPKLAELRVGESNLNGDEPTQCSRHLCLQALSASVTHPSIV<br>KETLPLLLQHLWQVNRGNMVAQSSDVIQVCSLRQMAKCKQDDP<br>ESCWYFHQTAIPCLLALAVQASMPKEKPSVLRKVLEDEVLAAM<br>VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSLFNPENSPSRF<br>QPFQDGSSGQRRLLALLMAFVCSLPRNVSEHIWEVLLFNLDKVT<br>PG |
| 6661       | 179  | 430  | GVHAASGTLSATWLAELAKMFDLSLAKAGKYLQAAKLMIGMPDYD<br>NYVEHMRVNHDPDQTPMTYEEFFRERODARYGGKGARCC   |
| 6662       | 185  | 423  | RSLPKPAPAQASITHCARFSGVTPTAKTAMSDGNTAFNALMYC<br>GPKADDGNI FSAACAPASSAVKASVVAQPGQAVIP  |
| 6663       | 3  | 1005   | RPVLSRVDVDFVPLPETSGRRKKLERMYSVDRVSDDIPIRTWF<br>PXENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAQTFERRER<br>SFPSRSWSDPTPMKADTSHDSRSDSLQSSHCTLDFAEDLDWDT<br>EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRDDPSII<br>PILYDHEHATFEDILEEIERKLVYHKGAKIWKMLIFCQGGPGH<br>LYLLKNKVATPAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM<br>GCYILGNPNGEKLFQNLRTLTMPYRVVTFBSPLELSAQGKQMIET<br>YFDPRLYRLWKSRLQHSKLLDFFDVL   |
| 6664       | 58   | 968  | PRLLRLPRSVVVMDSPWDELALAFSRTSMPPFFDIAHYLVSVMA<br>VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLAEPPPKF<br>LANHTNILLASSIWIYITFFCPHDLVSQGYSLPVQLLASGMKEV<br>TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIIITNFERL<br>VKGDWKPEGDEWLKMSYPAKVTLGSGVIFTFOHTQHLAISKHNL<br>MPLYTIFIVATKITMTTQTSTMTFAPFEDTLSSMMLFGWQPPFS<br>SCEKKSEAKSPSNGVGLSKPVDVASDNVKKHTKKNE   |
| 6665       | 171  | 1278   | DERRLACRQVVTQQRSELYPGFQKRQRFPLPKAGEZAAAQGGRLH<br>PGRWLGPCTQNPSCSVHTATGPEPRKLPLLPDPSNSGYKPEPA<br>ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCTVFPIDLAK<br>TRLQNQHGMKMYKGMIDCLMKTARAEGFFGMYRGAANLTLVTP<br>EKAIKLAANDFFRRLMEDGMQRNLKMEMLAGCGAGMCQVVVTC<br>PMEMLKIQLDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS<br>ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN<br>LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLLK<br>KGLGEDMYSGITDCAR                                |
| 6666       | 498  | 2868   | MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL<br>WSPGCWQPIQKEGVGLWDIRKPOSSLLRYGGNLSLQSAMSVRF<br>NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNCTMKSC<br>CFAGDRDQYILSGSDDFNLYMWRI PADPEAGGIGRVVNGAFMVL<br>KGHRISVNVQVRFPNPTMYMICSSGVEKIIKIWSPYKQPGCTGDL<br>GRIEDDSRCLYTHEEYISLVLSNGSGLSHDYANQSVQEDPRMA<br>PFDLSVRREIRGWSDDSDSLSESTILQLHAGVSESGYTDSES<br>SASLPRSPPTVDESADNAFHLGPLRVTTINTVASTPPTPTCED   |

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|------------|--|--|--|
|            |  |  | AASRQQLSALRRYQDKRLIALSNESDSEENVCEVLDLDFPR<br>PRSPPEDESSSSSSSSSEDEELNERRASTWQNRAMRRRQKT<br>TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSTSSPERST<br>STLEIQPSRASPTSDIESVERKIYKAYKWLRYSIYSNNKDG<br>TSLVTGEADEGRAGTSHKDNPAOSSKEACLNIMAQNRQDLPP<br>EGCSKDTFKEETPRTPSNGPGHEHSHAWAEVPEGTSQDTGNSG<br>SVEH7FETKKLNGKALSSRAEPPSPVPKASGSTLNSGSGNCP<br>RTQSDDSEERSLETICANHNNGRLHPRPPHNNQNLGELEV<br>AYSSPOHSDTRDNNSSLTGLLHKDCGSEMACETPNAGTRDP<br>TDTPATDSSRAVHGSHGLKRQRIELEDTSSENSSEKKLKT |
| 6667       | 171  | 1310   | AEVERLAAMRSDSLVPGTHPTPIRRRSKFANLGRIFKPKWKR<br>KKSEKFKHTSAALERKISMRQSRREELIKRGVLKEIYDKGELSI<br>SNEEDSLENGQSLSSSLSLPALSEMPPVMPDRDPCSVEVLQPS<br>DIMGDPDGPAPVKLPCLPVKLSPLPPKVMICMPVGGPDLPLV<br>SYTAQKSGQQGVAQHHTVLPVLSQIQHQLQYGHGQHLPTTGS<br>PMHPSGCRMIDELNKTAMTMQRLESSEQRVPCSTSYHSSGLHS<br>GDGVTKAGFMGLPEIRQVPTVVIECDONKENVPHESDYEDSSCL<br>YTREEEEEDEDDSSSLYTSSLAMKVCRCDSLAIKPSNRPSKR<br>ELEKNILPRQTDREERLELRQOIGTKL  |
| 6668       | 714  | 358  | TLAVATGPALTLRCHVCTSSSNCKHVVCPASSRFCKTTNTVPE<br>LRGNLVKDCAESCTPSYTLQGVSSSGTSQCCQEDLCNEKLH<br>NAAPTRTALAHSAISLGLALSLLAVILAPSL  |
| 6669       | 459  | 1207   | KDETRKDYDMLDHPERYSHYHYYSRRLAPKVDVRVVLVS<br>VCAISVFOFFSWNSYNKALSYLATVPKYRIQATEIAKQGLLK<br>KAKEKGKKSKEEIRDBEENIKNIKSKIDIKGGYQKPOICD<br>LLFQIILAPPHLCYIYVWYCRWIYNFNKKGKEYGEEERLYIR<br>KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEELK<br>KKLANDPRWKRYRRWMKNEGPGRITFVDD  |
| 6670       | 184  | 594  | VARI*GEAAKMSSEPPPPYPGGPTAPLLEKSGAPPTGRSSPA<br>VMQPPPGMPLPADIGPPPYEPGHPMPQPGFIPPHMSADGYM<br>PPGFPYPPGPHPPMGYPPPGPYTPGPYPGGGHTATVLVPSGAA<br>TTVT   |
| 6671       | 1  | 763  | LPAEKPRAPNMAGGRCGPQLTALLAAWIAAATAAGPEEAALP<br>PEQSRVQPMNTASNWTLVMEGEWMLKFPYAPWCPSQQOTDSEWAF<br>AKNGEILQISVGKVDVIEPGLSGRPFVTTLPAPFHAKDGIFFR<br>YRGPGEFEDLQNYILEKKWQSVEPLTGWKSASLTMSGMAGLFS<br>ISQKIWHLHNYFTVTGLIPAWCSYVFFVIATLVFGLSMDLVL*V<br>ISQCNWDPYPYRHVS*/RPSTNLGVHTAHTSEHLRL  |
| 6672       | 304  | 1089   | APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGILGLAYAMAHT<br>GVIFFLALLLCIALSSYSIHLLLTACIAGIRAYEQLGQRAFG<br>PAGKVVVATVICLHNVMGAMSSYLFIKSELPLVIGTFLYMDPEG<br>DWFLKGNLLIIIVSVLIIILPLALMKHLGYLGYTSGLSLTCLMFF<br>LVSVIYKKFQLGLCYRATMKQWSEALVGTPOPRDSTA AVKAQ<br>MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFOAQD   |
| 6673       | 1116   | 1963   | LQIQTHHTHHGARVTHLGSQHLLANAGTMLCRQSSSMAPAFSQ<br>SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV<br>WLCPCVAFHARGARPOAEEGGARWNSLVSSPWIIPNP*HSSIGAE<br>NAVPRP*QG*KVNPSSQGERQS\WVLPPLVPGEPLKLPGLPG*NK<br>SFSRV/SGSKGKWLPRQLM*AS*R\TPRFVPGTQWVPIW/PL<br>ITWH*SAPTPLKACAPAPRESDPCCSSCLSCPCVTOHPRFSDTGW<br>FGAGHCHSSCDFTRKGAAGGPG   |
| 6674       | 1  | 440  | LEFDYMCQDYVEVRDGDNRDQGIKRVCGNERPAPIQSIQSSL<br>HVLFSHDSKNGFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY<br>KCACLAGYTGQRCENLEERNCSDPG/WPSQWVPENNRGPWAYQ<br>PTPC*IGTRVAFFLT   |

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|------------|--|--|---|
| 6675       | 277  | 1678   | GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD<br>LEKIHPPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR<br>RRSNTAQRLERLRERQNIKCKNIQWKERNKQSAQELKSLFE<br>KKSLEKEKPPISGKQSILSVRLQCPLQNNPFNEYSKFDGKGHV<br>GTTATKKIDVYLP LHSSQDRLLPMTVVIMASARVQDLIGLICWQ<br>YTSEGREPKLNDNVSAyclHIAEDDGEVDTDFPPLDSNEPIHKF<br>GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM<br>KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH<br>HYKSFKVSMIHLRLFTTDVQL/GCALFPGVLRKRAAPVDCLRPS<br>ADTWQRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ<br>KASTKFWIKQKPIISIDSLCAC\DLAEE                  |
| 6676       | 277  | 1678   | GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD<br>LEKIHPPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR<br>RRSNTAQRLERLRERQNIKCKNIQWKERNKQSAQELKSLFE<br>KKSLEKEKPPISGKQSILSVRLQCPLQNNPFNEYSKFDGKGHV<br>GTTATKKIDVYLP LHSSQDRLLPMTVVIMASARVQDLIGLICWQ<br>YTSEGREPKLNDNVSAyclHIAEDDGEVDTDFPPLDSNEPIHKF<br>GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM<br>KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH<br>HYKSFKVSMIHLRLFTTDVQL/GCALFPGVLRKRAAPVDCLRPS<br>ADTWQRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ<br>KASTKFWIKQKPIISIDSLCAC\DLAEE                  |
| 6677       | 277  | 1678   | GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD<br>LEKIHPPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR<br>RRSNTAQRLERLRERQNIKCKNIQWKERNKQSAQELKSLFE<br>KKSLEKEKPPISGKQSILSVRLQCPLQNNPFNEYSKFDGKGHV<br>GTTATKKIDVYLP LHSSQDRLLPMTVVIMASARVQDLIGLICWQ<br>YTSEGREPKLNDNVSAyclHIAEDDGEVDTDFPPLDSNEPIHKF<br>GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM<br>KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH<br>HYKSFKVSMIHLRLFTTDVQL/GCALFPGVLRKRAAPVDCLRPS<br>ADTWQRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ<br>KASTKFWIKQKPIISIDSLCAC\DLAEE                  |
| 6678       | 221  | 865  | GPSNQSSGSLSLIVTGCSYWS*INDTCTILRVLSSNFRGQ*LR<br>PFPCSQQLPMSQGLWHLDCCPWVPYIPGQWRKGRQMRN*QS<br>LLGSDQESVGLDLCVFNFLHVLGLFP*PHELFLLPVVDLG<br>FLFPLLLQGGCHCLVLPANLVSAPOIGKLSCLRLQTHDELSRN<br>HHPLFLVVRWDVAKHLETVQSGLASLGFVGQHTSHGPP   |
| 6679       | 2  | 786  | LEFARGAMPFLGQDWRSPGQNWKTVDGWKRFLEKSGSFVSDL<br>SSYCNKEVYNKENLNSLNYD/SCSQEKEGHAE*ONQNS\DPH<br>QEKWIYVHKGSTKBRHGYCTLGEAFNRDLDFSTAILDSRRFNIVV<br>RLELEIAKSQTSLSGIAQKNFMNILEKVVLKVEDQONITLIR<br>ELLQTLTYTSLCTLVVRVGSVVLGNINMWVYRMETILHWQQQLN<br>NIQITRVSGQAQPPPGSGSLHRTDGTQTRQDFEPTPVTESGLF  |
| 6680       | 1498   | 2951   | PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE<br>P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP<br>/NQVSPPOPM*GAENGQDQGGKEEAGEELHRSSSGLTAAPGF<br>EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS<br>MQRSQAGLPWEAGLVESPTHIPALRPSGTNATGEAPPSTTCS<br>SGP\PAFPGPTGLRPGGSSSGGHG*PGLPVGV\GALGAAQD<br>POSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS<br>TIPKKGTRGFGEGGVQLQERNRWVVGRAQGFSAAGTAPPGV<br>*LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVANGRHGPGVQ<br>AQCCPPGAGCWGSPRGSQRCPRTYTHSLGHGRAPCPRCWH*<br>WQDPPSSPRTGCLPGIPARQAYSAPRTSRPGIRTGRAAYGFIR<br>FQGGGGG |

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|------------|--|--|---|
| 6681       | 1169   | 511  | INVIYYNQQRFAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE KMTVGVLTQTVGPPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL LAQEADELTLRQNLNRKSPHA\VVTLLINTKGHH*LINARLTRYQ TLLCENPHKTIEVSNT/LNPATLLLVTBSPVKHNCLEVLDSVYS SRPNLRDHP*TSVDWELVVDGSGFANPCKVTLKKETSPAPVTPR S  |
| 6682       | 109  | 1238   | TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDQVD VRRRIELIQDFEMPTVCTTIKVS KDQYILATGYTKPRVRCYDT YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRIEFHSQSG FYYKTRIPKFGDRDFS YHYPSCDLYFVGASSEVYRLNLEQGRYLN PLQTDAAENNVCDINSVHGLFATGTIEGRVECDWPRTNRNVGLL D\AP*TVSQQIQR*TSLP TISALKFN\GALTMVGTITGQVLLY DLRS DKPLLVDHQYGLPIKSVHFQDSL DILSADSRIVKMWNK NSGKI FTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL GPAPRWCSFLDNLTEELNPESEN                            |
| 6683       | 109  | 1238   | TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDQVD VRRRIELIQDFEMPTVCTTIKVS KDQYILATGYTKPRVRCYDT YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRIEFHSQSG FYYKTRIPKFGDRDFS YHYPSCDLYFVGASSEVYRLNLEQGRYLN PLQTDAAENNVCDINSVHGLFATGTIEGRVECDWPRTNRNVGLL D\AP*TVSQQIQR*TSLP TISALKFN\GALTMVGTITGQVLLY DLRS DKPLLVDHQYGLPIKSVHFQDSL DILSADSRIVKMWNK NSGKI FTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL GPAPRWCSFLDNLTEELNPESEN                            |
| 6684       | 111  | 527  | GLRGSTSRGRAGREPEFAAGVLCVWAGFCQSPCPPGGRGREAPA PP\SGRRHA*RPA*WLGPGGDSGGREEGGS/GEQRAMESKMG ELPLDINIQEPRWDQSTFLGRARHFFTVDPRNLLLSGAQLEAS RNIVQNYR  |
| 6685       | 258  | 1473   | KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL QGVIDMKNAVIGNNKQKANLIVLGAVPRLLYLLQOETSSTELKT ECAVVLGSLAMGTENNVKSLDCHIIPALLQGLLPDLKFIEAC LRCLRTIFTSPVTPPELLYTDATVIPHMLALLSRRYTQYEQICQ IFSHCCKGPDHQTILFNHGAQVQNIHLLTSLSYKVRMQALKCF S VLA FENPQVSM TLVNLVDGELLFQIFVKMLQORDKPIEMQLTSA KCLTYMCRAGAIRTDNCIVLKTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSVSAITDIK RLDHDLKHAHELQAAFKLYASLGANDEDIRKKVSLGEGRPPVL TASRQGVIST |
| 6686       | 310  | 927  | DSVTFDDLAVDFTPKWTLTLDPTORNLYRDVMLENYKNLATGVY QLFKPSLISWLEQESRTVQRGDFQASEWKVQLTKELALQQDV LGEP TSSGIQIMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLT LHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT   |
| 6687       | 181  | 915  | EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSTSTNSGNETSGSST IGETSNRSDRDRYRRNRSSRSPGRQCRHRSRSDRRHGESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLGVP IIVQASQAEKNRLAAMANNLQKNGGPMR LYVGS LHFNITEDMLRGI FEPFGKV  |
| 6688       | 1025   | 1  | AEVPNYPRVFHKCPDSCWRFKFPQIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFI SPAGDSL D LPSDGGTGFFSLAGDSSSTRSLSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAPTSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGAGSGSASCSSRAGKTTEATAASSMPSGTSSSFSTC TMSELEELFSLFSPAPLLSKLFTSSGSIAICCDQSGPSTGRLS VCQLWLADSDTGKLSDCQEVVTVGDSGGTLCPELSGLRM*MSLL  |

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|------------|--|--|---|
| 6689       | 640  | 1299   | SSAIVPGYSSSSDSRLNTVPTVDLLCPFQTKSST<br>SSSASYATSATSISDTAFSGSLKLLKHGLLSALDSSSRTS*STSS<br>AEDSTFRICSPSVSDTSSDSSGSKDNVILFISKVSI*SCFSLSS<br>FFSDSISFCFSSSSFCR*FVSSKVSQNALSSRLSNGPGSSSK<br>QRNSLTARQLAMSL*ATKF*RNACNPNCSSKKSAL*LSLNQRF<br>GGSASRKPGNISFNSQKCSALSYCCNFV*IKPREVSVSSSENYPAF  |
| 6690       | 1  | 442  | GTRGKMAATLGPLGSWQQWRRCLSDGSRMLLLLLLGGSGQGP<br>QQVGAGQTFEYLRKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ<br>YIRLTPDMQSKQKALWNRVPCFLRDWELQVHF*IKHQGQKKNL\H<br>GDGLAIWYTKDRMQP   |
| 6691       | 287  | 1401   | LKTETSEEKARRYKDRPSQLNAVFQEQKKMQAQESITLEDVAV<br>DFTWEEWQLLGAQKDLRYDVMLENYSNLVAVGYQASKPDALFK<br>LEQGEQLWTIEDGIHSGACSDIWKVDHVLRLQSESLVNRKPKC<br>HEHDAFENIVHCSKSQFLGQNHDI*FDLRGKSLKSNLTLVNQSK<br>GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLITKSQF<br>ISPKHQKTRKLEKHVCSECGKAFIKKSWLTDHQVMHTGEKPHR<br>CSLCEKAPSRKFMTEHQRTHTGEKPYECPECGKAFLLKKSRLNI<br>HQKTHTGEKPYICSECGKGFQKGNLIVHQRIHTGEKPYICNEC<br>/GKGFQKTCIAHQRFITER |
| 6692       | 178  | 939  | WIKEGELSLWERFCANI*IKAGPMPKHIAFIMDGNRRYAKKQCOVE<br>RQEGHSQGFNKLAE*TLRWCLNLGILEVTYAFS*IEFKRSKSEV<br>DGLMDLARQKFSRLMBEKEKQKHGVCIRVLGDLHLLPLDLQEL<br>IAQAVQATKNYNKCFNLVCFAYTSRHEISNAVREMAWGEQGLL<br>DPSDISESLLDKCLYTNRS*PHPDILIRTSCEVRLSDFLWQTSH<br>SCLVFQPVLPWEYTFWNLFEAILQFQMNHSLVQK  |
| 6693       | 178  | 939  | WIKEGELSLWERFCANI*IKAGPMPKHIAFIMDGNRRYAKKQCOVE<br>RQEGHSQGFNKLAE*TLRWCLNLGILEVTYAFS*IEFKRSKSEV<br>DGLMDLARQKFSRLMBEKEKQKHGVCIRVLGDLHLLPLDLQEL<br>IAQAVQATKNYNKCFNLVCFAYTSRHEISNAVREMAWGEQGLL<br>DPSDISESLLDKCLYTNRS*PHPDILIRTSCEVRLSDFLWQTSH<br>SCLVFQPVLPWEYTFWNLFEAILQFQMNHSLVQK  |
| 6694       | 292  | 813  | SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAESRQHELPR<br>EVHSLGQILPQDGLTAEAGPPEAQDPNGSPGISLPAAHIGFAAA<br>LAVGPGSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV<br>NAAAGKFQVDTGAKFYRGMSLEYGIEADNPFDFLSVYFLP   |
| 6695       | 292  | 813  | SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAESRQHELPR<br>EVHSLGQILPQDGLTAEAGPPEAQDPNGSPGISLPAAHIGFAAA<br>LAVGPGSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV<br>NAAAGKFQVDTGAKFYRGMSLEYGIEADNPFDFLSVYFLP   |
| 6696       | 1  | 782  | PRVRGRVGERWAFSLVPAAMSSMEPLLAWSYFRRRKQFQCAD<br>LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML<br>DENAIQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL<br>RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML<br>TSPDGPPI*NLRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD<br>LAALSTEHSQYKDW*WK/DQIEKCYRVGM*YREAEKQIKSS  |
| 6697       | 3  | 782  | PPLFLRLNSRALRPGSRKVMVVPASLSGQDVGSFAYLTIKDR<br>IPQILT*VIDTLHRHKSEFFEKHGE*EGVEAEKKAISLSKLRNE<br>LQTDKPF*IPLVEKFVD*TDIWNQYLEYQ*QSLLNESDGKSRWFYSP<br>WLLV\ECYMYRRI*HEAI\IQSP*IDYF*DVFKESKEQNFYGSQES<br>I*IALCTHLQQLIRTI*EDLD\ENQLKDEFFKLLQISLNGEISVDL<br>SL\SGGESSSQNTNVLNSLEDLKPF*ILLNDMEHLWSLLSNCK  |
| 6698       | 668  | 754  | VGSCACAGSCKCKE*CKCTSCCKSECRAFP  |
| 6699       | 325  | 492  | EGELP/PARRVLPAMTAS*APRGRPGVGVGVVTSCKHPRCV<br>LLGKRKGSV*GAGSFQ*LPGGHLEFG*ETWEECAQRETWEEAALHLK<br>NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN  |

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|------------|--|--|--|
| 6700       | 1098   | 1392   | ESKRRIYNHAFPPQESKWSGGILQ<br>TQCWRSSTPGMRTHFRTPQ/RLECGGFSQOENGHCMDTNECQ<br>FFVFCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT<br>LLGLCNLLGK   |
| 6701       | 2  | 1485   | AAAGPRTTRVRAAAFEQGQSPSPGLGPTSDKAAAPRTPKRRRLW<br>RQRQ/HPAMLCYVTRPDAVLMEVEEAKANGEDCLNQVCRRLGI<br>IEVDYFGLQFTGSKGESLWLNLRNRISQOMDGLAPYRLKLRVKF<br>FVEPHLILQEQRHIFFLHIKEALLAGHLLCSPEQAVELSALLA<br>QTKFGDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTQ<br>ASAEYQVLQIVSAMENYGIENHSVRDSEKLLIGVPEGISIC<br>KDDFSPINRIAYPVVQMATQSGKNVYLTVTKEGNSIVLLFKMI<br>STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF<br>LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ<br>SPSHSLPKSSSESMNCSSCEGLSCQQTTRVLQEKLRKLKEAMLCM<br>VCCBEEINSTFCPCGHTVCCESCAALQVGESAAHFCLOPHLSL<br>LLTGSRSQVLAR                                    |
| 6702       | 397  | 1971   | PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK<br>RABALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV<br>NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL<br>LAASCDYFKGMFAGGLKEMEQUEEVLHGVSYNAMCQILHFIYTS<br>ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV<br>YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQPLEKVYSL<br>LSSNRLEVSCETEVEYEGALLYHYSLEQVQADQISLHEPPKLET<br>VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ<br>SPQTELRSDFQCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH<br>FTASLAPRMSNQGIAVLNNFVYLLGGDNNVQCFRAESRCWYDP<br>RHNRFQIQSLQOEHADLSVCVVGRIYIYAVAGRDYHNDLNAVER<br>YDPATNSWAYVAPLKREVIYAHAGATLEGKMYITCGRKGRIT |
| 6703       | 45   | 1244   | GVGPRAAMPLELELCFGRWVGQHPCTIAEIGONHQGDLDVA<br>KRMIRMAKECGADCAKFKSELEFKFNKALERPYTSKHSWGKT<br>YGEHKRHLFESHQYRELQRYAEVGIFFTAGSMDMAVEFLHE<br>LNVFFFKVGSQDNNFPYLEKTAK/TRGWHSVLRDVCVQLNDE<br>TSSWDVLGRVTSKEKVLMLVLDYSGRPMVSSGMQSMQDMKQ<br>VYQIVKPLPNPFCFLQCTSAIPLQPEDVNLRVISEYQKLFDPDI<br>IGYSGHETGIAISVAVALQAKVLERHITLTKTWGSDHSASLE<br>PGELAEVRSVRLVERALGSPKQLLPCEMACNEKLGKSVVAKV<br>KIPEGTILTMDLTVKVGEPKGYPPEDIFNLVGGKVLTVBDD<br>TIMEE  |
| 6704       | 82   | 1007   | TMNTRNRVNSGLGASPSRPTRDPODPSGRQELSPVEDQREG<br>LEAPKGPSRESVHVAGQRRTSAYTLIAPNINRRNBIQRIAEQE<br>LANLEKWKQNRAPVHLVPRRLGGSQSETEVRQKQQLQMQSK<br>YKQKLKREESVRIKKEAEAEALQMKAIQREKSNKLEBKRLQE<br>NLRREAFREHQYKTAEFL/RQTEHRIARQCLSKCCLWPTILN<br>MGQKLGLQ\DSLKAEENRKLQKMKDEQHQSSELLEKROQQEQE<br>RAKIHQTEHRRVNNAFDLRLQKGSQPGGLEQSGGCWNNMNSGNSW<br>GI  |
| 6705       | 2  | 786  | RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT<br>SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSED<br>LKVIYILVRPKAGQTLQHRVFQILD SKLFEKVEVRPNVHEKIR<br>AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRPDDTLRHA<br>VQLNVTATRQLLLMASQMPKLEAFIHIHISTAYSNCNLKHIIDEVIY<br>PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIIYTYTK  |
| 6706       | 130  | 531  | PTHSSSSHSQEMLGKLNMLRNDGHFCDTTIRVQDKIFRAHKVVL<br>AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT<br>LSINTENIIDVLAASYMQMFSVASTCSEFMKSSILWNTPN SQP<br>EK   |

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|------------|--|--|---|
| 6707       | 2233   | 1343   | YWSGIGYELQHFHWRKFFHEKKGPPSTCQERLYESRSRWPCIS*<br>GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS<br>FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV<br>SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNLLC<br>NRRVFSLLCEGPGHCYQGAVEREACAAASPGLDSAAEPHRLCEH<br>TD*LPK*GPGYIQHFHCDNLCILYNISFNLFYSYF*GVARYA<br>C*RWYFEWLLYNHCGDILVACL*RRQL*SSQ  |
| 6708       | 115  | 1729   | TVGSWSRSGRSPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT<br>GEIIRVVHPRPCALGSDGVRVTMESALTARDRVGVQDFVLL<br>ENFTSEAF:ENLRRRFRENLIYTYIGPVLVSVPYRDIQIYSR<br>QHMERYRGVSFYEEPPLLAVADTVYRALRTERRDQAVMISVES<br>GAGKTDATKRLLQLYAETCPAPQGGAVDRLLQSNPVLAEAFGN<br>AKTLRNDSSRFKYMVDVQDFKGAUVGGHILSYLLEKSRVWHQ<br>NHGERNFHIFYQLLECGEEETLRLRLGLEERNPQSYLYLVKGQCAK<br>VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH<br>FAANESNAQVTTENQLKYLTRLSSVEGSTLREALTHRKIIAKG<br>EELLSPINLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV<br>ESPSNRSTTVLGLLDIYGFVQFQNSFEQFCINYCNEKLQQLFI<br>ELTLKSEQEYEAEGIAWEPVQYFNNKICDLVEEKFKGII*SI<br>LDE\ECLRPGE   |
| 6709       | 3  | 894  | PPHEHLFPSEGERGPFSLVSRRLGPGKMGKKGKKEKKGRGAEK<br>TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCFP<br>PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK<br>DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ<br>FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAVKRQLILF<br>GGFHSTRDYIYYNDVYAFNLDTFTWSKLSPGTGTPRSGCQ\I<br>PSLPRAASSVYGGYSKQVRVKDVKGTRHSDMF   |
| 6710       | 158  | 980  | RHKMTNRYVSSSGRAARKMRLALMGPAFIAAIGYIDPGNFATN<br>IQAGASFGYQLLWVWVANLMAMLIQILSAKLGATGKNLAEQI<br>RDHYPRPVVWFYVWQABI IAMATDLAEFIGAAIGFKLILGVSL<br>QGAULTGIATFLILMLQRRGQKPLEKVIGLLLPVAAAYIVELI<br>FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI<br>WHSSLTQHLHGSRQQRYSATKWDVAIAMTIAGPVNLAIMATAA<br>SELNFYIGHTGVA  |
| 6711       | 3  | 347  | VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK<br>ELVRTDLHNLMLKENKNDQAI*HIMEDLDTNAHMQIIFKELIML<br>MAMLTWSYHDNMHDADYGPQOHRPG   |
| 6712       | 118  | 578  | PHGQKRTRYPQVRAPCQQPQAQLAMALCLKQVFAKDKTFRPRKR<br>FEPGTQRFELYKKAQASLKSGLDLRSVVRLLPPGENIDDWIAVHV<br>VDFFNRIINLIYGTMAERCS*TSQPMAGGPRIEYRWQDERQYRR<br>PAKLSAPRYMALLMDWIESLI  |
| 6713       | 2485   | 3  | QARGSDSEGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE<br>PDREMVRANKKKKKSGGFQSMGLSYPVFKGIMKKYKVPTPI<br>QRKTIPVILDGKDVAMARTGSGKTACFLPMFERLKTHTSAQTG<br>ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF<br>AALHENPDII IATPGRLVHVAVEMSLKLQSVEYVVFDEADRLPE<br>MGFAEQLEI IARI.PGGHQTVLFSATLPKLLVEFARAGLTPEVL<br>IRLDVDTKLEBQLKTSFPLVREDTKAAVLLHLLHNVPQDQTV<br>VFVATKHAEYLTLLTQRVSCAHIYSALDPTARKINLAKFTL<br>GKSTLIVTDLAARGLDIPLLDNVINYSFPAGKGLFLHRVGRVA<br>RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA<br>GVDGMLGRVPQSVDDEEDSGLQSTLEASLELRGLARVADNAQQ<br>YVRSRPAPSPESI KRAKEMDLVGLGLHPLFSSRFEEELQRLRL<br>VDSIKNYSRATIFEINASSRDLCSQVMRAKQKDRKAIARFQQ<br>GQOGRQEQEGPVGPAPSRPALQEKQPEKEEBEEAGESEVEDIFS<br>EVVGRKRQRSGPNRGAKRRREARQRDQEFYIPYRPKDFDSERG |

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|------------|--|--|---|
|            |  |  | LSISGEGGAFEQQAAGAVLDLMGDEAQNLTGRQQLKWDKRRKRVFGQSGQEDKKIKTESGRYISSYKRDLYQKWQKQKID*S*LGRRRGILTRRRPRTBEVGEARPLAQAGCIPGPHAPRHPLQAESALELKTQKQILKQRRRAQKAALSQRWNPQAALCPQ  |
| 6714       | 169  | 1416   | NNCQELLPFPAPMAHIPSGGAPAAAGAAPMGPOVCVCKVELSVSGQNLDRDVTSSKDPFCVLFTENNGRWIEYDRTETAINNLNPAF SKKFVLDYHFEEVQKLKALPDQDKSSMRLEHDFLGQFSCSLG TIVSSKKITRPLLLNDKPKAGKLITIAAQELSDNRVITLSLAG RRLDKKDLFGKSDPFLEFYKPGDDGKMWLVHRTVEVIKYTLDPVW KPFTVPLVSLCDGDMKPIQVMCYDYDNDGGHDFIGEFQTSVSQ MCEARDSVPLEFECINPKKQKQKKNYKNSGIIILRSCKINRDYS PLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP TNPFCSGVDGIAQAYSACL |
| 6715       | 32   | 493  | GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP GRPKHLGVPNGRMVLAVSDGELSSTTGPGQGGEGRGSSLSIHSL PSGSPSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS AENVTFWKACERFQIPASDT   |
| 6716       | 1  | 176  | GAGGPAPRSFGSEEPRAALERDKMSARAAAAKSTAMEETAIWEQ HTVTLHVRVSLCCSK  |
| 6717       | 115  | 896  | LFAMSGFENLNTDFYQTSYSIDDSQSQSYDYGGSGGPYSKQYAG YDYSQQGRFVPPDMMQPOQPYTGQIYQPTQAYTPASQPQFYGN FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG PMVFLAFGATLLLAGKIQFGYVYGISAIQCLGMFCLLNLMSMT GVSFGCVASVLGYCLLEPMILLSSPAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF  |
| 6718       | 290  | 599  | KQSTVPGTILPSLKWNSGLCKFPETGGKMTTFKEGLTFKDVA VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ   |
| 6719       | 1  | 691  | PTREEQDREDGKCHKMEMNPFISGNLNCPIAMSQCSSDHGCET DLSDDDDKIEKPNFMKDSAQDNGLSRKISRKRVCSDDSDSSL QVVKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLNVHT RSKNGRKKPLHLACTTAKKKLSDCGSESVHCEVPSEYACEGKPP DPDSEGSTKVLSQALNGDSDSEMLNSEHHRHTNIHKIDAPSK RKSSSVTSSG  |
| 6720       | 3  | 822  | HEVAEEAGGTVPQRGTMPGTRKFQHVIEPPEPGKWELTGYEAA VPITEKSNPLTQDLKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLEKPDGGLVVLGGGTSGRMAP LMSVSFNQLMKGLGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPFPRILRSLTVFPPLRAPHYQITSLLFSM SVVTLISE   |
| 6721       | 3  | 822  | HEVAEEAGGTVPQRGTMPGTRKFQHVIEPPEPGKWELTGYEAA VPITEKSNPLTQDLKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLEKPDGGLVVLGGGTSGRMAP LMSVSFNQLMKGLGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPFPRILRSLTVFPPLRAPHYQITSLLFSM SVVTLISE   |
| 6722       | 1  | 390  | RSWSKRTWQALPMAVFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPADPGK PGRIELRLIGNYSLWLEGSKEEDAGRYWCAVLGQHNNYQNW   |
| 6723       | 173  | 659  | VQCYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKQLALT GNEGRVSVENIKQLLSAHKESSFDIILSGLVPGSTTLHSAEIL AEIARILRPGGCLFLKEPVETAVDNNKSVKTASKLCSALTLSGL   |



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|------------|--|--|--|
| 6724       | 173  | 659  | VEVKELQREPLTPPEVQSVREHLGHESDNL<br>VCQYCTARMADFGISAGQFVAVVWDKSSPVREALKGLVDKLOALT<br>GNEGRVSVENIKQLLSAHKESSFDIILSGLVPGSTTLHSAEIL<br>AETARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL<br>VEVKELQREPLTPPEVQSVREHLGHESDNL   |
| 6725       | 356  | 722  | RRRTPPVILATMDDDLMLALRLQSEWNLQEAERDHAQESLSLVD<br>ASWELVDPTPDLOALFVQFNDQPFNGQLEAVEVKSVMRTLCAG<br>ICSYEGKGGMCSIRLSEPLKLRPRKDLVEVFFV   |
| 6726       | 98   | 714  | HLQKMERKINRREKEKEYEGKHNSLEDTDQGNCKSTLMTLNVG<br>GYLYITQKQTLTKYPTDFLEGIVNGKILCPFDADGHYFIDRDGL<br>LFRHVLNFLRNGELLPEGFRENQLLAQAEFFQLKGLAEVKS<br>RWEKEQLTPRETTFLITDNHDSRQGLRIFCNAPDFISKIKSRI<br>VLVSKSRLDGFPPEFSISSNIIQPKYFIK   |
| 6727       | 1  | 831  | FRMGDERPHYGYGKHGTPOKYDPTFKGPIYNRGCTDIYICCVLL<br>LAIVGYVAVGI IAWTHGDPKVIYPTDSRGFCGQKGTKNENKP<br>YLFYFNIVKCAPLVLLBFQCTPQICVEKCPDRYLYTLNARSS<br>RDFEYKQFCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF<br>PAIHAYKGLVMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA<br>RQLAMRIFEDYTVSWYWDIISLGIAAMSLLFIIILLRFLAGIMG<br>RGMIMGILVLGY   |
| 6728       | 486  | 935  | FCSSWLRLSLADSSLSWKMFVLGLTGGIAGSKSSVIQVQFQLGCA<br>VIDVDVMARKHVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD<br>LIFNQPDRRQLLNAITHPEIRKEMMKETFKYFLREPTSPRGKK<br>HVPSALKEADSLMRDT   |
| 6729       | 259  | 1191   | VLTGAQSGRTASMGDRDQRAVAGPALRRWLLGTVTVGFLAQSV<br>LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGVPGQGYNGPP<br>GLQGFPGLOGRGDKGERGAPGVTGPKGDVGARGVSGFPGADGI<br>PGHPGQGGPRGRPGYDGCNGTQGDSPGQPPGSEGFTGPPGPQG<br>PKGQKGEPYALPKEERDRYRGEPEPGLVGFQGPGRPGHVGM<br>GPVGAPGRPGPPGPGPKGQQGNRGLGFGYKGEKGDVGQPGPN<br>GIPSDTLHP IIAPTGVTFFHPDQYKGEKGESEGPGRGISLKGEE<br>GIM  |
| 6730       | 784  | 1015   | NMVDDYEVGLQRYASPEDIKKAYHKVALKWHDPKNPENKEEAE<br>RKFEVAAEAYEVLNDEKRDIDYKYGTGLNEF   |
| 6731       | 1  | 446  | GIRKRLHGAVVRVEVGCWPETRESEGVHLERPTSPLKNNDEGS<br>LDIYAGLDSAVSDSASKSCVPSRNCLDLYEILTEBGTAKATY<br>NDLQVEYKGCQLQMKELMKKFKETQNTQNFSLINENQSLKKNISA<br>LIKARVEINRKDEEI  |
| 6732       | 102  | 1205   | GRWQRRPPPPSPFLWCLQPGGSDPQQLTQLRHCLSHSPQDTPW<br>AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPSRHRHRQEN<br>LGSIKPSSRSSTKATSTTMAGDGRRAEAVREGWGVYVTPRPIRE<br>GRGRLAPONGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFF<br>PLVAKERSPVGKRTRLLEFRSDSAKEEVRESAYYLRSRQRRQPR<br>PQTEEMKTRRTTRLQQQHSEQPPLQPSVMTRRGLRDSHSSEE<br>DEASSQTDLSQTISSKKTVRSIQEAPAVSEDLVIRLRFPFLRYPR<br>YEATSVQKQVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG<br>DKTTRSSQYIESFW |
| 6733       | 613  | 1311   | RSCRQVMRSRNGGESASDGHISCPKPSIIGNAGEKSLSEDAK<br>KKKSNRKEDDVMASGTVKRLKTSCECERKTKKSLSELSKEDLI<br>QLLSIMEGELQAREDVHMLKTEKTPVLEAHYGAEPKVLRL<br>VLHRDAILAQESIGEDVYEKPISELDRLEKQKETYRRMLEQL<br>LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK<br>LLEQEKAYQARKE   |
| 6734       | 189  | 551  | SAAMPVVFSGCFQELQEKNSLELVSPFEVAVHFTWEWQDLDD<br>AQRTLYRDVMLETYSSSLVSLGHCITKPEMIFKLEQGAEPWIVBE  |

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|------------|--|--|---|
| 6735       | 280  | 558  | TLNLRSLGGGSKQVFSGICHRSLVELQEVHLV<br>KSRRAAGVTKMSNPFLKQVFNKDKTFRPKRFEPGTRQRFELHKKKQASLNAGLDLRLAVQLPPGEDLNDWVAVHVDFNVRVNLIIYGTIXDGCT  |
| 6736       | 195  | 808  | MNYELNFKREMPNISKSLGTLNLFLLKRLSSVLPITDYVYFENSSSNPYLIRRIEELNKTASGNVEAKVVCYRRRDISNTLIMLADKHAKIEEBESETTVADLTDKQKHQLKRELFLSROYESLPAATHIRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG EIRVGPRYQADIPEMLLEGTFFCFVFAVL   |
| 6737       | 150  | 1209   | PVIMPLHFSFGDIWRPSCCVSSSPKLRNNAHSRLESYRPDSDLSDREDTGCNLQHISDRENIDDLNMEFNPSPDHPRASTIFLSKSSQTDVREKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKTYIKCVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPDPYDKHNPEQKQIYRFVTLFSAQAOLTAECALVTLVYLERLLTYAEIDICP ANWKRIVLGAILLASKVWDDQAVWVNDYQCILKIDITVEDMNELE RQFLELLQFNINVPSSVYAKYFDFLRSLAEANLSPFPLEPLSRE RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPWSPAIIS                                  |
| 6738       | 148  | 653  | CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLWGAPWTHGRRSNRVITDENWRBLLLEGDWMIFFYAPWCPACQNLQPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFINFISSDKWKSTIEPVSSWF  |
| 6739       | 3  | 631  | SWPDMAEVEEVAKLEKHLMLLRQEVYVQLQKLAETEKRCALLAAQANKESSESSESFISRLLAIVADLYEQEQYSDLKIKVGDRIHSAHKFVLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLTELMLKANRFQQLLRERCEKGVMSLVNVRNCIRFYQTABELNASTLMNYCAEIIASHWVSEVEGVNKAL  |
| 6740       | 3  | 631  | SWPDMAEVEEVAKLEKHLMLLRQEVYVQLQKLAETEKRCALLAAQANKESSESSESFISRLLAIVADLYEQEQYSDLKIKVGDRIHSAHKFVLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLTELMLKANRFQQLLRERCEKGVMSLVNVRNCIRFYQTABELNASTLMNYCAEIIASHWVSEVEGVNKAL  |
| 6741       | 141  | 960  | PLTLPFSSRRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQAHSGICTRTVQHQSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMTGGEDCTARI WDLRSRNLQCCQRIQVFNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGCNCYVWNLTTGGIGDEVTO LIPKTKIP   |
| 6742       | 141  | 960  | PLTLPFSSRRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQAHSGICTRTVQHQSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMTGGEDCTARI WDLRSRNLQCCQRIQVFNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGCNCYVWNLTTGGIGDEVTO LIPKTKIP   |
| 6743       | 1  | 412  | MHSTQDKSLHLEGDFNPAAPTSTCAFRKMPKRISISKQLASVKALRKCSDLKAIATTALIFRNSSDSGKLEKAIKDLLQTQFRNFAEGQETKPKYREILSELDEHTENKLDFFDMILLLSITVMSDL LQNIR   |
| 6744       | 95   | 1343   | RTPARNRACAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRDRQKVSTVGYGMDEVEQDQHBARKELPDSFDTTGTGSLGQEELTDLCHMLSLEEVAPVLQQLLQDNLLGRVHFDQFKEALILLSRTLSENEHFQEPDCSLEAQPKYVRGGKRYGRSLPEFQESVEEFPEVTVIEPLDEEARPSHIPAGDCSEHWKTQRSEYEAEQQLRFWNPDDLNASQSGSSPPQDWIEEKLQEVCELDGITRDGHLNRKKLVSII   |

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|------------|--|--|---|
|            |  |  | CEQYGLQNVGEMLEEVFHNLDPDGTMSSVEDFFYGLFKNGKSLT<br>PSASTPYRQLKRHLMSQSFDESGRRITTSAMTSTIGFRVFSCL<br>DDGMGHASVERILDWQEEGIENSQBILKALDPGLDGNINLTEL<br>TLALENELLVTKNSIHQACI  |
| 6745       | 1  | 588  | TFRDQGWAAQRRLRLGCSWESWEAAIAAGPGLPSSTARQONNP<br>AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP<br>ELPVTSFDCAVCLVHLQPVTRCGHVFCRSCIATSLKNNKWTCT<br>PYCRAYLPSEGVPTDVAKRMKSEYKNCACEDTLVCLSEMRIHI<br>RTCQKYIDKYGPLELEETA  |
| 6746       | 110  | 492  | GATGAMAESAARHRRRRRSTPLTSSSTLPSQATEKSSYFQTTEI<br>SLWTVVAAIQAVEKKMESQAARLQSLGRTGTAEKKLADCEKMA<br>VEFGNQLGKWAVALGTLLOEYGLLQRRLENVENLLRNVRN   |
| 6747       | 247  | 484  | EAVTFKDVAVVFTEELGLDLAQRKLYRDVMLENFRNLLSVGH<br>QPFHRDTFHLFRLKEKFWMMDIATQREGNSVYAGVC  |
| 6748       | 201  | 665  | MTTFKEAVTFKDVAVVFTEELGLDLAQRKLYRDVMLENFRNL<br>LSVGNQPFHQDTFHLGKEKFWKMTTSQREGNSGGKIQIEMET<br>VPEAGPHEEWSQQIWEQIASDLTRQNSIRNSSQFPKEGDVPC<br>QIEARLSISXVQQPYRCNECKQ  |
| 6749       | 95   | 719  | RREVKGGDGVCPRARQSPQSQQFPSCAGGEGGLQSSGEALDGAM<br>SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVELEFDFKAF<br>VDVDLLGEIDPDQADITYEGRQKMTSLSSCFALCHKAQSVSQ<br>INHLEAQLVDLKSLETQAEKVLEKEVHDQLQLHLSIQLQL<br>HAKTGQSADSGTIKAKLSGSPVEELERELKAN  |
| 6750       | 3  | 428  | SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT<br>TAPGPIHLELCLDQKLMFELCNMDNKLVLWLEEIQEEAERMFTR<br>EFSKEPELMPKTPSQKNRRKKRRI SYVQDENRDPIRRRLSRRKS<br>RSSQLSSRR  |
| 6751       | 152  | 1417   | PTKATEMAGASVKVAVVRVPFNSREMSRDSKCI IQMSGSTTIV<br>NPKQPKETPKSFSFDYSYWSHTSPEDINVASQKQVYRDIGEML<br>QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQGGIIPQLCEDL<br>FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLVRRE<br>HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS<br>SRSHAVFNII FTQKRHDAETNITTEKVKISLVLDLAGSERADST<br>GAKGTRLKEGANINKSLTTLGKVISALAEKSGPNKNNKKKKT<br>FIPYRDSVLTWLLRENLGGSRTAMVAALSPADINYDETLSTLR<br>YADRAKQIRCNVINEDPNNKLI RELKDEVTRLRDLLEYAQLGLD<br>ITDMTNALVGMSPPSSLSALSSRN  |
| 6752       | 24   | 1834   | RNCVPLGCRYRVRVFKHSDIKMQYSHHCEHLERLNRKQREAGFL<br>CDCTIVIGEFQPKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ<br>VKADGFQKLLBFIYTGTLNLDSDNVKEIHQAADYLVKEEVVTKC<br>KIKMEDFAFIANPSSTEISSITGNIELNQOTCLLTLDYNNREK<br>SEVSTDLIQANPKQALAKRSSQTKKKKAFNSPKTGQNKTVQY<br>PSDILENASVELFLDANKLPTPVVEQVAOINDNSELELTSVVEN<br>TFPAQDVIHTVTVKRKRKGSQPNCALKEHSMNSIASVKSPEAE<br>NSGEELDQRYSAKPMCNCTCGKVFSEASSLRHRMRIHKGVPYV<br>CHLCGKAFTQCNQLKTHVRTHTEGKPYKCELCDKGFAQKQVLV<br>HSRMHHGEEKPYKCDVCNLQFATSSNLKIHKHSGEKPYPVCDR<br>CGQRFAQASTLTYHVRHTGEKPYVCDTCGKAFVSSSLITHSR<br>KHTGEKPFICELCGNSYTDIKNLKHKTKVHSGADKTLDSASD<br>HTLSEQDSIQKSPLESETMDVKPSDMTLPLALPLGTEDHMLLPV<br>TDQSPSTDTLLRSTVNGYSEPOLIFLQQLV |
| 6753       | 2  | 1305   | VPSLPYPQKVVAAHTEFTSSDSETANGIAKPDVPMPGGEKAS<br>PFGIKLRRTNYSLRFNCDDQAEQKKKRHSSTGDSADAGPPAAG<br>SARGEKEMEGVALKHGSPSLPQERKQAPSTRRDSAEPPSSRSVPV<br>AHPGPPPASSQTPAPEHDKAANKMPLAQKPAAPKPTSPTPAS  |

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|------------|--|--|---|
|            |  |  | PLSKLSRPYLVELLSRRAGRPDPPEPSEPSKEDQSSDRRPPSP<br>GPEERKQKRDDEEEATERKPASPPLPATQKEKPSQTPEAGRKE<br>KPMQLSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR<br>EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP<br>EEKRPETAVSRLEERREQLKKANTLPTSVTVEISYSSPAAPLVKE<br>VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK   |
| 6754       | 2  | 413  | FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSTALEKRE<br>LSPSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ<br>FLREMIQPGIAKANMGVSREDVTTFEDHPLNPNPDSRWNTYFKD<br>NEVLL   |
| 6755       | 298  | 1343   | PGLOQVALEADWFLDMPGGRGSPRQQLSRSSALPSLQTLVGGG<br>CGNGTGLNRNGSAIGLPVPPITALITPGPVRHCQIFDLFPVDS<br>LLEFFLFFIYLLVALFIQYINIKTVWWYPYNHPASCTSLNFHL<br>IDYHLAAPTVMMLARRLVWALISEATKAGAASMIHYMVLISARL<br>VLLTLCGVLCWTLVNLFRSHSVLNLFLGYPFGVYVPLCCPHQ<br>DSRAHLLLTIDYNYVQHEAVEESASTVGGGLAKSKDFLSLLES<br>KEQFNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS<br>LFSAYYVAFPLPCFVKVSGYLTFCFLDLCVNIWVFLV  |
| 6756       | 180  | 754  | IERALGSLPLSIPVSWGSLRLTKYQQQLRPVLLCQTRVQCHD<br>LRSIQPQPGGLKQSFCLRVLGLQTGATTGRLDLTCKELIILTE<br>REAQKRKKRKEKESGMALTQGPLTRDVAIEFSQEWSLDPVQ<br>KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSW<br>PFHYLTETEALLTHK  |
| 6757       | 2  | 459  | NSRVEAPEAHSRESQGS DAMRKHLSSWWNLATVCMLLFSHLSAVQ<br>TRGIKHRIKWNKALPSTAQITEAQVAENRPGAFIKQGRKLDID<br>FGAGNRYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ<br>AANQGEFQKPDNKLHQQVLW   |
| 6758       | 1  | 1008   | ASGPELPGRRPRDRAPLWLPARLLRGVLAVWVLSALGPGSFCRR<br>RVPSLAQLGHSEAAPSPDDVRSRVPDRCPEDRDRAWPPPPPS<br>LPPSFRNRMANNSPALTGNSQPOHAAAAAQQQQCGGGGATK<br>PAVSGKQGNVLPWGNKTMNLNPMILTNILSSPYFKVQLYELK<br>TYHEVVDEIYFKVTHVEPWEKSGSRKTAGQTMCGGVRGVGTGGI<br>VSTAFCLLYKLTFLKLRKQVMGLITHDTSPIRALGFMYIRYT<br>QPPTDLWDWFESFLDDEEDLDVKGAGGCVMTIGEMLRSLTKLE<br>WFSTLFPRIIPVPVQKNIDQIKTRPRKI  |
| 6759       | 1  | 513  | RKHNHSLDGTSTRAFHPTGLPLLSPPVQRKTQSGCFDLDSS<br>LLHLKSFSSRSPRCLNIEDDPDIHEKPFLLSSSAPPITSLSLG<br>NFEESVLNRYRFDPLGIVDGFTAIEVGASGAFCPHTLTPVEVSFY<br>SVSDDNAPSPYMGVITLESIGKRGYRVPPSGTIQVVCVL  |
| 6760       | 239  | 606  | VLSKKGLSABEKTRMMEIFSETKDVFLKDLKLEKAPKEGKIT<br>AMSVKEVLQSLVDGMVDCERIGTSNYWAPPKALHARKHKL<br>VLESQLESGSQKHASLQKSIEKAKIGRCETEERT  |
| 6761       | 29   | 1733   | ERTLRGLREVAAPSDVADAASRRGRCCCLHCTQTQVAQDCPS<br>SSSSVQRCELSLFSQSLHTMTSKKLVSAGCADDALAGLVACNP<br>NLQLLQGHRVALRSDLSLKGRLVALLSGGGSGHEPAHAGFIGK<br>MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLIVKNYTG<br>RLNFGlareQARAEGIPEMVVIGDSDAFTVLKAGRRGLCGTV<br>LIHKVAGALAEAGVGLBEEIAQVNVVTKAMGTLGVSLSSCSVPG<br>SKPTFELSADVELGLGIHGEAGVRRIKMATADEIVKMLDHTMT<br>NTTNASHVPVQPGSSVMMVNNLGLSLFELGIADATVRSLEG<br>RGVKIARALVGTFMSSALEMPGISLTLVDEPLLKLIIDATTA<br>AWPNVAASITGRKRSRVAPAEQEPDSTAAGGSASKRMALVL<br>ERVCSLLGLEEHLNADRAAGDGCCTHRAARAIQEWLKEG<br>PPPAPQALLSKLSVLLLEKMGSSGALYGLFLTAAQPLKART<br>SLPAWSAAMDAGLEAMQYKGAAPGDRMTLDSLWAGQEL |

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|------------|--|--|---|
| 6762       | 3  | 613  | ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMVLLSWLSLFI QVAFITLAVAAGLYLAELEIEYTVATSRRIKYMIWFSTAVLIG LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG LVVVNHYLAFQPFABEYYPFSEVLAYFTFCLWIIPFAFFVLSA GENVLPSTMQPGDDVVSNYFTKGRGK  |
| 6763       | 2  | 760  | SGPDFPGRFRFGCCCVRFPPAGAGMELGGHWDMSAPRLVSETAE RKQEQKTGTAEAADSGAVGARRFLLCLYLGGLDLFGVSMVVP LLSLHVKS LGASPTVAGIVGSSYGLQLQFSSTLVGCWSDVVGRR SSLLACILLALGYLLGAATNVFLFVLARVPAGIFKHTLSISR ALLSDVVPKEKRLPVIGHFNTASGVGFILGPVVGVI.TELEDGF YLTAFICFLVFIILNAGLVWFFPRREAKPGSTE   |
| 6764       | 80   | 438  | LKKMDTMMLSVRNLFELVRRVEILSEGNEVQFIQLAKDFEDFR KKWQTDHGLGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR RQRAEADCEKLERQIQLIREMLMCDTSGSIQ   |
| 6765       | 3  | 550  | ARYSRVDHFCRRRCRAVARAPRFLQFPSPGSRHFLAACVARWL RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDLLSGSVLSSPNS NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHRLKLPGEVTETE VIALGLPFGKVTNMLKGNQAFLELATEBAAITNGNYSAVT PHLRNQ  |
| 6766       | 1  | 1287   | BGGSFKASLTWLPGLGEMKLHCEVEVISRHLPALGLRNRGKGV RAVLSLCQQTSSRSQPPVRAFLLISTLKKRGTTRYELRENIEQFFT KFDVDEGKATVRLKEPPVDICLSKANSSSLKGFSLAMRLAHRGCV VDTPVSTLTPVKTSEFENFKTKMVIITSKDDYPLSKNFPYSLEHL QTSYCGLVVRVDMRLCLKSLRKLDSLHNHIKKLPATIGDLIHLQ ELNLDNDNHLESFVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ LQBLNKLKDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF RNLSLEYLDLFGNTFEQPKVLPVIKQLQAPLTLESSERTILHNR IPIYGSIIIPFHLQDLDLTAICVGRFCLNSFIQGTITMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI                               |
| 6767       | 336  | 919  | APMICLSSDLQFRYKEAFLDRGLQIGYCSVDDDPKMHFLNV GRQSQSDNEYKKDFAKSRSQFHSSTDPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQQLQSDVKYKSDLNLTRGVGWT PPGSYKVMARRAAELANARGLGQAGYRGAEAVEAGDHQSSEV NPDATILHVKKKKALL  |
| 6768       | 2  | 363  | PGSTISCYLLSEGLPLCMQVACGEEKHRAPTMTLRLARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL  |
| 6769       | 284  | 396  | MSTPDFSTAENNQELANEVSCKLAMLTLMQAMQAD   |
| 6770       | 1  | 397  | QRNYQVIWSSSTMAKLHDYKDEVVKLMTFNYNSVMQVPRVEK ITLNMGVGEAIDKKLLDNAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDPRGLSAKS  |
| 6771       | 3  | 378  | APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWNSLEG  |
| 6772       | 1  | 1400   | AAAFQCGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGNR\VLMTGSLVFALPHFTAG P**GWKLDAGVVRTCPANPR\PVCAG\HTSGLSRYQLVFMGLQFL HGVGATPLYTLGVTYLDENVKSSCSPYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTLETSPWVGAWVGLGSGAAFFT AVPILGYPQQLPGSQRYAVMRAAEMHQLKDSSRGEASNDFGKT IRDLPLSIWLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVKNLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSPVMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSVPCGSDGLMYFSLCHAGCPAATETNVDG QKVYRDCSCIPQNLSSGFGHATAGKCTST |

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|------------|--|--|--|
| 6773       | 1  | 630  | PWEAPKEHKYKAEHTVVLTVTGEPCHPFFQYHRQLYHKCTHKG<br>RPGPQPWCATTNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT<br>CVNMPSPGPHCLCPQHLTGNNHCQKEKCFEPQLLRFHKNIEWRT<br>EQAAVARCQCKGPDHACQRLASQACRTNPNCLHGCRCLVEGHRLL<br>CHCPVGYTGPFCDVGE*GSGASRRPAPRWDLGLAR   |
| 6774       | 146  | 389  | LTELSDDQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIIS<br>GLRIGFLTGPPLIERTVLHIQVSTLHPSTFNQLMISQ   |
| 6775       | 104  | 614  | TCPSQLRVLTARGGRRAPSPQLWTLVLALIEEKWRSHRILRMNS<br>GRPETMENLPALYTIFFQGEVAMVTDYGAFIKIPGCRKQGLVHRT<br>HMSSCRVDKPKSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN<br>QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRSPRLRLS   |
| 6776       | 3  | 1108   | HERHERHEGALSQDALLRISIPLDNSNMRPEKRRFVHPQWQLLH<br>LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDQSLS<br>TSVAKVFMAGMMVGGILGHLSDRFGRRFVLWVCYLQVAIVGT<br>CAALAPTFLIYCSLRFSLGIAAMSLITNTIMLIAEWATHRFQAM<br>GITLGMCPSGIAFMTLAGLAFIRDWHILQLVVSVPYFVIFLTS<br>SWLLESARWLIINNKPEEGLKELRKAHRSKMKNARDTLTLEIL<br>KSTMKELEAAQKKKPFILGERLHMPNICKRISLPPFTKPFANFMA<br>YFGLNLHG/LKHLGNNVFLQLTFLGAV/TPPGQLVLHLGHWSG<br>RVSSRGRVNCGLGLFVLQVW   |
| 6777       | 779  | 63   | CFHFGPAWRDCEVRATFAKKQGSQGIISCIASFPAQPLYACGSY<br>GRSLGLYAWDDGSPALALLGGHGGITLHCFHPDGNRFFSGARKD<br>AELLCWDLRQSGYPLWSLGREVTTNQRIFYDLDPTGQLVSGST<br>SGAVSVWDTDGPNDGKPEPVLSFLPQKDTNGVSLHPSLPLLG<br>HCLPVSVCFLSPTESGGRRRGAGPSLGSRRHVHLECRQLLWWC<br>GGCARLQHP**SPRARKGR  |
| 6778       | 311  | 805  | IQSITDESRSIRRRKNPANTRLRNLNVP\BETAGDSE/ERSPEEE<br>VQADPRIRASAPKCPPTSSPFFKGRSPEGEGET\DPKVFHFGPG<br>KDKSVAEKN\KGP/SPVSSSEGIKDFFSMKPEWENLNQSNVRRMH<br>T\AVRLNEVIVKSRDAKLVLNMPGPPRRNRNGDENY   |
| 6779       | 2  | 535  | RALRRQPRLLAANGIEPESMAISEPIKGRKPCVNKEELAKRKP<br>MAKCAWKGPPEPPQDARAESAESPGGASESDQDGGHESPPKKAV<br>AWVSAKNPAPMRKKKVSLSGPVSVVLVDSDEGRKKPMPKKGPG<br>SRREASDQKAPRQQPAEATASTRGPKAKPEGSRRRATNESRK<br>V  |
| 6780       | 3  | 403  | HEVNDNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKD<br>SGNLGEIVCKLHGHHGFKLQKTYENNYLILTNATLDREKRSEYS<br>LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE<br>K  |
| 6781       | 1  | 1269   | APTRPVFPPTLQDLSSSKPEPSNSLNLPHSNELCSSLVHPELSEVS<br>SNVAPSIIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT<br>SAALPTHLQSALMSTVVTMPNAGSKVMVSEGSAAQSNARPPQFI<br>TPVFINSSSIIQVMKGSQPSTIPAAPLTNNSGLMPPSVAVVGPL<br>HIPQNIKFSSAPVPPNALSSSPAPNIQTGRFLVLSRRATPVQLP<br>SPPECTSSPVVPSHPVQVQVKELNPFDEASQVNTSADQNTLPSSQ<br>STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC<br>KKVTGSLEKGEEQGADGETEGGLDITAPGLMGTEQLSTELDS<br>KTFTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT<br>LVPELISAVPTTKSNHGGIASESLAG |
| 6782       | 3  | 1327   | RRBTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFTSVSGKLS<br>NVERTRNLESNHPQGTGGFVVPRLPPRPVNGKTIPTQQPPTK<br>VPPERPPPKLSATRRSNKKLPFNRSSSDMLQKKQSNLATGLS<br>KAKSQVFNQDPVLPVRPKPGHPLYSKYMLSVPHGIANEDIVSQ<br>NPGELSCKRGDVLMVKQTENNYLCQKGEDTGRVHLSQMKLIT<br>PLDEHLRSRPNPFPSPKAPSHAQKPVDSGAPHAVVLHDFPAEQV  |

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|------------|--|--|--|
|            |  |  | DDLNLTSGEIVYLLEKIDTDWYRGNCNRQIGIFPANYVVKVIIID<br>PEGNGKRECVCSSHCVKGSRCVARFEYIGEOKDELSFSEGEIII<br>LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV<br>PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSTFKRGDR<br>I  |
| 6783       | 3  | 1750   | SYHHHHAQQSAAASPNTASQKTVTTTSMITTKTLPLVLKAATA<br>TMPASVVGQRPTIAMVTAINSQAVALSDVQNTPVNLQTSSKVT<br>GPGAEAVQIVAKNTVTLOVQATPPQPIKVPQFIPPPRLTPRPNF<br>LPQVRPKPVQNNIPIAPAPPPMLAAPQLIQRPVMTKFTPTTL<br>PTSQNSIHPVRVVGQTATIAKTFPMAQLTSIVIATPGTRLAGP<br>QTVQLSKPSLEKQTVKSHETDEKQTESRTITPPAAPKPKREEN<br>PQKLAFMVSGLVTHDLEEIQSKRQERKRRTANPVYSGAVPE<br>PERKKS AVTYLNSTMHPGTRKRGRPPKYNALGFGALTPTSPOS<br>SHPDSPENETETTTFFPAPVQPVSLPSPTSTDGDIHEDFCSVC<br>RKSGQLLMCDTCSR VYHLDCLDPLKTI PKGMWICPRCQDQMLK<br>KEEAI PWPGLT LAIVHSYIAYKAAKEEEKQLLKWSSDLKQEREQ<br>LEQKVQLSNSISKMEMKNTILARQKEMHSSLEKVKQLIRLIH<br>GIDLSKPVDS EATVGAINSGPDCTPPANAATSTPAPSPSSQSCT<br>ANCNQGEETK |
| 6784       | 3  | 1750   | SYHHHHAQQSAAASPNTASQKTVTTTSMITTKTLPLVLKAATA<br>TMPASVVGQRPTIAMVTAINSQAVALSDVQNTPVNLQTSSKVT<br>GPGAEAVQIVAKNTVTLOVQATPPQPIKVPQFIPPPRLTPRPNF<br>LPQVRPKPVQNNIPIAPAPPPMLAAPQLIQRPVMTKFTPTTL<br>PTSQNSIHPVRVVGQTATIAKTFPMAQLTSIVIATPGTRLAGP<br>QTVQLSKPSLEKQTVKSHETDEKQTESRTITPPAAPKPKREEN<br>PQKLAFMVSGLVTHDLEEIQSKRQERKRRTANPVYSGAVPE<br>PERKKS AVTYLNSTMHPGTRKRGRPPKYNALGFGALTPTSPOS<br>SHPDSPENETETTTFFPAPVQPVSLPSPTSTDGDIHEDFCSVC<br>RKSGQLLMCDTCSR VYHLDCLDPLKTI PKGMWICPRCQDQMLK<br>KEEAI PWPGLT LAIVHSYIAYKAAKEEEKQLLKWSSDLKQEREQ<br>LEQKVQLSNSISKMEMKNTILARQKEMHSSLEKVKQLIRLIH<br>GIDLSKPVDS EATVGAINSGPDCTPPANAATSTPAPSPSSQSCT<br>ANCNQGEETK |
| 6785       | 1  | 528  | LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNOAGETALDIARR<br>LKATQCEDLLSQAKSGKFNPHVHVEYEWNLQREEIDESDDDLDD<br>KPSPVKKERSPRQSFCHSSSISPDKLALPGFSTPRDKQRLSY<br>GAFTNQIFVSTSDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR  |
| 6786       | 1820   | 1397   | RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ<br>INHIRNGIDILVGTGPRIKDHLQSGRLDLSKLRHVVLDEVDQML<br>DLGFAEQVEDI IHESYKTDSEDNPTLLFSATCPQWVYTTVA\KK<br>YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPVIGDVLQ<br>VYSGSEGRAIFCETKQNVTEMAMPHIKQNAQCLHGDIAQSQR<br>EITLKGFPREGSPKVLVATNVAARGLDIPEVDLVIQSSPPQDVS<br>YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG<br>VPSTMDLVKSKMDAIRSLASVSAAVDFFRPSAQRLEEEKGAV<br>DALAAALAHISGASSFEPRSLITSDKGFTVMTLESLEEIQDVSC<br>AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERLQAE<br>WHDSDWILSVPAKLPEIEEYDGNNTSSNSRQSGWSSGRSGRSG<br>RSGGRSGRSGRSGRSGRSGRSGRSGRSGRSGRSGRSGRSGRSG<br>FD*VFYHVLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS<br>SVWN    |
| 6787       | 2646   | 2270   | PSSFPPKNVPLEELEPPK*KRSGLSLTPKSQIQNGP*PQTEFF<br>FELGSPSGVISAHCNLRLGSSDSPAPASRVAGIIGTCHHAWLI<br>LVFLVBMGFHHVQAGLKLTL\VIHPPWPPKVLGLQT   |
| 6788       | 16   | 936  | GGTVDLR\DM LAVSVLA AVRGGR/ATVRRRVRESNVLHEKSKGKT<br>REGAEDKMTSGDVLNRRKMFYLLKTAFFSVQINTEEHVD\ELDQ  |

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|------------|--|--|---|
|            |  |  | EVILWGS*DS*GYPKKG*LLPKEVPSR/RVLLSGLTPLDATQE\FTEDELSK\YVTTMVCVAVNGKPMGLGVIHKPFSEYTAMAMVDGGS NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTFGNQTTIIPAGG AGYKVLALDVPDKSQEKADLYIHVTYIKKWDICAGNAILKALG GHMTLSGEEISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT GHK   |
| 6789       | 2  | 678  | GNGINVLKIAPESAIKFMAYEQIKRLVW*PGDS*GF/YERLVA GSLAGAIQSSSIYPMEVLKTRMALRKTGOYSGMLDCARRILARE GVAIFYKGYVFNMLGIIPYAGIDLAVYETLKNALQHYAVNSAD PGVFLVLLACGTMSSTCGQLASYPLALVTRMQAASIEGAPEVT MSSLFKHILRTEGAFGLYRGLAPNFMKVIIPAVSISYVYENLKI TLGVQSR   |
| 6790       | 2  | 4068   | APPAGRRRMAAPRAGCGAALLWIVSSCLCRAWTAPSTSQKCD EPLVSGPLPHVAFSSSSSISGSYSYSPGYAKINKRGGAGGWSFSDSD HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW KPYHQDGNIAWPPGNINSOGVVRHELQHP IARYVRIPLDWNG EGRIGLRIEVYGCYVADVINFDGHVLPYFRNKKMKTLDKDI ALNFKTSESEGVILHCEGQGGDYITLLEKAKLVLSNLGSLNQL GPIYGHTSVMTGSLDDHWHVSVVIERQGRSINLTDRSMQHFR TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG VNITDLARRKKLEPSNVGNLSFSCVEPYTPVPVFNATSYLEVPG RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTSKVG VHINITQTKMSQIDISSGSGLNDGQWHEVRFLAKENFAITIDG DEASAVRTNSPLQVKTGEKYFFGGFLNQMNSSSVLQPSFQGC MQLIQVDDQLVNLVEVAQRKPGSFANVSIDMCAIDRCVPHNCE HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT SNYYWIDPDGSGPLGPKLVYCNMTEDKVTIVSHDLQMOTPVVG YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSFYCKMSRLL NTPDGSPPYTWVVGKANEKHYWGGSGPGIQKACGIERNCTDPK YYCNCADADYQWRKDAGFLSYKDLPLVSVQVVGDTDRQSEAKL SVGPLRCQGRNYWNAASFPNPSYLHPSTFQGETSADISFYFK TLTTPWGVFLENMGKEDFIKLEKSAATEVSFSFDVNGGPVEIVVR SPTPLNDQWHRVTAERNVQASLQVDRLPQQIRKAPTEGHTRL ELYSQLFVGGAGGQGGFLGCTIRSLRMNGVTLDLEERAKVTSGFI SGCSGHCTSYGTNCENGKCLERYHGYSCDCSNTAYDGTFCNKD VGAFFEEGMWLRYNFQAPATNARDSSSRVDNAPDQONSHPDLAQ EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG GTREPYNIDVDHRNMANGOPHSVNIIRHEKTIPLKLDHYPSVSY HLPSSSDTLFNSPKSLFLGKVIETGKIDQBIHKYNTPGFTGCLS RVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPM SSATDPWHLDDLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVI A\VVIFTPLSLCTP\VL*SR*HVS*PHKGTLP*IPNEAKGAGSRQK KPGRRPMSMNNDPPTSQRPIDESKKEWPHLRGGYLANG |
| 6791       | 1801   | 1193   | TGHEGAKGEKGDKGLGPRGERGQHGPKGEGYFPGIPPEL/PGW SAVV*SWLTAASTKVQAILLPOPLE*LGLQIAFMASLATHFSNQ NSGII FSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMKHEDEV EEVYVYLMHNGNTVFSMYSYEMKKGSDTSSNHAVLKLAKGDEVW LRMGNGALHGDHQRSTFAGFLLETK   |
| 6792       | 33   | 1073   | VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTI LAVERNKVL PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAGRCLCAV CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHQAV TCLEASVTFFSLVSGSQDCTCILWDLHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIITGSDQGMVVRWKT/VGCEDEVCSWTASRRG APGSASKPKRPQVGEPEGLESRAGR*HCFDREAQQNQ\PV TAL AVSRNHTKLLVGDERRGRIFCWSADG*EERGSRGSGTTVPG   |



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|------------|--|--|---|
| 6793       | 2340   | 805  | GRKEANY\YGSLTQAGTVSLGLDARGQEVFPFSAVLPMVAPND LVFDGWDISSLNLAEMRRRAKVLWDWGLQEQLWPHMEALRPSPSV YIEFIAANQSARADNLIPGSAQQLEQIRRDIRDFRSSAGLDK VIVLWTANTERFCEVIPGLNDTAENLLRTIELGLEVSPSTLFAV ASILEGCAFLNGSPONTLVPGALELAWQHRVFGGDDFKSGQTK VKSVLVDPLIGSGLKTMISIVSYNHLGNNDGENLSAPLQFRSKEV SKSNVVDMMQVSNFVLYTPGEEPDHCVVIKYVPYVGDSSKRALDE YTSMLMGGTNTLVLHNTCEDSLLAAPIMLDLALLTELQORVSF CTMDPPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI ENILRACVGLPPQNHLLEHKMERPGPSLKRVGVPVAATYPMLNK KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP HDPTLKAPTNGKGRCHFPSPSTWGSWGL   |
| 6794       | 169  | 1349   | DDVKRKPEASAH*EKPGPPSPGVRGGERACGRGSHGARSCR\ EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGKTYTQRCRLFVG NLPTDITEEDFKRLFERYGEPSEVFINRDGFGFIRLESRTLAE IAKAELDGTILKSRPLRIRFATHGAALTVMKNSPVVSNELLEQA FSQFGPVEKAVVVDDRGATGKGFVEFAAKPPARKALERCQDGF AFLLTTPRPVIVPEPMQFDDDEGLPEKLMQTKQYHKEREQPP RFAQPGTTFEYASRWKALDEMEKQREQVDNRNIREAKEKLEAE MEAAARHEHQLMLMRQDLMRQEEELRRLEELRNQELQKRKQIQLR HEEHRRREEEMIRHREQEELRRQEEGPKINYMENYVCHFLR  |
| 6795       | 1740   | 1010   | GPRRQTQVRDIIELDSF*DWAAQETDCAQNSGERL*KGVL/ENFS TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ EKVNQIQKTVIEPLKKFGSVFPSLNMVAKRREQAQDYRRLOAK VEKYEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEEMPR FYGSRLDYFQPSFESLIRAQVVYSEMHKIFGDLSHQLDQPGHS DEQREERENEAKSELRLALSIVADD  |
| 6796       | 48   | 683  | GKEIQIPTIKLAWLLFGL*PVGALGKGVVSF**SHVALGQLGW LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSVPGACPSLNPPET SVQEGRDWCQR*LPRLFSALVGQPGCWPGQAPPERCV*PGRCKW HLQSQVLR*ERRRCCCLPRFA*GWRRRHQRLGLGIHPAPLGS STPHPEGNSQQCRR*GWAELRLPSSVVL*GKLGC*  |
| 6797       | 1620   | 211  | TERMTPSOPTRGSSCTRFSSMLWTSTWRCLTCHWAGMRMSVVG V TLGPMAGQLLSASGTTTEATWTPTHTLIRWLLTASRVDPPE ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP LTSRASSIMRSRTAIPAS*SRLTTKHTVGGSPSAWRPRPTSRS VSTPVSSSTETTASGSLTWNSSSPAPCPSSAPAHSEASCK TSLWGS CGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS* RSASRPRTWRATTSAASSWAPRCWCWGA*SAT*PSSTTTISS PHCGWPCPASCASAAWLSSTWATASVAGSCWGPIM*SSAHS PW CLSACSRSSMGTTCL*RSPP\SGASRAAAWCGSSPSSTFTPSS ASSSTWCSASSSRSSPAPTTPSSI PAQAQRRASCRIPTSHSART APPPASSAAGAARPAAFSAAAGCTPRRSIRCW   |
| 6798       | 3894   | 1696   | STISWESLESWLNKATNPSNRQEDWEYIIGFCQDQINKELEG*VS ALWGQLRGSLGRGTTMAKEGQGPSRLSALECVLLVPQ\ PQIA VRLLAHKIQSPQEWELQALTYLGDVSEKVKTKVIELLYSWTM ALPEEAKIKDAYHMLKRQGIQVSDPPIPVDRTLIPSPPRPKNP VFDDEEKSLLAKLLKSKNPDDLQEAANKLIKSMVREDEARIQKV TKRLHTLEEVNNNVRLLEMLLHYSQEDSSDGDRELMKELFDQC ENKRRTLFLKLASETDNDNSLGDILQASDNLRSVINSYKTIIEG QVINGEVATLTLPDSEGNSSQCSNQGTLIDLAEIDTTNSLSSVLA PAPTTPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL SWLDEELLCLGLADPAPNVPPKESAGNSQWHLQREQSDLDFFS PRPGTAACGASDAPLLQPSAPSSSSSQALPPPPFPAPVVPASVP APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL DQLEAEAKVTSGLVKPTTSPLIPTTPARPLLPFSTGPGSPFLQ |

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|------------|--|--|--|
|            |  |  | PLSFQSQSGSPPKGPELSLASHVPLESIKPSALPVTAYDKNGF<br>RILFHFAKECPCPPGRPDVLLVVVSMNTAPLPVKSIVLQAAVPKS<br>MKVKLQPPSGTELSFSPPIQPPAAITQVMLLANPLKEKVRRLRYK<br>LTFALGEQLSTEVGEVDQFPFVEQWGNL  |
| 6799       | 3894   | 1696   | STISWESLESWLNKATNPNSNRQEDWEYIIGFCDQINKELEG*VS<br>ALWQQLRSGSLGRGTTMAKEGQPGSPRLSAECVLLVPQ\FOIA<br>VRLLAHKIQSPQEWELQALTYLGDVSEKVKTKVIELLYSWTM<br>ALPEEAKIKDAYHMLKRGIVQSDPPIPVDRTLIPSPPPRPKNP<br>VFDDERKSKLLAKLLKSNPDQLQEANKLIKSMVREDEARIQKV<br>TKRLHTLEEVENNVRLLEMLLHYSQEDSSDGDRELMKELFDQC<br>ENKRRTLFLKASETEDNDNSLGDILQASDNLRSVINSYKTIIEG<br>QVINGEVATLTLDPSEGSQCSNQGTLLDLAELDTNSLSVLA<br>PAPTTPSSGIPILPPPQASGPPSRSSSSQAEATLGPSSSTSNAL<br>SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQDLDFFS<br>PRPGTAACGASDAPLLOPSAPSSSSSQAPLPPFPAPVVPASVP<br>APSAGSSLFSTGVAPALAPKVEPAVPGHGLALGNSALHHLDAL<br>DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLFPSTGPGSPLFQ<br>PLSFQSQSGSPPKGPELSLASHVPLESIKPSALPVTAYDKNGF<br>RILFHFAKECPCPPGRPDVLLVVVSMNTAPLPVKSIVLQAAVPKS<br>MKVKLQPPSGTELSFSPPIQPPAAITQVMLLANPLKEKVRRLRYK<br>LTFALGEQLSTEVGEVDQFPFVEQWGNL |
| 6800       | 404  | 1646   | RRSPSTGLSPVPQFSSPSLSDSYIPWSLLLSGTIAWATPGK*AG<br>*PQAW*LGLAPAIIFI/GLTRGRKQNKKEKMAEGSGDVDDAGDC<br>SGARYNDWSDDDDDSNESKSIWVYPPWARIGTEAGTRARARARA<br>RATRARRAVQKRASPNDDTVLSQBELQKVLCLVEMSEKPYILE<br>AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL<br>IVLNNLSVNAENQRRLLKVMNQVCDTITSRNSSVQLAGRLRL<br>TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLNLAIE<br>NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN<br>FKWEENEPTQNOQFEGGSLFFFLKEFQVCADKVLGIESHHDFLVK<br>VKVGKFMAKLAHEMFPKSQE   |
| 6801       | 2  | 1755   | SAEEFESQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL<br>YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHRKL<br>REQAQSYIAQNFKQLSHMGSIREETLADTLAQLLAVLRDLSD<br>VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEDQD<br>YLEGLLTKPIVKKYCLDVIEGALQMRYGDLLYKSLVPVPSNSS<br>/R*QQQLSCICSRKSTPETGYVCQGDGDLWTPORSLS\RYDPY<br>SGDIYTMPSPLTSAHTKKTVTSSAVCVSPDHDIYLAQPRKDLW<br>VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPTITGVK<br>LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM<br>LCYDP SHNMWLN CASLKRSDFEACVFND EICYICDIPVMKVYN<br>PARGEWRRISNIPLDSETHNYQIVNHDQKLLITSTTPQWKNR<br>VTVVEYDTRDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG<br>QSFI TEEDDARSESSTEWLDGFSELDSESGSSSSFSDDDEVWVQ<br>VAPQRNAQDQGGSL   |
| 6802       | 157  | 1341   | ETFFLFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHEKCAE<br>PSTRKNLMNSLEQKIRCLEKQKRELLEVNQWDDQPRSMKELYE<br>RKVAELKTKLDAAEFLSTREKDPHQQRKDDRRQREDDRRDLT<br>RDLQREKEKEKRLNEELHELKEENKLLKGNLTKANKEKHYEC<br>EIKRLNKALQDALNIKCSFSEDCLKSRVEFCHEEMRTEMEVLK<br>QQVQIYEEDFKKERSDRERLNQEKELQINETSQSQLNRNLSQ<br>IKACOMEKEKLEKQLKQMYCPCNCGLVFHLQDPWVPTGPGAVQ<br>KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR<br>TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRE<br>G   |
| 6803       | 1  | 2203   | KLSGRPYRHMGLVGTSKLYDIRKTI FTFTPQFIDQQQFYALDN   |

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|------------|--|--|--|
|            |  |  | KMIVEMLRDTLSYLCSSRWMTGQPTITFPISHSMLEDEGTSLSNS<br>SILAALRKMQDGYFGGARVQTGKLEFLTSCCTHLSFMDPGPE<br>GKLYSEDDNDYDYLESGNWMNDYDSTSHARCDEAVARYLDHLL<br>AHTAPHPKLAPTSQKGGDRFQAQAVQTTCDLMSLVTKAKELHVQ<br>NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD<br>QSGEVDKALVLQKETSLSLQEQADILYMLYTMKGPDWNTLYN<br>ERSATVRELLTEL VGKVG EIRHWGLIRYISGILRKKVEALDEAC<br>TDLLSHQKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM<br>SISILTQEI MVYLAMYMTQPG LFAEMFRLRIGLIIQVMATELA<br>HSLRCSAEAEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR<br>PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS<br>ISAESQSPGTSMTSPSSGSPFSAIDQSSKDSRQGWQRRRLDG<br>ALNRVPVGFYQKVVKVLQKCHGLSVEGFVLPSSTTREMPGEIK<br>FSVHVES\VLNVLRLRPEYRQLLVEAILVLTMLADIEIHSIGSII<br>AVEKIVHIANDLFLOEQXTLGP/DDTMLAKDPASG\ICTLR\YD<br>SAPSGRFGTMYLS\RAA\ATYVQEFLP\HSICAMQ  |
| 6804       | 1  | 951  | GSFGKKEKAKNKESLCMENSNSSSSDEDEEETKAKMTPTKKYN<br>GLEEKRSKSLRTTGFYSGFSEVAEKRIKLLNSDERLQNSRAKDR<br>KDVWSSIQGWPKKTLKELFSDSDTEAAASPPHPAPEEGVABES<br>LQTVABEEESCSPSVELEKPPPNNVDSKPIEEKTVEVNDRAEFP<br>SSGSNFA* IPLPYLHLNRLHQLS*QKGSRRQSSVTVPSEPLAPN<br>QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*COCEL<br>KQ**SARTTS*KSLYRSEKSEKSGRRKFIKKAKKP*SNSGK<br>QQKEGKRHX  |
| 6805       | 1539   | 206  | RQPDLYFGKSFVSVSESSSLLSNDLPKFDAGIKARNRNQNYL<br>VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNQQTQESPE<br>IEVHTAEDVP IAEVHAISEYDIETENNSSESLQDQTDPEPPA<br>KLCKILDKSQALNVTAQKQWPLLRANSSGLYKCELFNSKYFS<br>DLKQHMLKHKRTDSNVCRCESFSTNMLLIEHAKLHEEDPYI<br>CKYCDYKTVIFENLSQHIADTHFSHLYWCEQCDVQFSSSELY<br>LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVNEHACKLIELSD<br>KYNNGEHGQYSLSKITFDKCKNFFVCQVCGFRSLHTNVNRHV<br>AIEHTKIPPHVCDGCGKGFSSMLE\IAKHLSHLSSEGYLQCQYW<br>EYSTQIIDLKIHLDLPHKSDLPKCSCLMRFGNERELISHLP<br>VHETT  |
| 6806       | 272  | 3794   | VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQV<br>GFLGSCGVFLALTTDACCQGLPKAQTGEVAAFKNPPLSWLVI<br>DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGTVSHA<br>SLLAQCRALTQACGYSEATLTNVLDFKRDAQLWHGVLTSMNR<br>MHVSVVPYALMKANPLSWIQKVC FYKARAALVKSRODMHWSLLAQ<br>RGQRDVLSLRLMLIVADGANPWSISSCDAFLNVFQSRGLRPEV<br>ICPCASSPEALTVAIRRPDLGGPPPRKAVLSMNGLSYGVIRVD<br>TEEKL SVLTVQDVGVMPGANVCVVKLEGTPLYLCKTDEVEGICV<br>SSSATGTAYYGLGITKNVFEAVPVTGGAPIFDRPFTRTGLLG<br>FIGPDHLVPIVGKLDGLMVTGVRNRNADDVVATALAVEPMKFVY<br>RGR IAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID<br>SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGLTHPCN<br>VLMCPHTCVTNLPKPRQKQPEVGPMIVGNLVAGKRIQAASGR<br>ELAHLESDQARKFLFLADVLQWRAHTTPDHPLFLLNAGTGT<br>STATCVQLHKRAERVAALMEKGRLSVGDHVALVYPPGVDLIAA<br>FYGCLYCGCVPTVRPPHPQNLGTLTPTVKMIVEVSKSACVLTT<br>QAVTRLLRSKEAAAAVDIRTWPTILDITDDIPKKKIASVFRPPSP<br>DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIIKLQCELYPSRQ<br>IAICLPDYCGLFALWCLCSVYSGHQSVLVPPLLESNSVSLWLS<br>AVSQYKARVTFCCYSVMEMCTKGLGAQTGVLRMKGVNLSVCRVC<br>MVVAERP\RIALTQSFSLFKDLGLPARAVSTTFGCRVNVAIC |

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|------------|--|--|---|
|            |  |  | LOGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGRIL PGVKVIAHTETKGPLGDSHLGEIWVSSPHNATGYTIVYGEAL HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY VVGSLEDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWNTLL VVVVELDGLEQDALDLVALVTNVVLEEHYLVVGVVIVDPGVIP INSRGEKQRMHLRDGFLADQLDPIYVAYNM   |
| 6807       | 1444   | 606  | VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTIVSGGNG SVFOAGFQLOALANLEARRSGIGAALSSRDVSGLPVYAQSGEPR RLTOAQVAAPFGENALEHSSDQDTWDSLRSPGFCSPSSGGGAE SLPPGGPGHAEAGHLGKVCDFHLNHQOPSPSTVLPTEVAAPPLE KLLSVDSVAVDCAYRTVPKPGPQPGPHGSLTEGCLRSLSGDLN RFP CGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLDRSR FLFRLPMGLSCPLQVQ  |
| 6808       | 2063   | 737  | GVGSGAASALARSRLASRLSSRRRTAPRSGAMORLAMDRLML SRELSLYLEHQVRVGFSGVGLSLILGFSVAYAFYLLSSIAKK PQLVTGGESFSRFLQDHCVPVTETTYPTVWCWEGRGQTLRPF\ ITS KPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRTI LLLPGLTGTSGESVILHMIHLSEELGYRCVVFNNRGVAGENLLT PRTYCCANTEDLETVIIHVHSLYPSAPFLAAGVSMGGMILLNLYL GKIGSKTPLMAAATFSVGWNTFACESLEKPLNWLLEFNYYLTTC LQSSVNHKRRHMFVKQVMDHVMKAKSIREFDKRFTSVMFYQTI DDYYTDASPSRLKSVGIPVLCNSVDDVFSPSHAIP IETAKQN PNVALVLTSGYGHIGFLEGINPRQSTYMDRVFKQFVQAMVEHGH BLS                                     |
| 6809       | 939  | 65   | DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPO TDEAAQTD SQPLHPSDPTTEKQPKRLHVSNI PFRFRDPDLRQMF GQFGKILDVEIIFNERGSKGFGFVTFTETSSDADRAREKLN GTIV EGRKIEVN NATARVMTNKKTG NPYTNGWKLPVVGAVYGPEFYA VTGFPPYPTGTAVAYRGALHGRGRAVYNTFRAAPPPPIPTYG AVVYQDGFYGA EI\LEATQPTD TLSPLQRRQPTATVTAESTQLP TRTITPSGERRPTALEPCETFHRLG  |
| 6810       | 939  | 65   | DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPO TDEAAQTD SQPLHPSDPTTEKQPKRLHVSNI PFRFRDPDLRQMF GQFGKILDVEIIFNERGSKGFGFVTFTETSSDADRAREKLN GTIV EGRKIEVN NATARVMTNKKTG NPYTNGWKLPVVGAVYGPEFYA VTGFPPYPTGTAVAYRGALHGRGRAVYNTFRAAPPPPIPTYG AVVYQDGFYGA EI\LEATQPTD TLSPLQRRQPTATVTAESTQLP TRTITPSGERRPTALEPCETFHRLG  |
| 6811       | 1522   | 658  | DLTVVWSFVDCRVIASTHGH\KSWVSVAADFPTTSVEEGDPME FSGSDEDFQDLLHFGDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHNTVMNATSPAGSN GNSVTTPGNSVPPPLPRSNLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDKERHHEKDHKRNSMGMHISKSSDKLNLVTKT TDPAKTLGTPLCPMBEDVPLEPLICKIAHERLTVLIPLEDCEI VTACQEGFICTWGRPGKVVSNP  |
| 6812       | 4001   | 1682   | EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEFGALRYRIEQ KGLQHRILILHAKHQD SGALVGFSCPGVQDSAAITIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVESELL VVKMDGRKHRLILPEAKVQDSGEFECECTEGVSAFFGVTVDPPV HIVDPREHVFVHAITSECVM LACEV\DR\EDAPVRWYKDGQVE ESDFVLENEGPHRRLLVLPATQPSDGGEGFCVAGDECAFTVTI TDVSSWIVYPSGKVYVAARLERVLTCELCRPAEVRWTKDGE EVVESPALLQKEDTVRRLVLPVAVQLEDSEYLCEIDDESASFT VVTBPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK DGLEVESEALVLERDGPRLVLPAAQPEDGGEFVCDAGDDSA FFTVTTEPPVQFLAETTPSPLCVAPGEPVVLSCELSRAGAPV |

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|------------|--|--|--|
|            |  |  | VSHNGRPVQEGEGLELHAEGPRRVLICQAGPAHAGLYTCQSG AAPGAPSLSFVTQVAEPPVVRVVAPEAAQTRVRSTPGGDLELVH LSGPGGPVVRWYKDERLASQGRVQLEQAGARQVLRVQCARSGDA GEYLCDAPQDSRIFLVSVEEPLLVLKLVSDLTPLTVHEGDDATFR CEVSPPDADVTLWRNGAVVTPGPQRQSCCSYGGCRMCGQRKART CVSKWRQAEVWVRGPGCAGCEVGSPCPTTLACPNPRMGTSTASSS MVSYNWTRAPTAARATTIAPWPGSA  |
| 6813       | 9  | 836  | SSTQQRPGVPAGPRPLDGYLGVAADHKPLKMHCRDCAVLTSSGHL LHSRQGSQIDQTECVIRMDAPTRGYGRDVGNRSTSLRVIAHSSI QRILNRHDLNVSQGTVFIFWGPSSYMRRDGGQGVNNLHLLS QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGW F TMTIALELCDRINVYGMGPPDFCRDPNHSPVPYHYEFPFGPDEC TMYLSHERGRKGSRRFITEKRVFKNWARTFNIHFFQPDWKPES LAINHPEKNKPVF  |
| 6814       | 3  | 737  | KFRREQAN/ARERNRMHGLNDALDNLKRVVPCYSKTQKLSKIET LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG CLQLNARSFLMGQGGEEAAHHTRSPYSTFYPPYHSPELTTPPGHG TLDNSKSMKPYNYCSAYESFYESTSPECASPFEGPLSPPPIN Y NGIFSLKQETLDYGNKYNNGMHYCAVPRGRLGQGMFRLPTD SHFPYDLHLRSQSLTMQDELNAVPHN  |
| 6815       | 906  | 553  | QGLDPASQTKVVELLDKSGRRGRDRSSRDMAAGAGPRSESDLE DVGPTAEWNGDGSGLRRSGSFGKLRDALRRSEMLVKKLQGGT PQEPPNPRMKRASSLNFLNKSVEEPTQPGG  |
| 6816       | 1  | 803  | NLLKTHKF\LLGQDEDSLHVPVQAQMGNYQFYLKTLASPLERID PDQPKRLHTFGNPFKQDKKGMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRRSMALLLRKPQTPTVTNHVGGKGPSSASWFPSPYN LIKPTLVHTDATIIHDGHEEKMEHQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMENTLQITPAMAQGINADIKHQLMKSEVRKF GRSK  |
| 6817       | 172  | 3457   | LGMMDSPKIGNLFPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKERKGLKALKTYRISFQESI FLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLANSKKTNRNIA IDGGKVLNSKHNGEVYDETSNNLPDSSGQONP IRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSQNEGCTSKLEMPLESKC TSFPQALCVQWKNAALCWLDCILSALVHSEELKNTVTGLCSKE ESIEFWRLLTKNQANTLLYTSQLSGVKDGDKKLTSEIFAEIET CLNEVRDEIFISLQPOLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLFQNDLQHYAFHF EGCLYQITSVIQRANNHFI TWILDADGSWLECDLKGPCSERH KKFVPPASEIHIWIERKISQVTDKEAACLPKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILLPTLEETIQKTASVSQNLSEAF\LENKPV AENTGILKTNLLSQESLMASVSAPCNEKLIQDQFVDISFP SQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPI SKPPAGPP SSGTAAHPHAAHAEVLEKSGSTSCGAQLNHSSYNGNIGSSANH EDLVEGGIHLRLKLRKKLKAEEKKLAALMSSPQSRTRSENLE QVPQDGPNDCKSIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEILAEELSPTPVSTELSENGEGDFRYLGMGDSHI PPVPS EFNDVSONTHLRQDHNYSPTKNPCQEVQDLSLTNNACVRTNL ESPMKTDFIEFFSSSALNALANDTLDPHFDEYLFENY |
| 6818       | 2  | 240  | RGFDKVLWT/LSGAVK\CVQFSRISPDGEGYPGELKVWVTYTL  |

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|------------|--|--|---|
|            |  |  | DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI   |
| 6819       | 1  | 961  | GIPCTEMGNFDNANVTGEIEFAIHCFKTHSLEICIKACKNLAY<br>GEEKKKCNPNYKTYLLPDRSSQGRKKTGVQRNTVDPTFQETLK<br>YQVAPQLVTRQLQVSVVHGLTLARRVFLGEVIPLATWDFEDS<br>TTQSFWRHPLRAKADKYEDSVQSNGLTVRAKLVLPSRPRKLQ<br>EAQEGTDQPSLHGLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP<br>DQQLRLKSPVLRKQACQWKHSFVPSGVT\PAQLRQSSLELTW<br>DQALFGMNDRLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS<br>PNLWTDMTLVLH  |
| 6820       | 1014   | 340  | GDMVYIVGHVPPGFFEKTQNKAWFREGFNKYLKVVRRKHHRVIA<br>GQFFGHHHTDSFRMLYDDAGVPIAMFITPGVTPWKTTLPGVVN<br>GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGT\PRWELEY<br>QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYVYNSVSYSAG<br>VCDEACSMQHVCMARQVDIDAYTTCLYASGTTFPVQLPLLLMAL<br>LGLCT  |
| 6821       | 1088   | 518  | EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGSPSTVHPIQSPQN<br>RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT<br>FFAFSLIEGYI\SIIVMDAETQKKFPSDLLTSSSGELWRMVRIG<br>GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFHDHALVPEDGI<br>GSVIEVLQRRQEGLAS   |
| 6822       | 1088   | 518  | EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGSPSTVHPIQSPQN<br>RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT<br>FFAFSLIEGYI\SIIVMDAETQKKFPSDLLTSSSGELWRMVRIG<br>GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFHDHALVPEDGI<br>GSVIEVLQRRQEGLAS   |
| 6823       | 654  | 221  | PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPPWRSVQTAC<br>GIPQLLEAVLKLLPLDITYVESPAAVMELVPSDKERGLQTPVWTE<br>YESILRRAGCVRALAKIERFEFYERAKKAFVAVTGETALYGNL<br>ILRKGVLALNPLL  |
| 6824       | 858  | 104  | LLLAQRWGWG\CCFFSLAVSVKMNVLFPAGLLFLLLTQFGFRG<br>ALPKLGICAGLQVVLGLPFLLENPSGYLSRFDLGRQFLPHWT<br>NWRFLPEALFLHRAFLALTLTAHLTLLLLFALCRWHRTGESILS<br>LLRDPSSKRKVPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV<br>WYFHTLPYLLWAMPARWLTHLLRLVLGLIELSWNTYPTSTCSS<br>AALHICHAVILLQLWLGPPFPKSTQHSKKAH   |
| 6825       | 3  | 1173   | SSGEFLQASDIMWTISDTGWILIILCSLMEFWALGACTFVHLL<br>PKFDPLVILKTLSSYPIKSMGAPIVYRMLLQODLSSYKFPHLQ<br>NLAGGESLLPETLENWRAQTGLDIREFYGTETGLTCMVSKTM<br>KIKPGYMGTAASCYDVQIIDDKGNVLPGETEGDIGIRVKPIRPI<br>GIFSGYVDNPKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD<br>IINSSGYRIGPSEVENALMEHPAVVETAVISSPDVVRGEVVKAF<br>VILALQFLSHDPEQLTKELQHVKSVTAPYKYPRKIEFVLNLPK<br>TVTGKIQRA\KLDRKWKMSGKAPCAVRHLRDIHLDSPLLSLSF<br>PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC  |
| 6826       | 2304   | 954  | LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP<br>LYFEDEVRYLQSTQAIHDFVSQYKNTARQYAYFYKVIQTHPHA<br>NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPW<br>DMCNHTNGLITTGYNLEDDRCCEVALQDFRAGEQIYIFYGTRSN<br>AEFVIHSGFFFDNNSHDRVKIKLGVSXSDRLYAMKAEVLARAGI<br>PTSSVFALHFTPEPISAQLLAFLRVFCMTEELKEHLGDSAD<br>RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLKTYKTIEEDKS<br>VLKNHDLVRAKMAIKRLGEKEILEKAVKSAVNREYYRQOME<br>EKAPLPKYEESNLGLLESSVGSRLPLVLRNLEEEAGVQDALNI<br>REAIKAKATENGLVNGENSI PNGTRSENESLNQESKRAVEDAK<br>GSSSDSTAGVKE |

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|------------|--|--|---|
| 6827       | 1  | 779  | SSVVEFGLSVLGGFLFLFVLENMGLLRHRLRPRCCRRKRNL<br>ETRNLDPENGSGMALQPLQAAPEPGAQCGQREKNSQHPALAPP<br>HQGHSHGHQGGTDITWVLLGDGLHNLTDGLAIGAFAFSDGFSSG<br>LSTTLAVFCHLPHLPGDFAMLLQSGLSFRRLLLSLVSGGLGL<br>GGAVLGVGLSLGVPVPLTPWVFGVTAGVFLYVALVCMPLPFPSS<br>GAPAYA\HVLQGLGLLLGGCLMLAITLLEERLLPVTTTEG  |
| 6828       | 3  | 1654   | KSQHG/WILQMHSCKEGYVVDLKGPNGLHRAMLDLNGTRFSE<br>LGHLSQTASLKRGSFQSGRDDTWRYKTPHRVAFVEKLTKLVL<br>QLPNFWKLMISYVNGSLFSETAEKSGQIERSKNVRQONDPKKM<br>IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA<br>HAIQTVRLTHESLTALEIPNDLLQTIQDLILDRLVRVCMATLQH<br>TAEIIRLAEKEDWIVDNEGLTSLPCQFQCI VCSLQSLKGVLE<br>CKPGEASVFQPKTQEEVCQLSINIMQVFIYCLEQLSTKPDADI<br>DTTHLSVDVSSPDLFSGIHEDFSLTSEQRLLIVLSNCCYLERHT<br>FLNIAEHFEKHNFGQIEKITQVSMASLKELDQRLFENYIELKAD<br>PIVGSLEPGIYAGYFDWDCPLPTGVRNVLKEALVNI IAV:AEV<br>FTISKELVPRVLSKVIEAVSEELSRMQCVSSFSKNGALQARLK<br>ICALRDTVAVYLTPESSKSSFKQALEALPQLSSGADKKLLEELLN<br>KFKSSMHLQLTCQAASSTMMKT |
| 6829       | 1  | 782  | MRMEAGEAAPAGAGGGAAGGKWKVRLNVGGTVFLTTRQTLCR<br>EQKSFSLRSLCQGEELQSDRDETGAYLIDRDPYTFGPIILNFRHG<br>KLVLQKDMAEEGVLEAEFYNIGPLIRI IKDRMEERDVTVTQVP<br>PKHVYRVLCQGEELTQMVTMSDGRFEQLVNISSSYNGSED<br>QAEFLCVVSKELHSTPNGLSSESRKTKSTEOLLEOQQQEEV<br>EEVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVP I  |
| 6830       | 1  | 939  | MEPGSVENLSIVRSRDFLVNKHWDVRIKAWRETLTLQKQL<br>RYRFPPELADPDTCYGFRCFQDLDFSTSGALCVALKAAAGSAYR<br>CFKERRVTKAYLALLRCHIQUESRVTISHAIGRNSTEGRAHTMCI<br>EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL<br>RV\HCSALGHFVVGDLTYGEVSGREDRPFMRMLHAFYLRIPDT<br>ECVEVCTPDPFLPSLDACWSPHTLLQSLDOLVQALRATPDPPPE<br>DRGPRPGSPSALLPGPRPPPPPTKPPETEAQRGPCLQWLSEWT<br>LEPDS  |
| 6831       | 3  | 1087   | SLFFGSSTPDNKAQEEDLETQSPSPSVEKAVTVIDEGTIPTNF<br>NVAEKPADHSLSEVKLKTADPRGTLVKSGDQNVKEKSMILSN<br>VEDLQQPKFISEVSREDEYKKEISGDSEMNINSVVTSAADGENL<br>EIQSYSLIGELVMEEAKTIVPPHVTDSEKRVQKPAIAPPKWN<br>SIFKEEPRSDQKQKSLSDVVDKVPQPKSASSNFASKNITKE<br>SEKPEIILPVEESKGLIDFSEDRLKEMQNPTSLKISEEETK<br>LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKONSV\APLELRDS<br>NEIGKTQITLGRSSTELKESKADAMPQHFYQNYEDYNERPKIIVG<br>SEKEKDEKKKK   |
| 6832       | 1809   | 412  | MGSLISGPPQDNGEALKEPERAQEHSNLPFAGGQHFFFEYLLV<br>VSLKKRSDEDDYEPITTYQFPKRENLLRGQEEERLLKAIPLF<br>CFPDGNEWASLLEYPRETFVLTNVDGSRKIGYCRLLPAGPG<br>PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAYIPFMQGL<br>REAAFPAPGKTVTLSKFIPOSGTFISLTRPLDSHLEHVDFFSSL<br>LHCLSFQILQIFASAVLERKIIFLAEGSLTSLQCIHAAALLY<br>PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFOQEVMDSPME<br>EVLVLNLCGTFMLSVGDEKIDILPPKLQDDILDLSLQGINELKT<br>AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK<br>ALTSKTNRRFVKFKVKTQLFSLFIQAEKSKNPPAGYFQOKILE<br>YBEQKKQ/TETKGNCEIRAVVNKND   |
| 6833       | 1  | 1129   | PLMTLSQCGGIPGHGSHGGHGHGLPKGPRVKSTRPGSSDIN<br>VAPGEQGPQDEETNTLVANTSNSGLKLDPADPENPRSGDTVEV<br>QVNGNLVREPDMLEEDRAGQLNMRGVFLHVLGDALGSVIVVV  |

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|------------|--|--|--|
|            |  |  | NALVFYFSWKGCEGDFCVNPFDPCKAFVEIINSTHASVYEA<br>GPCNVLYLDPTLCVVMVCILLYTTPYLLKESALILLQTVPKQID<br>IRNLIKELRNVEGVVEVHVLHVWQLAGSRIIATAHIKCEDPTSY<br>MEVAKTIKDVFNHGHATTIQPEFASVGSKSSVVPCELCARTQ<br>CALKQCCGTLPOAPSGKDAEKTPAVSISCLBLSNNLEKKPRRTK<br>AENIPA\VVIEIKN\IPNK\QPESSL  |
| 6834       | 78   | 1151   | AGQERPAPIWRLLWLTTPSVSRKAEPAHIPINR*GA*E*RGGLP<br>LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP<br>CSKLVLSGARGIVGTTVQVLVEAQQLLLLLFTGVWGLNLRAGEE<br>SRAL*LIBEVTVRD AHLGNVAVGCAQCLSQGQVGSALAKALLE<br>AAAARVDCKEVLTVSGDKQAEVSVRL*VRDVCVEEAGCVFEGQ<br>AHGRPGLALAKGRGGTNEVEEQVQVDGVQLVLSAHECHELVAG<br>QQDGEDQAARTRLQAGAHSAHGRRQQAAPCRPHQAGVSCHE<br>LQQVVGDA*ARE*APQIIVLLLLLEDVAQLRTGKKA*DLVVDVE<br>QLLRQL  |
| 6835       | 1  | 834  | GIPAADR\EASLELIKLDISRTFPNLCIFQOGGPPYHMLHSILG<br>AYTCYRPDVGIVQGMSTFAAVLILNLDADAFIAPSNLLNKPCQ<br>MAFFRVHDHGLMLTYFAAFEVFPEENLPKLFPAHFKNLTPDIYL<br>IDWIFTLYSKSLPDLACRIWDVFCRDGEEFLFRTALGILKLF<br>DILTMDFIHMAQFLTRLPEDLPABELFASIIATIQMSRNKKWA<br>QVLTALQKDSREMRREGKSVPTLRLQREFALGTNQSEMPRLCC<br>FRLTPGQPRRTDAL  |
| 6836       | 1  | 850  | MSCGRPPPDVDMITLKV\DNLTyrTSPDLSRRVFKEYGRVGDV<br>YIPREHTKAPRGFAFVRFHDRDAQDAEAMDGAEIDGRELRV<br>QVARYGRRDLPRSRQRRHAAGPEAA/RYGRRSRYSRGRSRSPR<br>RRHRSRSGPSCSRSRSRYSRYSRSPYRSRSPYRSRYSR<br>PYSRYSRYRESRYGGSHYSSSGYSNRYSRYSRSHSKSGSSTS<br>SRSASTSKSSSARRSKSSSVSRSRSRSSMTSPRVSRRKS<br>KSRSRSKRPPKSPPEEGQMSS  |
| 6837       | 1  | 1369   | TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP<br>PNPPAQGDGTSLSPTYTLESTSGNDGKPVSGGGGRGRGRKRDS<br>GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAGVSSAGET<br>RGAPTPEKALTSPPSWGKGAELLGDDQDPLIGSLDGGAKSDSSS<br>PNVGEFASDEVSTSYANDEVSSSDNPAQVKAASRPLVTGSP<br>KLPPRGVAGEHCPKAPPALGLGIMSNSTSTPDSYGGGGGPGH<br>PGTPGLEQVTRPTSSSGAPPDEIHPLILQAIQLQRQOFSIS<br>EDQPLGLKGGKKGECAGVAGSAQNGDSELGSCCSEAVKSAMSTI<br>DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPQNPNS<br>KEAHDLPANKASASQPGSHLQCLSVHCTDDVDGAKARASVPTWR<br>SLHSDISNRFGTFVAALT |
| 6838       | 16   | 499  | LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMETLTWQODEE<br>DQTRDMELVETRPAGDGTQKWAADVVPSEGE/Q/RYMCHVQHE<br>GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC<br>RKNSDRVSYSEAASSDHAQGSVSLTACKV  |
| 6839       | 1  | 1195   | AAPAGGGPDPEALSAPFGRHLSGLSWPQVKRLDALLSEPIPIHG<br>RGNFPPLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGAASHVL<br>HPESGLGYKDLDLVFRMDLRSEASFQLTAKAVVLACLLDFLPAGV<br>SRAKITPLTLKEAYVQKLVKCTDSDRWSLISLNSKSGKNVELK<br>FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG<br>ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLYCHLLVRGFR<br>PRPSTDVRLAQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD<br>AARRYACLVTLHRVNVNSETVCLMNHERRQTLDLIAALALQALAE<br>QGPATAALAWRPPTDGVVPATVNYVTPVQPLLAHAYPTWLP<br>CN   |
| 6840       | 4254   | 2061   | ELQGDVSPVDPVPSMAWCENSICVGFKRDIYLLIRVDGKGSIKEL<br>FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW  |



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|------------|--|--|--|
|            |  |  | TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPFI<br>TSGGSNIIVASNHFWRLIPVPMATQIQQLLDQKQFELALQLA<br>EMKDDSDSEKQQQIHHIKNLYAFNLFQCKRFDESMQVFAKIGTD<br>PTHVMGLYPDLLPTDYRKQLQYPNPLVLSGAELKKAHLALIDY<br>LTQKRSQVLVKKLNDSDHQSSSTPLMEGTPTIKSKKKLLQIIDTT<br>LLKCYLHTNVALVAPLLRLLENNHCHIESEHVLKKAHYSELI<br>LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL<br>HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPDRVLGFLIEN<br>FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKKEYLL<br>SFPAGKTPVPAGEEEGELGEYRQKLLMFLEISSYDPRGLICDF<br>PFDGLLEERALLGRMGKHEQALFIYVHILKDTMABEYCHIKHY<br>DRNKDGNKDVLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA<br>LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLLENAQKK<br>RFNVQLKNLLHABFLRV\QEERILHQQVKCIITEEKVCMVCKKK<br>IGNSAFARYPNGVHVHYFCS\KEVNPADT  |
| 6841       | 1  | 3206   | TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA<br>REKRDSSRMNEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD<br>MCPETRLDRTGSSPTQGIWNKAFGINTDSLYHELSTAGSEVIGD<br>VDEGADLLGEFSGMGKEVGNLLENSQLLETKNALNVKNDLIA<br>KVDQLSGEGEVLRGELEAAKQAKVKLENRIKELEELKRVKSEA<br>IARREPKEEAEDVSSYLCTESDKIPMAORRFRTRVEMARVLMR<br>RNQYKERLMELQEAVRWTEIRASREHPSVQEKKKSTIWQFFSR<br>LFSSSSSPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPIASG<br>SRPLEFFPDDDCTSSARREQREQYRQVREHVRNDDGRLQACGW<br>SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA<br>AGVNLSGWRPNEDDAGNVKPAAGRDPLTCDREGDGEPKSAHTS<br>PEKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD<br>QFTVCNAHVLCISSIPAASDSYPPGEMFLDSVNPEDPGADGV<br>LAGITLVGCATRCNVPRSNCSRGDTPVLKDGOGEVATIANGKV<br>NPSQSTEEATEATEVDPGPGSEPETATLRPGPLTEHVFTDPAPT<br>PSSGPPQSGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMMWL<br>AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD<br>GTLAI FHRGEDGQWDLNHYHLMDLGHPHHSIRCMVAVVYDRVWCG<br>YKNKVHVVIQPKTMQIEKSFDAHPRESQVRQLAWIGDGVVVSIR<br>LDSTLRLYHAHTHQHLQDVDEPYVSKMLGTGKLGFSFVRITAL<br>LVAGSRLVWGTGNGVVISIPLETETVVLHRRQ\LLG\LRANKTSP<br>TSSEG\ARPGG\IIHVG\DDSSDRAARSFIYCSMAQAQLCFH<br>GHRDAVKFFVSPGNVLTNGSVLDSPAEGPGPAAPASEVEGQ<br>KLRNVVLVSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLKKA<br>ERSHIIVWQVSYTPE |
| 6842       | 3  | 926  | RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP<br>RRLEFQSVKLHCPKCHLLQEVPHGEDLDIIFQDGATKTPDVKLON<br>TSLYDSKIWTTKNQGRKVAVHFVRNNGILEPLSNECLLLIEGGT<br>LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC<br>KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFMFTFT<br>LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSDMIMDMFC<br>PPGIKIDAYPWLECFIKSYNVNTNGTDNQICYQIFDTTVAEDVI   |
| 6843       | 2  | 851  | NHRKVLGSAKRYECNECGKSFAYTSSLIKHRIHTGERPYECSE<br>CGRSPAENSLLIKHLRVHTGERPYECVECGKSPRRSSSLQHQ<br>VHTRERPYECSECGKSFSLRSNLIIHQRVHTGERHECGCGKSF<br>SRKSSLIHLRVHTGERPYECSDCGKSFSAENSLLIKHLRVHTGE<br>RPYECIDCGKSFHSSSFRHQRVHTGMRPYK*SKFWKFCSPGF<br>LLLOGQRVHTGSRCECDKWGIFFS*NASFFT*KSAPTEEVFFE<br>CNECEKAFSPSLSVTTTFT   |
| 6844       | 244  | 642  | ZHQLAGFELRKTQTSMLGTTREKTRVKTAYLSPQLEEDVFPY<br>QYDVKSEIYSFGIVLWEIATGDIPOGCNSEKIRKLVAVKRQQS  |

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|------------|--|--|--|
|            |  |  | PLGEDCPSBELREIIDECAHDPSPVRPSVDILKKLSTFSK*CIK I   |
| 6845       | 3  | 1519   | VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLEYRIRTLG<br>GALENAQNLYGQAKPANESADSGLEVCPEDIYGVQVHVNGAV<br>GLAFELYHHTTQDLQLFREAGGWDVVRVAEFCRSRVESPREE<br>KYHLRGVMSPDEYHSGVNVSVYTNVLVQNSLRFAAALAQDLGLP<br>IPSQWLAVADKIKVPFDEQNFHPEFDGYPEGVEVVKQADVLLG<br>YPVPFSLSPDVRKNLEIYEAVTSPQGPANTWSMFVAVGMELKD<br>AVRARGLLDRSFANMAEPFKVWTENADGSGAVNFLTGMGGFLQA<br>VVFCTGFRVTRAGVTDFPVCLSGISRVSVSGIFYQGNKLNFSF<br>SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLPGHKVSPFRS<br>AGRIQMSPPKLPGSSSEFPGRFTFSDVRDPLQSPFLWVTLGSSSP<br>TESLTVDPASE*SGTGASETSLGPSLWFLHPPLLTLLACHPS<br>PAARLSGKVHAANPEFKAFCL |
| 6846       | 213  | 1258   | LYFLKTIK*LNRLAEHP*YENEKLTCLRNTIMEQYTRTEESARG<br>IIFTKTQSAYALSQWITENEFKFAEVGVKAHLIGAGHSSEFKP<br>MTQNEQKEVISKFTGTGINLLIATTVAEEGLDIKECNIVIRYGL<br>VTNEIAMVQARGRADESTYVLVAHSGSGVIEHETVNDFREKM<br>MYKAHCVQNMKPEEYAHKILELQMQSIMEKKMTKRNIKHYK<br>NNPSLITPLCKNCVSLACSGEDIHVIEKMHVNMTPEFKELYIV<br>RENKTLQKKCADYQINGEICKCGQAWGTMVHKGLDLPCLKIR<br>NFVVVFKNSTKKQYKKWVLEPITFPNLDYSECCLFSDSD   |
| 6847       | 1450   | 348  | SMCWNSDRLEMPILDLALILYPPSYVPYTGHLSDDSLRSKYCLT<br>WFDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQ<br>PPAYGTLTVRSLDTRHCLNEFNFPDPYSKVQRENGVALRCF<br>PGVVRSLDALGWEERQALVKGLLAGNVFDWAKAVSAVLESOP<br>YFGFEEAKRKLQERPWLVDSEWLQRLKGPPIKCALIFADNSG<br>IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE<br>RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR<br>ERGADLVVIEGMRVHTNYHAALRCESLKLAVIKNAWLAERLG<br>GRFSLVIFRYEVPAE   |
| 6848       | 19   | 16   | AMWNSLDGIRNIVLSNPKKRNLTSLAMLSLQSDILHDADSND<br>LKVIIISAEQPVFSSGHDLKELTEEQGRDYHAEVFQTC SKVMH<br>IRNHPVPVIA MVNGLATAAGCQLVASCDIAVASDKSSFATPGVN<br>VGLFCSTPGVALARAVPRKVALEMLFTGEPI SAQEALLHGLLNK<br>VPEAEQEETMRIARKIASLSRPVVS LGKATFYKQLPQDLGTA<br>YYLTSQAMVDNLALRDGQEGITAFLOKRPVWSHEPV*VEH  |
| 6849       | 70   | 821  | SLGVDGSCLEQGSAPRPPQTDTSF*PVGWATQEDLYHQSYEC<br>VCVLFASVPDPKFEFYSSENINHEGLECLRLLEI IADFDLLSK<br>PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGT<br>VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPPVAVGIGA QKPKQ<br>YDIWNTVNVASRMESTGVLGKIQTETEAWALQSLGYTCYSRG<br>VIKVKGKQLCTYFLNTDLTRTGPPSATIG   |
| 6850       | 2  | 1235   | ARGLNHEWTFEKLQHISRNAQDKQLHLFMSLGVDPDAVFDLTD<br>LDVLKLELIPRAKIPAKISQMTNLQELHLCPCPAKVEQTAFSFL<br>RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLSENKMI<br>GLESRLRELRLKILHVKSNTLVPSNITDVAPHLTKLVIHNDGT<br>KLLVLNLSLKKMMNVAELELQNCLELIPHAIFSLSNLQELDLS<br>NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL<br>YFSNNKLES LPVAVFSLOKLRLCLDVSYNNISMIPIEIGLLQNLQ<br>HLHITGNKV DILPKQLFKCI KLRTNLNGQNCITSLPEKVGQLSQ<br>LTQLELKGNC LDRLPALQGCRLKKSGLVVDHLFDLPLEVK<br>EALNQDINIPFANGI   |
| 6851       | 1765   | 660  | VSAQVSAREGENCLGWNADSSQESYKSLEEAEDCYPPSLTLTD<br>LRDLFNQVEQGPLLSCPKAGTDLMSGRAREVGWMAAGLMIGAGA<br>CYCVYKLTIGRDDSEKLEEEGEEWDDDDQELDEEEDPIWDFET   |

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|------------|--|--|---|
|            |  |  | MARPWTEGDGDTPEGAPGGTDRPSGGKANRAHPIKQRPFPYE<br>HKNTWSAQNCNGSCVLDLSKCLFIQKLLFAEPKADAGFPFSQD<br>INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM<br>YINEVCRETVSRCNSFLQQAGLNLLISMTVINMMLAKSASDLK<br>FPLISEGSGCAKVQLKPLMGLSEKPVLAGELVGAQMLFSFMSL<br>PIRNGNRRIILETPAP   |
| 6852       | 1  | 407  | RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT<br>GFILNSIAVLNCLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ<br>IAETLWEQVLKPLGDNLMENIROSVTNSIKAGLTDOVSHHARL<br>KTD   |
| 6853       | 3  | 469  | GDSCAVCIELYKPNLVRILTNCNHFHKTCVDPWLLHRTCPMC<br>KCDILKALGIEVDVEDGVSLSQVPVSNEIFNSASSHEEDNRSET<br>ASSGYASVQGTYPPELLEHVQSTNESLQLVNHEANSVAVDVIH<br>VDNPTFEEDETPNQETAUREIKS  |
| 6854       | 1148   | 585  | HESYIGTFDPGELCVCAATQWLQDNSASYFLNRKLVYEPSTQAK<br>PVKNTPLRMWYISHHIYQODLRKKILDVVGKRLDVTGFCMTGKPG<br>IICVEGFKHECEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR<br>LFHSFEELLLLEAGDYGLRNDYHMLNGQFLFLKHKSEHVFI<br>LFGIESKSSDS   |
| 6855       | 1913   | 1148   | GRVGGRVGRITCSPLSGANEYIASTDTLKTEEVLLFTDQTDLLAK<br>EPTSLFQDSETKGSGLVLEGDKIHIQIFEDLDKLLALASRF<br>YIPEGCIQWAAEMVVALDALHREGIVCRDLNPNLLNDRGHI<br>QLTYFRWSEVEDSCSDAIERMYCAPEVGAI TEETEACDWWSL<br>GAVLFELLTGKTLVECHPAGINTHTTLNMPWVSEEARSLIQQL<br>LQFNPLERLGAGVAGVEDIKSHPFPTPVDWAEMLR  |
| 6856       | 1617   | 997  | VTQLYVSVDASTKDSLKKIDRPLFKDFWQQLDLSLKALAVKQOR<br>TVYRLTLVKAWNVDLQAYAQVLVSLGNPDFIEVKGVTYCGESSA<br>SSLTMAHVPWHEEVQFVRELVDLIPEYBIACEHEHSNCLLIAH<br>RKFKIGGEWWTWINYRNFQELIQEYEDSGGSKTFSADY MARTP<br>HWALFGASERGFDPKDRHQKRNKSKAISGC   |
| 6857       | 1  | 617  | KGPEATAMVCVCSHPNCRQNHKPSHSAQQTCCGSPTPASAPNH<br>KLMAEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF<br>DLQQLSDDEGTNMHLQLVRQEMAVCPQLSEFLDSLRLQYLRT<br>TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSLCKAF<br>RHVKVDTLTSLQPEALSRLVPAAWCTVGRD   |
| 6858       | 2  | 669  | RSRGIKDFENDPPLSSCGIFQSRIAGDALDLSGIRISSVFASPA<br>LRCVQTAKLILBELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM<br>SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ<br>IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR<br>KIPSLGCMCFCEENKEBGKWEVLNPPVKTLLTHCANAAFNRNWNIS<br>GN  |
| 6859       | 1  | 1150   | GETMPKKAKTKAKKKPRKRSDSGGYNLSDTIQSPSTGLLKSG<br>KTNSVESLPELLTSDSEGSYAGVGSPLDLQSPDFTTGFSKDIE<br>AKVKPYVNGTSPVYSREDLPWEKSPILKISAPQPIPSNRIDTT<br>SSASWVAGSPSPVSPVVDLRTIMEIESRQKCGATPKSHLGKT<br>VSHGVKLSQKQKRMIALTKENNSGMNSMETVLFPSKAPKPVN<br>AWASSLHVSSSKSFDFLLEEKSVTSHSGSDHVKVSKFSGIEN<br>SQAPKIVRCSTHGTGPEGNHISDLPLDPSNPNWLSSTVAPSM<br>VAPVTFASIVEEELQOEALIRSREKPLALTIQIEEHAIQDLLVF<br>YEAFGNPEEFVIVERTPOGPLAVPMWNKHGC |
| 6860       | 1889   | 1515   | DKDKKQKQKRGIFPKVATNIMRAWLFQHLTHPYFSEEQKKQLAQ<br>DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP<br>MGSFVLDDQQHMGIRPAGPMSGMGMNMGMGDGQWHYM   |
| 6861       | 1889   | 1515   | DKDKKQKQKRGIFPKVATNIMRAWLFQHLTHPYFSEEQKKQLAQ<br>DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP  |

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|------------|--|--|--|
| 6862       | 2  | 471  | MGSFVLDGQQHMGIRPAGPMSGMGMMGMDGQWHYM<br>EEIDREFHNKLLKEDRLEKQKPVNGEDKGDGSDVTQNSEGNA<br>DEEDPLGPNCYYDKTKSFFDNISCDNRERRPTWAEERRLNAET<br>FGIPLRPNRGRGGYRGRGGLGFRGGGRGGGGGTPTAPRGRFG<br>GFRGGGRGGREFADFEYRKTAFGP   |
| 6863       | 2216   | 487  | PQEPALKSEFSQVANSNTIPLPLPQPNCTCKDNGPCKQVCSTVGGSS<br>AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSSF<br>YCVNHTVLCADGYILNAHRKCDVINECVTDLHTCSRGEHCVNTL<br>GSFHCYKALTCEPGYALKDGEDVDECAMGTHTCQPGFLCQNT<br>KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI<br>NTVGSYTCQRNPLICARGYHASDDGKTCVDVNECETGVHRCGEG<br>QVCHNLPGSYRCDCKAGFQDAFGRGCDVNECWA SPGRLCQHT<br>CENTLGSSYRCSASCGLLAADGKRCEVNECEAQRCSQECANIY<br>GSYQCYCRQGYQLAEDGHTCTDIDECAQAGILCTFRCLNVPGS<br>YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEATCHNIQGS<br>FRCLRFECPPNYVQVSKTKCERTTCHDFLEQNSPARITHYQLN<br>PQTGLLVPAHIFRIGPAPAFGTIALNIKGNEEGYFGTRRLLN<br>AYTGVVYLQRAVLEPRDFALDVEMLWRQGSVTTFLAKMHIFFT<br>TFAL   |
| 6864       | 2  | 2933   | LADSSPSNLQIITIKELLSMHQPDPAITKEFDYLPVDSRSSSG<br>FVGLRNGGATCYMNAVFOQLYMQPLPESLLSVDDTDNPDDSV<br>FYQVQSLFGLHLMESKLQYYPENFWKIFKMNKELYVREQDAY<br>EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSQKICKDCPHRY<br>EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK<br>EKRIITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFP<br>WMLNMEPYTVSGMARQDSSSEVGENGRSVDOGGGSPRKVALT<br>ENYELVGVIVHSGQAHAGHYYSFIKDRGCGKGKWKYKFNDTVIE<br>EFDLNDETLEYECFGGEYRPKVYDQTNPYTOVRRRYWNAIMLFY<br>QRVSDQNSPVLPKKSRVSVVRQEAEDLSAPSSPEISQSSPR<br>PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRENLEKF<br>MKNRDVYSSDYFSFVLSLASLNATKLKHPYPCMAKVSLOLAIQ<br>FLFQTYLRTKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS<br>SEGRELIIKIFLECNVREVRVAVATILEKTLDSALFYQDKLKS<br>HQLLEVLALLDKDVPENCNKCAQYFFLNTFFVQKQIRAGDLL<br>LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFCNLHNTVALL<br>VLHSDVSSQRNVAPGIFKQRPPIAIPSSPLLPLHEEVEALLFM<br>SEGKPYLLEVFMALRELTSLLALIEMVVYCCFCNEHFSFTMLH<br>FIKNQLETAHPHELKNTFQLLHEILVIEDPIQVERVKVFETEN<br>GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH<br>WSNAVQWLQKKMSEHYWTLQSNVSNSTSTGKTFQRTISAQDTLA<br>YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSSESPMMIGEL<br>RSDLDDVDP |
| 6865       | 1820   | 1242   | DPERWKHLSKVTPPGSSVSTTPVQVRLQSPQSQGSMMPSCNRS<br>CSCSRGSPVEDGKWYGVRSYLHLFEYEGYAVFPKLEGIGEGFLV<br>LDQRAADYNQALGTCLAGTALCVAAGVLLAICLPWAMIGWLSQ<br>DTKAEPDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS<br>PFGQSSVQTIQPKRDS  |
| 6866       | 1571   | 495  | DCPRPYTLYGLRATCMRDLDWAWINAVSAFKALEQDLVPNIKF<br>IEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP<br>AITYGTRGNSYFMVEVKCRDQDFHSGTGGGILHEPMADLVALLG<br>SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLSEYRNSR<br>VEKFLFDTKKEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRV<br>IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKNVVSMTL<br>GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF<br>QEIVHKSVVLIPLGAVDDGEHSQNEKINRNWYIEGTKLFAAFL<br>EMAQLH  |

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|------------|--|--|---|
| 6867       | 2833   | 1704   | GTRIMSPQKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQSP LQSAESSPTAGKKLEVPVPEEEEEQEAWNALLGRIFWDFLGEK YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILOAF KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGEPLVEALK VGEIGKEGCRPRAFCLADSDESSSAGSSEDDAPEPSGGDKQL LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE VSNTPLLLTVEVQECRGTAVNIPPPPTDRVWYGFRRKPPHVELK AREKLGEREVTLVHVTDWIEKKLEQEFQKVFPMPNMDVYITIM HSAMPDRSTCLLKDPVVEAADQP   |
| 6868       | 1  | 346  | RPTRPPTRPBEIKNLILPYISDMNFVQDLCEDFYELFKTDKGF D KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG GSQGRIVHLSNSFTOTVNCRKPFPSW   |
| 6869       | 3  | 1619   | MYMERMDKRALISFWESVEHLKANKNEIPQLVGEIYQNFFVES KEISVSEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYPS FIVSDLYEKLKIEEEKHASQMSINKDEMGPRDEAGEAEVDDGT NQINEQASFAVNKLRELNEKLEYKQALNSIQNAPKPKKIVSK LKDEIILIEKERTDLQLMARTDWECENLGMWKASITSGEVTEE NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLRKLSEC VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQNLKFLQNLDSER LCQSEALYAFSPSPDYLVKVIDVQGGKNSFSLSSFLERLPRDFF SHQEEETEEDSDLSYDGDVDRGDALAEPCFMLIGEIFELRGM FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIF RDAFWPNGKLAPPTTIRSEKQSQETKQRAQQKLENIIPDMLQSL VGQQNARHGIIKIFNALQETRANKHLLYALMELLILLICPELRV HLDQLKAGQV |
| 6870       | 1  | 1566   | MAAVVAATRWQQLLVLSAAGMGASGAPQPPNILLMLDMDMGWG DLGVYGEPSRETPNLDMAAEGLLFPNFYSANPLCSPSRAALLT ORLPPIRNGFYTTNAHARNAYTPQEIYVGGIPDSEQLPELKKAG YVSKIYGVKWHLGHPRQFHPKKGDFDEWFGSPNCHFGPYDNKARP NIPVYRDWEMVGRYYEFPINLKTGEANLTQIYLQEALDFIKRQ ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDVREIDDS IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGSNGPFLC GKQTTFEGCMREPALAWPGHVTAGQVSHQLGSIMDLFTSLAL AGLTPPSDRAIDGLNLLPTLLQGRIMDRPIFYRGDTLMAATLG QHKAHFWTWTNSWENFRQIDFCPGQNVSGVTTHNLEDHTKLPL IFHLGRDPGERFPLSFASAEYQEALSRTISVVQQHQEALVPAQ QLVNVCNWAVMNWAPPGEKLGKCLTPPESIPKKCLWSH                  |
| 6871       | 209  | 1126   | RMSLNPPIFLKRSEENSSKRFVETKQSQTTISASEDPLQNLCLAS QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPYEQIPLV KLPKIDIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPYE EKDEHALIFPGPQISIKDISFHLQKRIQNNVRGKNDPDKPS FKRKRTEEQEFCDLNSCKGTTLKKIIFIDSTWNQTNKIFTDE RLQGLLQVELKTRKTCFWRHQGKPDFTLSTIEAIYYFLVDYHT DILKEYRGQYDNLFFYSFMYQLIKNAKCSGDKRETGKLTH  |
| 6872       | 880  | 459  | FGLLMVLSLIFMKGNCVREDLTFNFLFKLGLDVRETNGLFNGT KKLITEVFVRQKYLEYRRIPYTEPAEYEFWGPRAFLETSKMLV LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG PTSRPPPR   |
| 6873       | 1929   | 955  | DEQAVLCSKDKTYDLKIADTSNMLLFI PGCKTPDQLKKEDSHCN I IHTEIFGFSNNYELRRRRPKLKKLLMENPYEGPDSQKEK DSNSSKYTTEDLLDQIQASEEIMTQLQVLNACKIGGYWRILEF DYEMKLLNHVTQLVDSESWSGFKVPLNTCLQELGPLEPEEMIEH CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKNLAEF QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE DNQERFNSLSLEKWTEDDIAPYIQDLCEGKQTIGALLTKYSH SSMQNGVKVYNSRRPIS  |

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|------------|--|--|---|
| 6874       | 1  | 307  | DSIADHVNSAAVNVEEGTKNLGKAARYKLAALPVAGALIGGMVG GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMEKLTSSCPDLPSQTDKKCS  |
| 6875       | 1688   | 349  | VIGTGERGNSASEKWEIMFNEELGDPFIIHSISLLNAEEHSIA TLLLRIEKEELDMKSGFYVSLWVTISKKNQDNKKYETIKRDI LRGKSVPHYAAIEPDGNLMIVSYKSLTFVQAGQDLEENMDEDI SEKIKEPLYWQQTEDDLTVTIRLPEDNTKEDIQIQLPDHINI VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW PELVIGDKQGELIRDSAQCAIAERLMHILTSEELNPNPDKEKPP CNAQELEECDIFFEESSSLCRFDGNTLKTTHVNLGSNQYLFVS IVDPKEMPCFCLRHVDVALLWQPHSSKQDDMWEHIATFNALGYV QASKRDKKFFACAFNYSYAALCECLRRVFIYRQAPMSTVLYNR KEGRQVGQVAKQVVASLETNDPILGFQATNERLFVLTTKNLFLLI KVNTEN |
| 6876       | 41   | 1285   | VGEMTLINRHLRLCLVTSAPRILEMHPFLSLGTSRTSVTKLS LHTKPRMPPCDFMPERYQVIFLVNSGSEANELAMLMARAHNNI DIISFRGAYHGCSPYTLGLTNVGIYKMEPLGGTGCCQPTMCPDVF RGPWGGSHCRDSPVQTIRKCSAPDCCQAKDQYIEQFKDTLSTS VAKSIAGFFAEPIQGVNGVVQYPKGLKEAFELVRARGGVCIAN EVQTGFGRGLGSHFWGFQTHDVLDPDIVTMAKGIONGFPMMAVITT PEIAKSLAKCLQHFNFTFGGNPMACAIGSAVLEVIKEENLQENSO EVGTYMLLKFAKLRFDEFIIVGDVVRGKGLMIGIEMVQDKISCRPL PREEVNQIHEDCKHMLGLVGRGSIFSQTFRIAPSMCITKPEVDF AVEVFRSALTQHMERRAK                          |
| 6877       | 1  | 778  | GTSPSPARAYAPPTERKRFYQNVSTIQEGGCFEINLDHRKLKTP QAKLFTVPSEALAIIVATEWDSQDITIKYTTMHLTLCNTSLDN PTQRNKDQLIRAAVKFLDITICVRVEEPETLVELQRNEWDPPII EWAEEKRYGVEISSSTSIMGPSIPAKTREVLSHLASYNWALQG IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWN IEWADHYELQELRARTAGTLFIHLCESTTVKHKLKE  |
| 6878       | 931  | 263  | QTLQGDFFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQON LEEDTVTLVLVAPVPSCEVPSSALSCTVVELRCQDKENGPAP EYTWFKDGI RLLENPRLGSSQSTNSSYTMNTKTGTLOFNTVSKLD TGYSCEARNVGYRRCPPGKRMQVDDLNSGIIAAVVVVVALVIS VCGLGVCYAQRKGYFSKETSFSQKSNSSSKATTMSENDFKHTKSF II  |
| 6879       | 3  | 845  | IRVIGESDIMQEFLESSEDENYNGVSDVELRVALPDGTTVTVRVK KNSTTDQVYQAIKAVGMDSTTVNYFALFEVISHSFVRKLAPNE FPHKLYIQNYTSAPVPGTCLTIRKWLFTTEBEILLNDNDLAVTF FHQAVDDVKKGYIKAEKSYQLQKLYEQRKMMVYLNMLRTCEGY NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEOLEENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRVVKIFTYPFNYMHE CFERVFCELRKWKKEY   |
| 6880       | 2110   | 1437   | RKONCTAKEWTFPEAKWNTTARVFSHIRLGMHVLIIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFOGLSVAFILKFLDNMFH VLMAQVTTVIIITTVSVLVFDFRPSLEFFLEAPSVLISFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEELRLTKPKSDESD EDTF  |
| 6881       | 2638   | 2244   | NDSKWEDIHVITGALKMFFRELPEPLTFNHFNDVNAIKQEPER QRAVAVKDLIRQLPKPNQDTMQILFRHLRRVIEGKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNVQIVELILLELSSIFGR   |
| 6882       | 1  | 850  | GTPAQWLWYIPVKSCKGVVPVSEACTAMGLRSGNLRDRFWLVIN QSGNMVITARQEPRLVLSLTCDGDTLTLSAAYTKDLLLPKPTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK   |

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|------------|--|--|--|
|            |  |  | KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI<br>LTTVDPTGVMRSRKEPLETLKSYRQCDSERKLYGKSPLEFGQYF<br>VLENPGTIKVGDPVYLLGQ  |
| 6883       | 2794   | 2256   | NSKLLNQNKLKLFITLTQVLSLHGWGPGIHLQKEGAPFVTQNR<br>ALQLLYDLRYLNI VLTAKGDEVKSGRSKPDRIEKVTDHLEALI<br>DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSSTF<br>NSQEPHNILPLASSQIRFGLPLSMTSTRKAKSTRNIETKAQYD<br>ANC   |
| 6884       | 2  | 99   | EFERVTAEAVKPRETSEPRAAQRFCEKFPFL  |
| 6885       | 297  | 1554   | STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFQDV<br>LCDSPYQLILSAFDFIKNSGQEASFMITGDSPPHVPVPELSTD<br>TVINVIITNMTTIIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV<br>YNAVANLWKPWLDEEAISTLRKGGFYSSQKVTNPNLRIISLNTN<br>LYYGNIMTLNKTDPANQFEWLESTLNNSSQNKKEKVYIIAHVPV<br>GYLPSSQNTAMREYYNEKLIDIFQKYSVDIAGQFYGHTRHDSI<br>MVLSDKKGSPVNSLFVAPAVTPVKS VLEKQTNNGIRLFQYDPR<br>DYKLLDMLQYYLNLTEANLKGESIKWLEYILTQTYDIEDLPQES<br>LYGLAKQFTILDSKQFIKYNYFFVSYDSSVTCDDTKCAFAQICA<br>IMNLNISIYADCLQOLYIKHNY                                  |
| 6886       | 2  | 1341   | QCGGIPGREGGSSRPLEEGTGSSSPACVRGAAPGSEDAFYPTRAK<br>QARVSQELKKAARTVSISEGPDTLGDGMRERETALALAPEPEP<br>LEKEACEKWKRPFRSASATSLTSLHSCVDVVKGLDPKRRGHSI<br>GGAPEQRYQIIPVCVAARLPTRAQDVLD AHLSEVNAVRFQPNSS<br>LLATGGADRLIHLWNVVGRLEANTLLEGAGGSITSVDPDFSGY<br>QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA<br>VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN<br>DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT<br>LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD<br>GALYIWDVDTGKLESRLQGP HCAAVNAVWCYSGSHMVSVDQGR<br>KVVWLWQ |
| 6887       | 1047   | 116  | WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGCCPRGPWGPQHG<br>GQORAAGPTLPRGERGPPQSGPGLAAQTPPTSKQVAVRAFLTG<br>TYRSQSPRSPAGPFRGGTGWPEPAVCLCVAVGPQRLSSPGLVY<br>NAGSEHCYDIYRLVHSCADPTGCGTGP DARAWDYQACTEINLT<br>FASN NVTDMFPDLPTDELQRQRYCLDTWGVWPRPDWLLTSFWGG<br>DLRAASNIIFSNGLDPWAGGGIRRNLSASVIAVTIQGGAHLD<br>LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL<br>SL   |
| 6888       | 1  | 992  | FVAYVKKIPIHIVVTHCLNPHALVIKTLPTKLRDALFTVVRVI<br>NFIKGRAPNHLRFQAFEEIGIEYSVLLFHTMRWLSRGQILTH<br>IFEMYEEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE<br>LSASMQRGTGMNTVSAREKLSAFVRKFPFWQKRIEKNFTNFPFL<br>EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI<br>LDPFLFNIDFVDDSYLMKNDLAE LRASGQILMEFETMKLEDFWC<br>AQFTA FPNLAKTAL EILMFFATTYLC ELGFSITFTFQNKVPEAA<br>LILSDDIRVAISKKVP SFLGHH   |
| 6889       | 1  | 1534   | LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLTTT<br>AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDIIASVV<br>ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW<br>ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVS GVKHKNISL<br>WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEVSKRQ<br>KNKSGETVVLKLDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP<br>EGKFNLAHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI<br>EVS DVVNILVYVGIKAGNGILSKAGILKKFEEDLDDILKRLK<br>DSSEIPGALWHIYAGKVDKIREFLQKISKEQGLEVLPEHDP<br>IR<br>DQSWYVNNKLRQLLEBYGVRTWTLIQFLGDAIVLPAGALHQVQ               |

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|------------|--|--|---|
| 6890       | 3  | 667  | NFHSCIQVTEDFVSPFHLVSEPHLTQELRLKKEINYDDKLQVK<br>NILYHAVKEMVRALKIHEDEVDDMEEN<br>THACGMNIPLYLHRALVVHKTAEACNSPPCCAKDLSIFGAITCF<br>TGFLGVDTGAGATRWCRCLKTQRADPLVCAVGMGLGSAIFICLIFV<br>AAKSSIVGAYICIFVGETLLFSNWAITADILMVVVIPTRRATAV<br>ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA<br>LMLCPFVVVLGGMFFLATALFFVSDRARAQQVNLAMPASVK<br>V  |
| 6891       | 1980   | 1262   | LRHQELLSKELKLLRGITTESIIHIGLAAGKEQFMQDASNVMO<br>LLLKTQSHLYNMEDNNPEVRQAAAAYGLGVMAQFGDDYRSLCSE<br>AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVDF<br>EVLPHWLSWLPPLHEDKEEAIQTLFLCDLIESNHPVIGPNNSN<br>LPKIIISIIAEGKINETINYEDPCAKRLANVVRQVQTSSEDLWLEC<br>VSQLDDEQEQEALQELNLFA   |
| 6892       | 3  | 876  | RSVAAASGPGAWGTDHYCLELLRKRDRYEGYLCSSLLPAESRSSV<br>FALRAFNVELAQKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH<br>QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNKELE<br>NYAENTQSSLLYLTLEILGKIDLHADHAASHIGKAQGIIVTCLRA<br>TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA<br>SQAHLLHLKHARSFHKTVPVKAFFAFLQTVSLEDFLKKIQRVDFD<br>IFHPSLQKQNTLLPLLYLIQSWRKTY   |
| 6893       | 1  | 842  | DGERKMSVERTFSEINKAEEOYSLCOELCSELAQDLQKRLKG<br>RTVTIKLKNVNFVVKTRASTVSSVSTAEIIPAIKELLKTEID<br>ADFPHLRLRLMGVRISSFPNEEDRKHQORSIIGFLQAGNOALS<br>ATECTLEKTDKDKFVKPLEMSHKKSFFDKKRSEKWSHQDTFKC<br>EAVNKQSFQTSQPPQVLKKMNENLEISENSDDCQILTCVCFR<br>AQGCISLEALNKHVDECLDGPSEISENFKMFCSHVSATKVNKKE<br>NVPASSLCEKQDYEAH  |
| 6894       | 1742   | 1463   | TTLCKPLVPREHFYETLPAEMRKFTTQYKGSQLEGLPHWRG<br>DVRDRGHGRPWQPSLEPSLPPTLCFPLSSFSSSWPSAQHLTPS<br>VFNPW   |
| 6895       | 2379   | 478  | VTVVELCDLASPTALLIMRTVLDLIVEDLQSTSEDEKQQYTSOT<br>TRLALALYALASHKACKLAILHLINGTIKGDERYAEIFQDLAL<br>VRSPGDSVIRQQCVYVTSILQSLCDQDIALILPSSSEGSISEL<br>EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCTVRTMMFL<br>AEHDYGLFHLKSSLRKNSSALHSLKRVVSTFSKDTGELASSFL<br>EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL<br>QSKEESPENLFLELEKLVLEHSKDDDNLDLLDSVVLKQMLLES<br>SGDPLPLSDQDVEPVLAPESLQNLFNRTAYVLADVMDDQLKS<br>MWFTPFQAEIIDDLDLVKVDLIELSEKCCSDFDLHSELEERSFL<br>SEPSSPGRTKTKTGFKLGKHKHETFTSSGKSEYIEPAKRAHV<br>PPPRGRGRGGFGQGI RPHDI FRQRKQNTSRPPSMHVDDFVAES<br>KEVVPQDGI PPPKRLKVSQKISSRGGFSGNRGGRGAFHSQNR<br>FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG<br>PLPPLRPLSSTGYRPSPRDRASRGGGLGPSWASANSQSGGSRG<br>KFVSGSGRGRHVRSFTR |
| 6896       | 1  | 555  | GNIVIQKKKYNKQHIIPLENTIDSIKDEGLRNGWLKTPTKS<br>FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAADVVPD<br>SEATVCMRCQAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ<br>SSKPVRICDFCYDLLSAGDMATCQPARSDYSQSLKSLPLNDMSD<br>DDDDDDSSD   |
| 6897       | 3  | 920  | GDGLMHEVNGLMERPDEWETAIQKPLCSLPAGSGNALAASLNHY<br>AGYEQVTNEDLLTNCTLLCRLLSPMNLSSLHTASGLRLRFSVL<br>SLAWGFADVDLESEKYRRLGEMRFTLGTFLLRLAALRTYRGLA<br>YLPVGRVGSKTSPASVVVQQGPVDAHLVPLEEPVPSHWTVVPDE<br>DFVLVLALLHSHLGSSEMAAPMGRCAAGVMHLFYVRAGVSRAML  |



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|------------|--|--|---|
|            |  |  | LRLFLAMEKGRHMEYECPLYVVPVVAFLBPKDGGKGVFAVDGE<br>LMVSEAVQQGVHPNYFWMVSGCPEPPPSWKPPQMPPEEPL   |
| 6898       | 919  | 346  | QKTVTAVASLLKGRQGIYTENERRMGAVIKIRFFKIMLVLIICW<br>LSNINIESLLFYLEMQTDINGGSLKPVRTAAKTWTFIMGILNPA<br>QGFLLSLAFYGTGCSLGFQSPRKEIQWESLTTSAEGAHPSPPL<br>MPHENPASGKVSQVGGQTSDEALSMLSEGSASTIEHTASESC<br>NKNEGDPALPTHGDL  |
| 6899       | 120  | 827  | MKVRKNNDAYLLDKNKINMDCFISCFKKMLTLMFSHSGILSL<br>LEHGEETTFSLPCAYARSILTVPWVELGGKVSVMCAKTGYSASI<br>TFHTKPFYGGKLRHVTAEVKHNITNTVVCRVQGEWNSVLEFTYS<br>NGETKYVDLTKLAVTKKRVPRLEKQDPFESRRLWKNVTDLSLRES<br>EIDKATEHKHTLEERQTEERHRTETGTPWKTRYFIKEGDGWVY<br>HKPLWKIIPPTQPAE   |
| 6900       | 3  | 451  | TEVLGSKGIHELRSSTSALHHALESASLLTMFWRAALPSTHIP<br>VLPKGVGESTERELLELRKTVSQEQQLQSTTEHLKNANQKES<br>MEQFIVSQLRTHDVLKKARTNLEVRKLLHQSEAPSLSPTHHP<br>LADLVGDSWPALRFQEK  |
| 6901       | 1  | 201  | DDNMVQRLETDFFKMTLQQQSTLEQWAAWLDNMVMQALKPYEGRP<br>SFPKAAARQFLLKWSFYRYHLGFS   |
| 6902       | 2  | 267  | GAPPPPPSQPPRPQAPSSPHSDLTNFPSSALEGQAGAQA<br>SDMPEPSLDLLPELTNPEDELLSYLDPDLPSNSNDLLSLFENN  |
| 6903       | 1  | 149  | RINQVYRQGTGIHILVIDQMVFQDESCFLFSTVKAESSDGI<br>HIILK  |
| 6904       | 464  | 2092   | MEASLPVSLSCVLACGDVEGKFDILFNVRVQAIQKKSGNFDLLC<br>VGNFEGSTQDAEWEYKGTGKKAPIQTYVLGANNQETVKYFQDA<br>DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPYGSF<br>SPKDVSSLRMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD<br>TKKGSALVSSLATGLKPRYHFAALEKTYERLPYRNHIIQEN<br>AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAELVKQPPD<br>VTENPYRKSGQEASIGKQILAPVEESACQFFDLNEKQGRKRSS<br>TGRDSKSSPHPKQPRKPPQPPGCPWFLASPEVEKHLVNVNIGTH<br>CYLALAKGGLSDDHVLIILPIGHYQSVVLSAEVVEVEKYKATL<br>RRFFKSRGKWCVVFNRYKSHHLQQLVIVPISCSSTDDIKDAF<br>ITQAEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR<br>IKKNFPLQFGREVLASEAILNVDPKSDWRQCQISKEDEETLARR<br>FRKDFEPYDFTLDD |
| 6905       | 1  | 226  | VSKTGEAETITSHYLFALGVYRTLYLFNWIWRVHFEGFFDLIAT<br>VAGLVQTVLYCDFFLYLITKVLKGGKLSLPA   |
| 6906       | 3  | 611  | SYDDHNGHIDFITAASNLRAKMYSEPADRFKTRIAGKIIPAI<br>ATTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPVVFETET<br>TEVRKTKIRNGISFTIWRWTVHGKEDFTLLDFINAVKEYGIE<br>PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLKVPTEKKYVDLTV<br>SFAPDIDGDEDLPGPPVRYFFSHDT   |
| 6907       | 2  | 2228   | LRGVPVWAAGAFRFGSSGEESTSHLIMSRRSQRTRYSGQDDGGS<br>SSSGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS<br>DAHTSYSESLVHESWFPFRSSLEELHGDANWGEDLRVRRRGT<br>GGSESSRASGLVGRKATEDFLGSSSGYSEDDYVGYSVDVQSS<br>SSRLRSVAVRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTAA<br>SLLDVFLVTRRFSSSLKTLFWLLPLLLLTCLTYGAWYFYPYGLQ<br>TFHPALVSWWAAKDSRRADGWEARDSSPHQAEQVRVMSRVHSL<br>ERRLEALAAEFSSNWQKEAMRLERLELRQCAPQGGGGGLSHED<br>TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAHQDSE<br>DLFKKIVRASQSEARIQQLKSEWQSMQTESQESSVKELARLE<br>DQLAGLQQELAALAKQSSVABEVGLLPQQIQAVRDDVESQFPA<br>WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGS                      |

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|------------|--|--|--|
|            |  |  | AREAASLSLTLOKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA<br>DYALES GGASVISTRCS EYETKTALLSLFGIPLWYHSQS PRVI<br>LQPDVHPGNCWAFQGGPQGFVVRLSARIRPTAVTLEHVPKALSP<br>NSTISSAPKDFAI FGFEDELQOEGTLLGKFTYDQDGEPIQTFHF<br>QAPTMATYQVVELRILTWNHGHEPTCTIYRFRVHGEPAH  |
| 6908       | 3  | 780  | QVPSAAWLMVAVCGLSRLGLGSRGLGQCGFAARLLYPRFQSRG<br>PQGVEDGDRPQSSKTPRIPIYTKTGDKGFSSTFTGERRPKDD<br>QVFEAVGTDELSSAIGFAELVTEKGHTFAELQKIQCTLQDV<br>GSALATPCSSAREAHLYTTTFKAGPILELEQWIDKYTSQLPPLT<br>AFILPSGGKISSALHFCRAVCRAERRVPLVQMGETDANVAKF<br>LNRLSDYLF T LARYAAMKEGNQEKIYKKNDPSAESEGL   |
| 6909       | 3  | 409  | GRLLAVGTDLYGQRSSAPEQELLVQDATPVNSLLPEKAFSDIP<br>SPYLRGTIKMMQAVRQAFQDQDDRTWDGRPLTMAATFDDCLYA<br>LCVVDITKRSSQTGEWQNIAMTEPELSPAYLISEAMRRSRMS<br>LYC  |
| 6910       | 1  | 1068   | LVPVVVIDSYVYKGLVIAPLNIIVLYNIPTPHGPDLYCTEPWYFY<br>LINGFLNPNVAFALALLVPLTSLMEYLLQRFHVQNLGHPYWL<br>LAPMYIWFIIFFIOPHKEERFLFPVYPLICLCAVALSALQHSF<br>LYFQKCYHFPQRYRLEHYTVTSNWLALGTVFLFGLLSFSRVA<br>LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF<br>PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ<br>NLEEPSRYIDISKCHYLVDLDTMRETREPKEYSSNKEEWISLAY<br>RPF LDASRSSKLLRAFVVPFLSDQYTVVYNYTILKPRKAKQIRK<br>KSGG        |
| 6911       | 1184   | 966  | GEDAEEMETGNVANLISIFGSSFSQLLRKSPPGGGEEEEEGEESG<br>PEAAEPGGICCDKPVLRDMNPWSTAIVAF   |
| 6912       | 1  | 844  | AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI<br>SGGTDIIISCFMGHNSFLPVYKGEIQARNLGMAVEAWNEEGKAVW<br>GESGELVCTKPIPCQPTHFNDENG NKYRKAYFSKFPGIWAHGD<br>YCRINPKTGGIIVMLGRSDGTLPNGVRFSGSEIYNIVESFEEVE<br>DSLCPVQYNKYREERVILFLKMASGHAFQPDVVKRIRDAIRMGL<br>SARHVPSLILETKGIPYTLNGKKVEAVKQIIAGKAVEGQGAFS<br>NPETLDLYRDIPELQGF  |
| 6913       | 1643   | 1558   | KKSHEESHKEELSYGAQASLPLPCSDFR   |
| 6914       | 1251   | 615  | ELAAECKSAGYPGTILIPYRCDLSNEEDILSMFSAIRSQHSQVDI<br>CINNAGLARPD TLLSGSTSGWKDMFNVNVLALSICTREAYQSMK<br>ERNVDDGHIININMSGHRVPLPSVTHFY SATKYAVTALTEGLR<br>QELREAQTHIRATCISPGVVETQFAFLHDKDPEKAAATYEQMK<br>CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT   |
| 6915       | 254  | 652  | GRSLSFKTFLIWLISYIYQGGILMYGALVLFESFVHVVAISFT<br>ALILTELLMVALTVRTWHWLMVVAEFLSLGCVVSSLAFLNEYFD<br>VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS  |
| 6916       | 254  | 652  | GRSLSFKTFLIWLISYIYQGGILMYGALVLFESFVHVVAISFT<br>ALILTELLMVALTVRTWHWLMVVAEFLSLGCVVSSLAFLNEYFD<br>VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS  |
| 6917       | 254  | 652  | GRSLSFKTFLIWLISYIYQGGILMYGALVLFESFVHVVAISFT<br>ALILTELLMVALTVRTWHWLMVVAEFLSLGCVVSSLAFLNEYFD<br>VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS  |
| 6918       | 28   | 921  | PEAGTRSWREPDPEDLRRFLLSACRSFPQWLPGGGGGQVSSCS<br>DTDVPYLLAVKSEPGRFAERQAVRETWGSAPGIRLLFLGSP<br>VGEAGPDLDLSLVAWESRRYS D LLLWDFLDVFPNQTLKDLLLAW<br>LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSYLGE<br>VFTQAMP LRPKGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW<br>LLRAAARVAPFFEDVYTGLCIRALGLVPQAHGFLTAWPADRT<br>ADHCAFRNLLVRLPGPQASIRLWKQLQDPRLQC  |

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|------------|--|--|--|
| 6919       | 850  | 41   | QGRRELSGSVFCFFIQOEPKEMLTLSYHERVRSQGOQLQQLQA<br>ELDXLHKEVSTVRAANSERVAKLVFQRLNEDFVRKPDYALSSVG<br>ASIDLQKTSHDYADRNTAYFWNRFSWNYARPPTVILEPHVFPF<br>NCWAFEGDQGVVVIQLPGRVQLSDITLQHPPPSVEHTGGANSAP<br>RDFAVFFLLSFTHQGLQVYDETEVSLGKFTFDVEKSEIQTFHL<br>QNDPPAAPPKVKIQILSNWGHPRFTCLYRVRAGVRTSEGAEGS<br>AQGP   |
| 6920       | 1418   | 591  | EAQGPSKVHLLTKKKK   |
| 6921       | 2  | 1711   | MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI<br>PAHRLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLV<br>QYAYTGVQLQKEDTIESLLAAACLLQLTQVIDVCSNFIKQLHP<br>SNCLGIRSGDAQGCETELNVAHKYTMHFIEVIKNQEFLLLP<br>NEISKLLCSDDDINVPDEETIPHALMQWVGHVQNRQGLGMLLS<br>YIRLPLLPOLLADLETSSMFTGDLECCQLLMEAMKYHLLPERR<br>SMMQSPRTKPRKSTVGALYAVGGMDAMKGTITIEKYDLRTNSWL<br>HIGTMNGRRLLQFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK<br>IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTERWDP<br>EGRQWNYVASMSTPRSTVGVALNNKLYAIGGRDSSCLKSMBY<br>FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGHDAPASNHC<br>SRLSDCVERYPKGDSSWSTVAPLSVPRDAVAVCPLGDKLYVVG<br>YDHTYLNVTVESYDAQRNEWKEEVPVNIAGRAGACVVVVKLP<br>LTFFAGIRHEVRDREREREREREREKFLDSTGSELKQNIHSIT<br>GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA<br>VNTPKDAAQDAKAEENKKEPLCRQKQHRKVLKKGKPEDVMPV<br>KGAQERLPTVPLSGMYNKSGGKVRITFKLEQDQLWIGTKERTK<br>LPMGSIKNVSEPIEGHEDYHMMAFQLGPTESYVWVWVPTQY<br>VDAIKDTVLGKWQYF |
| 6922       | 1075   | 369  | LGLFCILPIDTLCAVLERDITLSIRESRLFGAVVRWAEACQROQ<br>LEVTFGNKQKVLGKALSIRFPLMTIEEFAAGPAQSGILSDREV<br>VNLFLHFTVNPKPRVEYIDRPRCLRGKECCINRFQQVESRWGY<br>SGTSDRIRPTVNRRIISIVGFLYGSIHGPTDYQVNIQIIEYEKK<br>QTLGQNDTGFSCDGTANTFRVMFKEPIELPNVCYTACATLKGP<br>DSHYGKGLKKVVHETPAASKTVFFFSPPGNNGTSIEDGQIP<br>EIIFYT   |
| 6923       | 2469   | 1660   | PEERVICFVEYYLTAFHEGRKALAKKPYNPIIGTFHCSWEVP<br>KDRVKPKRTASRSPASCHEHPMADDPKSYKLRFVAEQVSHHP<br>ISCFYCECEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLL<br>HGEEYVFTLPSAYARSILTIIPWVELGGKVSINCAKTGYSATVIF<br>HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNN<br>ETKVIDTTTLPVYPKKIRPLEKQGPMSRNLRREVTRYLRGDI<br>DAATEQKRHLEEKQVREERKRENLRTPWKPKYFIQEGDGSILQ<br>SPLESTLMGLEVQSFPV   |
| 6924       | 2210   | 1235   | RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL<br>SCLQSMPSVRCQLQISNGTSSVIVSRKRPSEGNVQKEKDLCKIYF<br>DQWSESDQVEFVEHLISRMCHYQGHINSYKPLQDFITALP<br>EQGLDHAENILSYLDARSLCAELVCKEWRVISEGMLWKKLI<br>ERMVRTDPLWKLSERRGWDQYLFKNRPTDGPNSFYRSLYPKI<br>IQDIETIESNWRGCRHNLQRIQCRSENSKGVYCLQYDDEKII<br>LRDINSIKWDKTSLLECLKVLTGHTGSLVCLQYDERVITGSSDS<br>TVRVWDVNTGVLNLTLIHNEAVLHLRFNSGLMVTCSKORSIAV<br>WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVV<br>STSTCEFVRTLNHKGRIACQLYRDLVVGSSDNTIRLWDIEC<br>GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP<br>RAPASTLCRLTVEHSGRVFRLQFDEBFISSSHDDTLIWDPL<br>NVPPSAQNETRSPRTTYTISR   |
| 6925       | 2  | 1653   | SGRVAMDGLGLQFPEQGFAGPPLLPHPHMGHYRDCQSLGAPPL  |
| 6926       | 1  | 733  |  |

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|------------|--|--|--|
|            |  |  | DGYPLPTPDTSPLDGVDPPAFFAAPMPGDCPAAGTYSYAQVSD<br>YAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVYVGAMGS<br>PGAGGGRGFQMPPQHQQHQQHPPGPGQPTPPPEALPCROGT<br>DPSQPAELLGEVDRTFEQYLHFVCKPEMGLPYQGHDSGVNLPD<br>SHGAISSVVS DASSAVVYCNYPDV   |
| 6927       | 2  | 1484   | LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS<br>CQGFATWATDLSTDLESQSVSCCKYEANBILQFRDLKSQNPHEH<br>YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAEQQLW<br>KKSFCFEKGIHNFESIEDATNAALLCNTGRLMRICAQAHCGA<br>GDELKREFSPEEGLYNNKAIDYVLKALRSLGTRDIHPAVWDSVN<br>WELSTTYFTMATLQDDYAPLSRKAQEQIEKEVSEAMKSLKYCD<br>VDSVSARQPLCQYRAATIHRLASMYHSLRNQVGDHLRKQHR<br>VLADLHYSKAAKLFQLLKDAPCELLRVQLERVAFAEFQMTSQNS<br>NVGKLTLSGALDLMVRTEHAFQLIKELIEEFQPKSGDAAAA<br>ADASPSLNREBVMKLLSIFESRLSFLLOSILKLSSTKKKTSNN<br>IEDDTILKTNKHIYSQLLRATANKTATLLERINVIHLLGQLAA<br>GSAASSNAVQ |
| 6928       | 1085   | 777  | EAIDLINNLLQVKMRKRYSDKTLSPWLQDYQTWLDLRELECK<br>IGERYITHESDDLWEKYAGEQGLQYPTHLINPSASHSDTPETE<br>ETEMKALGERVSIL  |
| 6929       | 1749   | 607  | RDQGRYRDRSPAREPGDVSARTSRGGGGRSATTAMPFPVNG<br>NLHQHDPQDLRHNGNVVAGRPSCSRGPRRAIQKPPAGGRRSG<br>RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE<br>QEVNRQGOARTNSTSAQKNERESIRQKLALGSFFDDGPGYITSC<br>SKSGKPSLSSRLQSGMNLQICFVNDSGSDKSDADDSKTETSLD<br>TPLSPMSKQSSSYSDRDTTEESLDDMDFLTRQKKLQAEAKM<br>ALAMAKPMAKMQVEVEKQNRKKSVPADLLPHMPHISECLMKRSL<br>KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE<br>QDAMLVDIEDLTRAESQOKHMAEKMPAK  |
| 6930       | 131  | 545  | FKDTANVFVSLFQMRNFRHYFIEPSQLKLFYDVITWIVTQVAI<br>SYTVVPVLLSIKPSLTFYSSWYCLHILGILVLLLPPVKKTOR<br>RKNTHENIQLSQSKKFDEGENSLQNSFSTNNVCNQNEIASR<br>HSSLKQ   |
| 6931       | 2  | 659  | FVERLPNRPACLLVASGAAGVSAQSFLHCFTMASTAFNLQVAT<br>PGGKAMEFVDVTESNARWQDFRLKAYASPAKLESIDGARYHAL<br>LIPSCPGALTDLASSGSLARILQHFHSESKPICAVGHGVAALCC<br>ATNEDRSWVFDSSYSLTGPSVCELVRAPGFARLPLVVEDFVKDSG<br>ACFSASEPDAVHVLDRLVLTGQNASSTVPAVQNLFLCGSRK   |
| 6932       | 2  | 1131   | FVDSPGQGEQAEIEEGGIQMNRMRAHSPAEGASVESSSPGPKK<br>SDMCEGCRSLAAGHPGYISHDKETS IKYVSHQHPSPQLFSIVR<br>QACVRSLSCEVCPGREGPIFFGDEQHGPFVFSHTFFIKDSLARGF<br>QRWYSIITIMMDRIYLINSWPFLGKVRGIIDELQGKALKVFEA<br>EQFGCPQRAQRMNTAFTPFLHQRNNGNAARSLTSLTSDNWLACL<br>HTSFANLLKACGSRLEKLEGAFTEDTLVQMEKLADEESES<br>WONSEAEIEEKAPVLPSTEGRELTOGPAESSLSGCGSWQPRK<br>LPVFKSLRHMQRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL<br>KTLQEVTDLSLGGWMAQQVGII   |
| 6933       | 1431   | 890  | SLNLHCTLPPPPHQYPAGYPSDKGKKPKGQSKQPSGTTKRPI<br>SDDDCPSASKVYKASDSAEAEAFQLTPQQQHLIREDCQNQKLW<br>DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTTECFHNVC<br>DCLQRSFKAQVFSPACRHDLGQNYIMIPNEILQTLDDLFFFGY<br>SKGR   |
| 6934       | 3030   | 2588   | DRDHSQCGGIRVALARVSSVKLISKAKIRTVKMTPIIVLAFIV<br>CWTPEFFVQMWVWDANAPKEASAFIIVMLLASLNSCCNPWIYM<br>LFTGHLFHELVRFLCCSASYLKGRRLGETSASKKSNSSSFVLS<br>HRSSSQRSCSQPSTA   |

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|------------|--|--|---|
| 6935       | 886  | 543  | NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL<br>VAMDGHWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS<br>VGVAVLELLNFPPSSPTLSVSSTSL  |
| 6936       | 1347   | 567  | RSHRRQFLSRALLEFFGKSHPPPHRLPRKSLNVGLHYSHIPFLT<br>TCLHFLRRLQKQGVGLSVETSKPQVPVGGLSRKKVPQEPWATV<br>MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS<br>LPSPLPNLGPQGPALTPQENILHTTQTDYNNLAACLLQMEPV<br>NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL<br>AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG  |
| 6937       | 1  | 727  | AVEFRCCPGRRDPACFARGWRLDRVYGTCTCDQACRFTGDCCFDY<br>DRACPARPCFVGEWSPWGGCADQCKPTTRVRRRSVQQEPQNGGA<br>PCPPLEERAGCLEYSTPQGGDCGHYTVPAFITTSFANKERTROA<br>TSPHWSHTTSDAGYCMFKTESLTPHCALENRPLTRWMQYLRG<br>YTVCVDCQPPAMNSVSLRCSGDGLSDGNQTLHWQAIGNPRCQG<br>TWKVVRRVDQCSCPAVHSFIFI  |
| 6938       | 3  | 719  | NSRKLLEAERVDTFMQLKKRQSEKENDSGTLDTVGAVVVDH<br>EGNVAAAVSSGGLAKHPGRVGGAAALYGCNCNAENTGAHNPYST<br>AVTSGCGEHLVRTLARECSHALQAEADAHQALLETMONKFISS<br>PFLASEDGLVGGVIVLRSRCSAEPOSSQNKQTLLEVEFLWSHTT<br>ESMCGVMSAQDGKAKTHISRLPPGAVAGQSVAIIEGGVCRIGEP<br>SELTQAECESQRHFT   |
| 6939       | 3  | 810  | KVTAPRRPQRYSSGHGSDNSSLVSGELPPAMGRTALFHHSGGSS<br>GYESLRDSEATGSASSAPDSMSSEGAASPGARTSLKSPKKRA<br>TGLORRLIPAPLPDPTALGRKPSLPQGWVDLPPPLAGSLKEPF<br>EIKVYEIDDERLQRPPTPREAPTQGLACVSTRLLAERROQR<br>LREVQAKHKLCEELAETQGRMLLEPGRWLEQFEVDPELEPESA<br>EYLAALERATAALEQCVNLCKAHVMVTCFDISVAASAIPGPQ<br>EVDV   |
| 6940       | 1188   | 496  | GKMAAQPLRHRSCATPPRGDFCGGTERAIDQASFTTSMENDTQ<br>VVGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFCQAQCHAV<br>LADSVHLAWDLRSRLGAVVFSRVNNVLEAPFLVIGIEGSLKGS<br>TYNLLFCGSCGIPVGFHLYSTHAALALRGHFCLSSDKMVCYLL<br>KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS<br>EVTDPQSKPEN   |
| 6941       | 1  | 713  | SLSRADSDPHGPHTCGHVLNVIIGSNVLAALAEARQAEALGYQA<br>VVLAAAMQGDVKSMQFYGLLAHVARTRLTPSMAGASVEEDAQL<br>HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQSGG<br>RGRNQELALRVGAELRRWPLGPIDVLFLLSGGTGQDGPTEAAG<br>AWVTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGGAHLHTG<br>MTGTNVMMDTHLLFLRPR  |
| 6942       | 1  | 246  | GDYVERYDPKTDWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG<br>QTYLNTMESYDPQTNEWTQMASLNIAGRAGACVVVIKQP  |
| 6943       | 1  | 739  | PMATGDGAKTLAIHVKALTADSTRITWKATLPASSFRLSWRLG<br>HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY<br>VADETPVCAKAETADSYGPTTLNQEQNAGPMASPLAGIIGGA<br>VALVFLFLVLAICWYVHQAGELLTRERAYNRGSRKKDDYMESG<br>TKKDNSILEIRGPGQLMPLINPYRAKEEYVVHTIFPSNGSSLCK<br>ATHTIGYGTTRGYRDGGIPDIDYSYT  |
| 6944       | 960  | 156  | VANILLNGVKYSESLTGSSERAEPQLSVGRLCSTICNMPKALRT<br>LCVNHFLGWLSEFQMLLFYTFDMGEVVFQGDPAKAPHTSEAYQKY<br>NSGVMTGCWGMCIYAFSAAFYSAILEKLEEFSLVRTLFIAYLA<br>FGLGTGLATLSRNLVVLRLCITYGILFSTLCTLPYSLLCDYYQ<br>SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVGLPLTSA<br>VGSANGVMYFSSSLVSFLGCLYSSLFVIEIPPSDAADEHRPLL<br>LNV   |

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|------------|--|--|---|
| 6945       | 2067   | 179  | EGEDRGLEPRTMGAAAGTGTRLAPWPGRACGALPRWTPTAPAQGC HSKPGPARPVPLKKRGYDVTRNPHLNKGMFTLEERLQGIHGL IPPCFLSQDVQLLRIMRYERQSQDLKYIILMTLQDRNEKLFY RVLTSQVEKFMPIVYTPVGLACQHYGLTFRPRGLFITIHDKG HLATMLNSWPEDNIKAVVVDGERILGLGLGCVGMGIPVGKLA LYTACGGVNPQQCLPVLLDVGTNNELLRDPLYIGLKHQRVHGK AYDDLDEFFMQAVTDKFGINCLIQFEDFANANAFRLNKNYRNKY CMFNDDIQGTASVAVAGILAAALRITKNKLSNHVFGFQAGAGEAM G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH LNHEKEMFAQD\HPEVNSLEEVRVLVKPTAIGVAAIAEA\FTE QILRDMASPHERP\IIFALSNTSKAECTA\EKCYRVTEGPRGF FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG GPDGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR NVFLRIAIAKVF*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD YDSFYT/VDSYIWAQGMNVQTV   |
| 6946       | 133  | 2551   | SCEYSGITVAPGDCPCGVAHLLAPSMASDTPESLMALCTDFCLR NLDGTLGYLLDKETLRRLHPDIFLPSEI\CDRLVNEYVELVNAAC NF\EPHE\SFNPLFRDPRKQPASRIHL\RED\LVQD\QD\LE AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGV*AFFG C\TNILLRKENPGGL/CEDEYLFNPTCQVLVKDFTFEGFSRLR F\LLGRMIDWVPVES\LLRPLNSLAALDSGIQTSDA*\FLTQ WKDSL\VSLVL\YNMDSDDIIR\VIQHLKLRHLDISRDRLSS YYKFKLTREVLSLFVQKLGSLMSLDISG\HMILENCISIKIGKR EAGQTSI\EPSK\SSIIFFRGFEGGPQF\LGVF*GIFCGRLTH IPAYKVSQDKNEEQLNAIEAYTEHRPEITSRAINLLFDIARIE RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSYRSE QSVKLRQVIQVVLNGMESYQEVTVQRNCLTLCNFSIPEELEF QYRRVNELELLSLNPTRQDESIQRIAVHLCNALVCQVDNDHKEA VGMGFVVMTLKLTKQKLLDKTCDQVMEFSW\SALWNITDETPD NCEMFLNFMGMKFLDCLNEFPERQELHRNMLGLLGNVAEVKEL RPQLMTSQFISVFSNLLSKADGIEVSYNACGVLSHIMPDGPEA WGVCEPQREEVEERMWAAIQSWDINSRRNINYSFEPILRLLPO GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIKIM ATARQETKEMARKVIEHCNSFNKEENMDTSR |
| 6947       | 2  | 1682   | TSVSTIPRGLASARPQSRSWRCCPVWRSPGRARGRLKMLNVP SQSFPAPRSQORVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG LKGRLLIEVTEEBELKKHKKDDCWCICIRGFVYNVSPYMEYHGGGE DELMRAAGSDGTFLFDQVHRWVNYESMLKECLVGRMAIKPAVLK DYREBEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQDLSLVTI /EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A MRFRKIFLOGL/CESVGKIEIVLQKKENTSWDFLGHPLKHNHSL IPRKDTGLYYRKQQLISKEDVTHDTRLFCMLPPSTHLQVPIGQ HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPMNKYIYFLIK IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFOELEDLFLLA AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE KLAPKDKRLDVEFVLSAPISEWNGKQCHI SPALLSEFLKRNLDK SKVLVCICGVPVFTQGVRLHDLNFSKNEIHSFTA  |
| 6948       | 104  | 58   | PDGAHSFFPDEYFTCSSLCLSCGVGCKSMNHGKEGVPHEAKSR CRYSHQYDNRVYTKACYERGEVSVVPKTSASTDSPWMGLAKY AWSGYVIECPNCGVVYRSRQYWFQGNQDPVDTVVRTEIVHVWPGT DGFLKDNNAQAQRLLDGMNFMAQSVSELSGPTKAVTSWLTDOI APAYWRPNSQILSCNKCATSFKDNDTKHHCACGEGFCDSCSSK TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRT QETVB  |
| 6949       | 152  | 4656   | GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH QGPIKPYQQRQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC   |

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|------------|--|--|--|
|            |  |  | <p>SCSTDTSEVPRWPKEDHLVYADEESSNITDGRITPEPAVSNT<br/> EPPSTTTSTAST\YPDVLTRVSLYRSHLNFMSLESPALHCQPSTS<br/> SAFFIGSSGFLVKEIKDSTSQHDDNISTTSGFSSRASDKDIT<br/> VSKNTSLPPLWSPEAERSHLSQHTATSSKKPAFNLSAFGTLSP<br/> SLGNSSILKTSQGLDSPFPYPGKTTYGGAAAARQSKLRNTPYQA<br/> PVRQMKAKQLSAQSYGVTSSTARRILQSLKMSPLADAKRIP<br/> SIYSSPLNSPLDRSGIDITDFQAKREKVDSSQYPPVQRLMTPKPV<br/> SIATNRSVYFKPSLTPSGEFKRNQRIKDKCSTGYEKNMTPGQN<br/> REQRESGFSPNPSLPAANGLSSGVGGGGKMRERHAFVASKP<br/> LEEEEMEGPVLKISLPITSSSLPTFNFSPEITTSPPSPINSS<br/> QALTNKVQMTSPSSSGSPMFKFSSPIVKSTEANVLPPSSIGFTF<br/> SVPVAKTARLSGSSSTLEPIISSSAHHVTIVNSTNCKKTPPEDC<br/> EGPFRPAEILKEGSLVDILKSPGPASPKIDSVAAQPTATSPVY<br/> TRPAISSFSSSGIGFGLSKAGSSWQCDTCLLQNKVTDNKCICAC<br/> QAALSPRDATKQTGIEIPNKGKTTLSASGTGFGDKFKPVIKT<br/> WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVSESAET<br/> MTASSSSCTVTGTGLGFGDKFKRPIGSWECSVCCVSNNAEDNKC<br/> VSCMSEKPGSSVPTSSSSTVPVSLPSSGSLGLEKFKKPEGIWD<br/> ELCLVQNKADSTKCLACESAKPGTKSGFKGFTSSSSSSNAASS<br/> SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP<br/> MSEGF*FSKHIVGFKFGVSSSESKPEEVKKDSKNDNFKGLSFG<br/> SNPVFLTPFGVSNLQGEKKEELLKSSCAGFRFGTGVINSTR<br/> VPANTIVTSENKSSFNLTGITEKSVSVAPLKQTSSEAKKEEMPA<br/> TKGGFSPGNVEPASLPASVFLGRTEKQEPVTSLSLVFGE<br/> KLTMKPEKC\QPVFSFGEFORQTKDENSSTFSFMTKPESE<br/> SEQPAKATFAFGAQTNTTADQGAAPDLNLSYLNSSSSSSSTPAT<br/> AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSS\AFGNTAESST<br/> SQSLLSQDSKLATTSSTGTAVTPFVFGPGASSNMTTSGFGFG<br/> ATTSSSAGSSFVFGTGPSAPSASPAFGANQTPTFGQSQGASQP<br/> NPPGFGSISSTALFPTGSGQAPPTFTGTVSSSQPPVFGQQPSQ<br/> SAFGSGTTPNSSSAFQGSSTTNFNFTNNSPSGVFTFGANSSTP<br/> AASQPSGSGGFPFNQSPAFTVGSNGKNVSSSGTSFSGRKIK<br/> TAVRRRK</p> |
| 6950       | 2585   | 411  | <p>PRPGSRSGLCRRAGERGAVRAGGLSRRTAE*IMDELHYQDTS<br/> DVPEQRDSKCKVKWTHEEDEQLRALVRQFGQDWKFLASHFPNR<br/> TDQCCQYRWLRVLNPDLVKGPWTKEEDQKVIELVKKYGTQKQTL<br/> IAKHLKGRGKQCRERNHNLNPEVKKSCWTEEDRIICEAHKV<br/> LGNRWAEIAKMLPGRTDNVKNHWNSTIKRKVDGTGGFLSEKDC<br/> KPPVYLLELEDKQGLQSAQPTGQGSLLTNWPSVPPTIKEEN<br/> SEELAAATTSKEQEPITDLDVARTPEPLEEFPKREDQEGSP<br/> ETSLPYKVVVEAANLLIPAVGSSLSALDLIESDPDAWCDLSKF<br/> DLPEEPSAEDSINNSLVQLOASHQQQVLPVPPQPSA\LVPSVTEY<br/> RLDGHTISDLSSSRGELIPISPSTEVGSGIGTPPSVLKRQRK<br/> RRVALSPVTENSTSLFLDSCNSLTPKSTPVKTLPPSPSQFLNF<br/> WNKQDTLELESPLSTSTPVCSQKVVVTTPLHRDKTPLHQKHA<br/> VTPDQKYSMDNTPHTPTPFKNALKEYGLKPLPQTPHLEEDLKE<br/> VLRSEAGIELIEDDIRPEKQKRKPLRRSPIKKVRKSLALDIV<br/> DEDMKLMSTLPKSLSLPTTAPSNSSSLTSGIKEDNSLLNQGF<br/> LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTACGGTRDQLFMQE<br/> KARQLLGRKPSHTSRTLILS</p>  |
| 6951       | 1940   | 239  | <p>ACPDITMKRSIQALYQQLSFLILALTEALFAIQEPSPRESL<br/> QVLPSTGTPPGTMTAPHSSTRHTSVVMLTPNPDGPPSOAAAPMA<br/> TPTPRAEGHPPT\TPSPPSLRQ*PPPIKAP/SSTGPAPAMAT<br/> TSSKPEGRPRGOAAPTILLTKPPGATSRPTTAPPTTTTRPPRP<br/> PGSSRKAGGNSRPVPPAPGGHSRSKEGQRGRNPSTPLGQKRP<br/> LGKIFIQYKGNFTGSVEPEPSTLTPTPLWGYSSSPQPTVAAT</p>  |

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|------------|--|--|---|
|            |  |  | TVPSNTSWAPTITSLGPAKDKPGLRRAAQQGGSTFTSQGGTPDA<br>TAASGAPVSP/PSCPSAFSAPPPR*PTGWQPQ**LLAYCYP\CT<br>SRPLSTSSGVFTAATGPTAAFDTSVSAPSQGIPOGASTTPQAP<br>THPSRVSESTISGAKEETVA\PS*PTGCPVLSQWYPQQAIS<br>STAWSPPGPSLGGQQTSPMWPRGTNRSTEPSA*ARWISPG*S<br>WPSACPSPP\LCPADGVLHEEEEDRQPEQPEAYGNNTTHPGT<br>TFQOAC\RGAAAPGEIPVPLKPLRTLQSEPRSPANGDYRDTGMVPC  |
| 6952       | 658  | 304  | PESEGESGEMTDORYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE<br>PTPRLVLLHGLRPSQLLRHCGE*EQSASPLQLDGKDASALWT<br>ASRQARGELRLCLTTAVRGTSPPSVSPVCQSS   |
| 6953       | 1512   | 349  | NWGKTRALASGKHVFFGKQTNPNKS/VHCD*G**RRETTQDES<br>FSPHFRGKMGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD<br>PLLELCQCPLCQLDCGSREQLIAHVYOHAAVVSAXSYM\CPVC<br>GRALSSPGSLGRHLIHSQDQSNCAVCGARFTSHATFNSEKLP<br>EVLNMESESLPTVHNEGPPSSAEGKDIAFSPVYPAGILLVCNNCAA<br>YKLLAEATPSVRKWLRRQNEPLEVRLQRLERERTAKKSRDN<br>ETPEEREVRMRDRKRLQRMQETDEQARRLQDRREAMRLKR<br>AIETPEKQARLIREREAKRLKRRLEKMDMLRAQFGQDPSAMA<br>ALAAEMNFQLPVSGVELDSQLLGKMAFEEQNSSSLH  |
| 6954       | 819  | 1  | PPPPFITPSHPREAGT*AG*KRSGDSECSFFVEQ*A*TRAAQN<br>*PQR*RWTEGNSPOASAVATPGOGASPAAPRC*P*PSRRHRLP<br>PGARPPAG*AAPAPT*PWLAPASAPQGAAPLSPAPPLIRTR<br>*CAGAAARGRFRDRSPRPTPGGCSWSEPRTPPAVSASAQTPS<br>DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHPR<br>AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGAPPNQVGSS<br>VMQAMSTGI   |
| 6955       | 1968   | 782  | PPGRRQVRAQVAGAPVGHWGTRARQVKTGRRRRARRIMPFLGQD<br>WRSPGWSWIKTEDGWKRCESSQKLERENNHCNISHSIIINSE<br>GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK<br>ERHGYCTLGEAFNRDLDFSSAIQDIRRFNYVVKLLQLIAKSQLT<br>LSGVAQKNYFNILDKIVQKVLDDHNPRLIKDLLQDLSSTLCIL<br>/N*RSREVCISGKHQYLDLPIRNYSLATTATGSSDD*ASE\NG<br>LTLSDPLHMLNNILYRPSDGDWIIITLQVPTLYMLSEDRQLW<br>KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPKEQY<br>GDTLHFCRHCSILFWKDSGHPCTAADPDSCTFPVSPQHFDLFPK<br>F  |
| 6956       | 8605   | 3839   | QTSTSI PASPTSPVVLGESVLQDNSFDLNNGSDAEQEEMETQSS<br>DFPPSLTQAPDQSSITQLHPATSPAVSPTTSPAVSLVSPAAAS<br>PEISPEVCPAASTVVS PAVFSVVSPASSAVLPVAVSLEVPLTASV<br>TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEBITGEGLT<br>ASGSGDVMRRRIATPEEVRLPLQHGWRREVRICKGSHRWQGETW<br>YYPGCGKRMKQFPEVIKXLSRNVVSVRREHFSFSPRMPVGDFF<br>EERDTP EGLQWVLSAEIIPSRIOAITGKRGRPRNTEKARTKEV<br>PKVKRGRGRPPKVKITELLNKTDRPLKLEAQETLNEEDKAKI<br>AKSKKKMRQKVORGEQTTIQQAARNKRKQETKSLKQKEAKKKS<br>KAEKEKGKTKQEKLEKVKREKKEKVKMKEKEEVTAKAPACKAD<br>KTLATQRRLEERQRRQMILEEMKKPTEDMCLTDHQLPDPFSRVP<br>GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGLVQEG<br>LCQGDLSLGEVQDLLVRLKAAHDPGFFPSYCQSLKILGEKVEI<br>PLTRDNVSEILRCFLMAYGVEPALCDRLRTPFOAQPQQKAAV<br>LAFLVHELNGSTLIINEIDKTLESMSYRKKNKWIIVEGRRLRLKT<br>VLAKRTGRSEVEMEGPEECGRRRSSRIMEVTSMEEEEEESI<br>AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLLH<br>SSQMLRAVSLGQDRYRRRYWVLPYLAGIFVEGTGNLVPPEVIK<br>KETDSLKVAHAASINPALFSMKMELAGSNTTASSPARARGPRK |



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|------------|--|--|--|
|            |  |  | TKPGSMQPRHLKSPVRGQDSEQPOAQLQPEAQLHAPAQPPQQLQ<br>LQLQSHKGFLEQEGSPLSLGQSQHDLSQSFLSWLSQTQSHSSL<br>LSSSVLTPDSSPGKLDPPSPQPPPEEPDEAESSPDQALWFNI<br>SAQMPCNAAPTPPPAVSEDOPTSPQQLASSKPMNRPSAANPCS<br>PVQFSSTPLAGLAPKRRAGDPGEMPQSPGLGQPKRRGRPPSKF<br>FKQMEQRYLTQTAQPVPEMCSGWWIWDPEMLDAMLKALHPR<br>GIREKALHKLHNRDRLQEVCLRPADPIFEPRQLPAFOEGIM<br>SWSPKETYETDLAVLQWVEBLEQVIMSDLQIRGWTCPSPDST<br>REDLAYCKHLSDSQEDITWRGRGREGLAQQRKTNPDLAVMRL<br>AALEQNVRRYLRPLWPTHEVVLEKALLSTPNGAPEGTTTTEIS<br>YEITPRIRVWRQTLERCSAAQVCLCLGQLERSIAWEKSVNKVT<br>CLVCRKGDNDFFLLCDGCDRGCHYCHRPKMEAVPEGDWFCVT<br>CLAQQVEGEFTQKPGFPKRGQRKSGYSLNFSSEGDRRRRVLLR<br>GRESPAAGPRYSEGLSPSKRRRLSMRHHSDLTFCFIIILMEME<br>SHDAWPFLEPVNRLVSGYRRIKKNPDMFSTMRERLLRGGYTS<br>SEEFADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF<br>YQGKQGSVRQGRWGVTLWHLPPPTQTCTCHFLLMLPWVQTQV<br>RYNPDF   |
| 6957       | 82   | 3514   | HLIVAMPEPTKKEENVAPAPAPPPPEEPSKEKEAGTTFAKDWTLV<br>ETPPGEEQAKQNANSQSLIFIEKPGQGTGVKGEDITFIKVKKA<br>EDLSEKPTINGSRKWMDLAKAGKHLQLKETFERHSRVYTFEMO<br>IIKAKDNFAGNYRCEVTYKDKFSDSCFDLEVHSTGTTPNIDIR<br>SAFKRSGEGQEDAGELDFSGLLKREVKQEEBEPQVDVWELLKN<br>TKPSEYEKIAFYQESPTCSGMLKRLKRSIREKKSAFAKILDP<br>VYQVDKGGVRVFWELADPKLEVKWNKNGQELRPSTKYIFEDTR<br>COSILNIDNCQMTDDSEYVVTAGDEKCESTELLVREPPIMVTQOL<br>EDTDTYCGERVELECEVEDDAQVKNFKNGEIIILVQTRYRIRV<br>EGKKHILIIIEGATKADAADYSVMTTGGQSSAKLSVDLKLKILT<br>PLTDQTVNLQKEICLKCEISENIPGKWTNGLPVQESDRLKVH<br>KGRIHKLVIDHALTEDEGDYVFPADAYNVTLPKVVHVIDPPKII<br>LDGLDADNTVTIAGNKLRLLEIPISGEPPPKAMWSRGDKAIMEG<br>SGRIRTESYPSSTLVIDIAERDDSGVYHINLKNEAGEAHASK<br>KVVDVFPDPPVAPTVEVGDDWCIMNWEPPAYDGGSPILGYFIE<br>RKKKQSSRWMLNFDLCKETTPEPKKMEGVAYEVRIIPAVNA\I<br>GISKPSMPSRPFVPLAVTSPPTLLTVDSVDTTVMWRPPDHI<br>GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD<br>LIDTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE<br>IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFQKPRPELTWKD<br>GAEIDKNQINIRNSETDTIIIFIRKAERSHSGKYDLQVKVDKFE<br>TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTTPKDDGNAAIT<br>GYTIQKADKKSMEWLRLVIEHIIIEPVPHTELIGNYFRVFSN<br>MGLSEDAITMTKESAVIARDGKIYKNPVYEDDFDSEAPMFTQPL<br>VNRLCHSGYMATLNCVSRGNPKPKITWMKNKVAIVDDPRYRMFS<br>NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIQ<br>PRTSRVKTEGSQSSAMDFSVKVDIEKEVTCPICLELLTEPLSL<br>DCGHSFCQACITAKIKESVVISRGESSCPVCQTRFQGNLRPNR<br>HLANIVERVKEVKMSPOEGQKRDVCEHHGKKLQIFCKEDGKVIC<br>WUCELSQEHQGHQTFRINEVVKECQEKQLVALQRLIKENQAEK<br>LEDDIRQERTAWKNYIQIERQKILKGFNEMRVILDNEEQRELQK<br>LEEGERVNLNLAATDQLVQQRQDASTLISDLQRRRLRGSSVEM<br>LQDVIVMKRESWTLKKPKSVSKLKSFRVFDLSGMLQVLKE<br>LTDVQYYWVDVMLNPGSATSNAVISVDQRQVKTVRTCTFKNSNP<br>CDFSAFGVFGCQYFSSGKYYWEVDVSGKIWLGVHSGKISSLNK<br>RKSSGFADPSVNYSVKYSRYRPQYGVVIGLQNTCEYNAPEDS<br>SSSDPKVLTLMFMAV\LPVVLGFS |
| 6958       | 274  | 1663   | SLVHVVEFGRGIEDFPYLFQQLTHCQQRICSVTQAGVQWCDHSS   |
| 6959       | 1  | 1469   |  |

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|------------|--|--|--|
|            |  |  | LQPQTGGLNQSSHLSSRDYRMLSSFNFWQDRFWLPPNVWTELEDRDGRVYPHPQDLAALPLALVLLAMRLAFERFIGLPLSRWLGVRDQTRRQVKFNATLEKHFLTGEHRPKPEQLSLLAAQCGLTLQQTQRWFRRRNRQDRPQLTKKFCESWRFLFYLSFVGGLSLVHYHESWLWAPVMCWDYRPNQLTSCPAADSEA\SLYWWYLLLEGLFYLSLLIRLPFDVKRKGSGPSSIKPRPHYDPPSTA\DFKEQVIHFVAVILMTFSYSANLLRIGSLVLLHDSDDYLLBEACMVMYMQYQQVCDAFLIFSFVFFYTRLVLFPTQILYTTYESISNRGPFYGYFFNGLMLLQLLHVFWSCILRLMYSFMKGQMEKDIRSDVEESDSEEEAAAQEPQLQKNGTAGGPRPAPTGDGPRSRVAGRLTNHTTAT  |
| 6960       | 387  | 2068   | AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRSHLEPEEKQALKRLVEEELPMQVDEAASREDKLDLTKKGKRPTPCSDPBRKRFRFNSESESGSEASSPDYFGPPAKNGVASRSHTHPEENPRRA\SKAVEESSEDERQDLPAORGEESSEEEKGYKGRTRKKPVVKKQAPGKASVSRKQAREESEEAEAPVQRTAKKVEGNKGTKSLKESEQESEEEILAQKKEQREEEVEEKEEEDEEKGDWKPRTSRNGRRKSAREERSCKQKSQAKRLLGDSDEEEQKEAASSGDDSGRDREPPVQRKSEDTQLKGKGRKLSGSSSEDEDSGKGEPETKGSRKMARLGSTSGEESDLEREVSDEAGGPPQGERKNRSSKKS SRKGRTRSSSSSSDGSPKAGGKAGSGRRGEDHPAVMRLKRYIRACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCRALKEQREEAAEASLDVANIISGSGRPRRTAWNPLGEAAPPGELRYRLTLDSEERPRPAPDWSHMRGIISSDGESN |
| 6961       | 340  | 1646   | RPWSSPTMKPNFSLRLRIFFNLNCWGIPLYSKHRADRMRLGDFLNQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHFRSGIIGSGLCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSKGAVGLLVHLSGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKKADVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSSEGNMTMVPKNCYVSQQLKPFPPGVRIDYVLKYAVSGFYISCKSFETTTGFDPHRGTPSLDHEALMATLFVRHSPPPQNPSSSTHGP\AERSPL/MCVCLKEALDGSGLGLMA\QARWWA\TFA\SYVIGLGL\LLLALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNGLYRAQAEQLQHVLRGAREAQDLGPEPQLYALL\LGQQEGDRTKEQ  |
| 6962       | 340  | 1646   | RPWSSPTMKPNFSLRLRIFFNLNCWGIPLYSKHRADRMRLGDFLNQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHFRSGIIGSGLCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSKGAVGLLVHLSGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKKADVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSSEGNMTMVPKNCYVSQQLKPFPPGVRIDYVLKYAVSGFYISCKSFETTTGFDPHRGTPSLDHEALMATLFVRHSPPPQNPSSSTHGP\AERSPL/MCVCLKEALDGSGLGLMA\QARWWA\TFA\SYVIGLGL\LLLALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNGLYRAQAEQLQHVLRGAREAQDLGPEPQLYALL\LGQQEGDRTKEQ  |
| 6963       | 374  | 2618   | RVTPLILKLLKPKTAENQKASENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSINLHNFSNSVLETLNEQRNRGHFCVTVRIHGSMLRAQRCLVLAAGSPFFQDKLLLGYSIDIEIPSVVSQVSQVKLIDFMYSGVLRVQSSEALQILTAASILQIKTVIDECTRIVSQNVGDVFPQIQDSQDTPRGTPESGTSQSSDTESGYLSQHPQHSVDRIYSALYACSMQNGSGERSFYSGAVVSHHETALGLPRDHMEDPSWITRIHRSQOMERYLSTTPETTHCRKQPRPVRIQTLVGNIIHKQEMEDDYDYQGQQRVQILERNESEECTEDTDQAGTESEPKGESFDSGVSSSIGTEPDSVEQQFGPGAARDSQAEPTQPEQAAEAPAEAGGPQTNOLETGASSPERSENEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLRQTETLTSLNRLMPLTSTNTQVIGTAGNTYLPALFTTQAGSGPK                           |

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|------------|--|--|--|
|            |  |  | PFLFSLFQPLAGQQTQFVTVSQPGLSTFTTAQLPAPQPLASSAGH<br>STASGQGEKKPYECLCNKFTTAKQNYVKHMFVHTGEKPHQCSI<br>CWRSFSLKDYLIK\HMTHTGVRAVQCSICNKRFTQKSSSLNVHM<br>RLHRGEKSYECYICKKKFHKTLTLLERHVALHSASNGTTPAGTTP<br>GARAGPPGVVACTEGTTVYVCSVCPAKFDQIEQFNDHMRMHVSDG   |
| 6964       | 1  | 178  | SGRPFVFFSNTDVFYIKKVTNRWTAGSSYKMTMRKSGIKILL<br>QIFIG\NCSMFVLVI  |
| 6965       | 757  | 208  | NVFIETPIQGFMTSAHPGQKHPDFSMGLLFPLLAALEVCSCGS<br>SGSLGYNLPQNH\GLLGRNTLVLLGQMRRI SPFLCLKDRSDFRF<br>PQEKVEVSQLOKA\QAMSFLYDVLQOVFNFSHKALL\CCMEHDL<br>PGPTPHFTSSAAGTPGDLGAGDGRRRSWGQWVIEGSTLALRRY<br>FQESISTLE   |
| 6966       | 820  | 1867   | IITALGVRGMPGCPGCGMAGPRLLFLTALALELLGRAGGSQP<br>ALRSRGATACRLDNKESESWGALLSGERLDTWICSLGSLMVG<br>LSGVFPLLVIPLMGTMRLSEAGAWRLKQLLSFALGGLGNVFL<br>HLLPEAWAYTCSASPGGEGQSLOQQQQLGLWVIAGILTFLALEK<br>/HVPGQQGGGDQPGPQQRPHCCCRRAQWRPLSGPAGCRARPRCR<br>GP\DIKVSGLYNLLANTIDNFTHGLAVAASFLVSKKIGLLTTMA<br>ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLAGFA<br>ICTQSPKGVVEETAAWVLPFTSGGFLYIALVNVLPDLLEEDPW   |
| 6967       | 162  | 633  | GFLPFKYWILDLSASSRMETDCNPMELSSMSGFEESGLNGFEG<br>TDMKDMRLAEAAVVDVLFVANNMFVSKSLRCADDVAYINVTETK<br>ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLDLTL\<br>SPAYREAFGKR\LLQRLEALKRDGQS  |
| 6968       | 1  | 2265   | RGGGGGRGGPGAREREPGEPTERTNEAAAGRGCFQHPHGLQKT<br>LEQFHLSSMSSSLGGPAAFSARWAQEA YKKESAKEAGAAVPAPV<br>PAATEPPVHLPAIQPPPVLPGFFMPSDRSTERCETVLEGE<br>TISCFVVGGEKRLCLPQILNSVLRDFSLQINAVCDELHIYCSR<br>CTADQLEILKVMGILPFSAPSGLITKTDAERLCNALLYGGAYP<br>PPCKKELAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS<br>SPSAACIQCLD\CRLMYPPHKFVVHSHKALENRTCHWGF\DSA\<br>NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVR<br>RVSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS<br>LGCVHPRQRLSAFRPWPSPAVSASEKELSPHLPALIRDSFYSYKS<br>FETAVAPNVALAPPAQKQVVSPPCAAASRAPEPLATCTQPRK<br>RKLTVDTPGAPETLAPVAAPEBDKDEAEVEVESREEFTSSLSS<br>LSSPSFTSSSSAKDLGSPGARALPSAVPDAAPADAPSGLEAEL<br>EHLRQALEGGDLTKEAKEKFLHEVVKMRVKQEEKLSAALQAKRS<br>LHQELEFLRVAKKEKLREATEAKRNLKEIERLRAENEEKMKKEA<br>NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL<br>QHAEDREQLRADLLREREAREHLEK\VVK\ELQEQLWPRARPE<br>AAGSEG\AAELEP |
| 6969       | 1855   | 118  | AGTMHGRLLKVTSEBQAEAKRLEREQKLKLYQSATQAVFQKRQA<br>GELDESVELTSQILGANPDFATLWNCRRREVLOQLETQKSPEEL<br>AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPENWNTREL<br>ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFDTSLITR<br>NFSNYSSWHYRSCLLFQLHPQDPSGPGRLPEDVLLKELELVQN<br>AFFTDPNQSAWFYHRWLLGRADPDQDALRCLHVSDEACTVSP<br>SRPLLVGSRMEILLMVDDSP LIVEWRTPDGRNRP SHVWLCDL<br>AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE<br>QLFRCELSVEKSTVLQSELESCKELQELEPENKWL\LT IILLM<br>RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS<br>VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRRLTL<br>PPALAAALRCLEDPPPT\VLQASDNAIESLDGVTNLPRLQELLL<br>CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL<br>PSVSSVLT  |

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|------------|--|--|---|
| 6970       | 3  | 1528   | SFPPLLSPPSAVGEKVAAPCPGRSECARAKMAYIQLEPLNE<br>GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSSEDEVEILGPFA<br>QTPPWLMASRSSDKDGSVHTASEVPLTPRTNSPDGRRSSSDTS<br>KSTYSLTRRISSLESRRPSSPLIDIKPIBFGLSAKKEPIQPSV<br>LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLDEEILSKYQLGM<br>LHFSTQYDLLHNLTVRVIEARDLPPPISHDGSRDMAHSNPYV<br>KICLLPDQKNSKQTVGVRKTKQKPVFEERYTFEIPFLAQRRTLL<br>LTVVDFDKFSRHCVIGKVSVPCEVDLVKGGHWWKALIPSSQNE<br>VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVDSQSGSDPFVKI<br>QLVHGLKLVKTKTSFLRGTIDPFYNESPSFKVPQEELENASLV<br>FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRMLNTHRT<br>AVEQWHSLSRAECDRVSPASLEVT   |
| 6971       | 37   | 3702   | ACFYVPGSRSFKLI PRHGLVNMGRSGKLP SGVSAKLKRWKKGHS<br>SDSNPAICRHRQAARSRRFSPRSGRSDLTVDVAKLHNLQSGSL<br>RLGKSEAPETPMEEAEVLTEKSSGTFSLGSLSDCTNVTFPSKVQ<br>RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEFYFAALIRKA<br>AQHGVCSVLKGSFEMFEKAPAHHPAAISTAKFCIQIEKSGGSK<br>EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA<br>CAMQAFHSLFHARFGLSTLSAELNAQIITALYDYVPSENDLQPL<br>LAWLKVMEKAHINLVRQLQNDLGLGHLPRFFGTAVTCLLSPHSQV<br>LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV<br>EEGLTYKFAAASSVLQLLCVFFACGRQAHVPVRKCLQSLCDL<br>RLSPHPHTAALDOAVGAAVTSMGPEVVLOAVPLEIDGSBETLD<br>FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSAMDLAQAG<br>STVESKIYDTLQWQMTLLPGFCTRPTDVAISFKGLARTLGMAI<br>SERPDLRVTVQALRTLITKGCQAEADRAEVSRFAKNFLPILFN<br>LYGQPVAAAGDTPAPRRVLETIRTLYLTITDTQLVNSLLEKASEK<br>VLDPASSDFTRLSVLDLVALAPCADEAAISKLYSTIRPYLESK<br>AHGVQKAYRVLEEVCAAPQPGALFVQSHLEDLKKTLDSLSRS<br>TSSPAKRPRKLCLLHIVRKLKSAEHKEFITALIPEVILCTKEVSV<br>GARKNAFALLVEMGHAFIRFGSNQEEALQCYLVLIYPGLVGAVT<br>MVSCSILALTHLLEFEGKLMGTSTVEQLLENVCLLASRTRDVV<br>KSALGFIKVAVTVMDVAHLAKHVQLVMEAGKLSDDMRHRFRMK<br>LRNLFT\KFIPK\FGILTGWGKAVGPKYHRVLVNIRKAEARAK<br>RHRALSQAABVEEEEEEEEEEPAGGKGSIEEILADSEDEEDNE<br>EEERSRGKEQRKLARQSRRAWLKEGGGDEPLNFDLPKVAQRVLA<br>TQPGPGRGRKKDHSFKVSADGRLLIREADGNKMEEEGAKGED<br>EEMADPMEDVIRNKKHQKLKHQKEABEELEIPPQYQAGGSGI<br>HRPVAKKAMPAGEYKAKKAGDVKKGRPDYAYIPLNRSKLNRR<br>RKMKLQGFGLVKAQGRSQVGHKNRRKDRRP |
| 6972       | 2179   | 973  | PGGAILLPLWRRTRPREATVPRGAAQGRARSAGRIIPSSQSPS<br>PAEAGGATRSPPPRPPRPARPPGPSAPPLLRSDAGPGATVSA<br>AAATERARRGATMGAQLSTLGHMVLFPVWFLYSLMKLFQRSTP<br>AITLESPIKYPLRLIDREIISHDTRRFRFALPSPQHILGLPVG<br>QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK<br>FPAGGKMSQYLESQIGDTIEFRGPSGLLVYQGGKFAIRPDKK<br>SNPIIRTVKSVMGIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF<br>ANQTEKDILLRPELEELRNKHSARFKLWYTLDRAPFANDYGGQ\<br>FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIYACLPNL\DHVGH<br>PTERCVF   |
| 6973       | 1  | 1964   | LQPRCAHRGLRAQKCRPAFGVDAMVLCFVIGKLLHKRVVLA<br>SPRROEILSNAGLRFVVPKFKELDKASFATPYGYAMETAKQ<br>KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPDVKQDAY<br>RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSRFYETKV<br>KFSELSEELLWEYVHSGPEMDKAGGYGIALGMLVESVHGDFL<br>NVVGFPLNHFCQLVKLYPPRPEDLRRSVKHDSIPAADTFEDL   |

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|------------|--|--|--|
|            |  |  | SDVEGGGSEPTQDAGSRDEKAEAGEAGQATAEARCHRTRETLP<br>FPFTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPQKAADIAS<br>KVDASACGMERLLDICAAMGLEKTEQGYNTETANVYLASDGE<br>YSLHGFIMHNDLTWNLFYLEFAIREGNTQHHRALGKKAEDLF<br>QDAYYQSPETRLRFMRMHGTMKLTACQVATAFNLSRFSSACDV<br>GGCTGALARELAREYPRMQVTVDLPDIIELAHFQPPGPQAVQ<br>IHFAGDFFRDPLPSAELYVLCRILHDWDDKVHKLRSVAESC<br>KPGAGLLLVETLLDEEKRVQALMQSLNMLVQTEGKERSLGEY<br>QCLLELHGFFHOVQVHLGGVLDAIL\PPKWPEQAQACSL   |
| 6974       | 3082   | 2172   | RSCAASFASFARFPLELFAPPGSHRSPPGRGVATSAQCALSVRK<br>LLAARPGLGTKYQATMVYKTLFALCILTAGRVRVQLSPTAPLSV<br>SLPTNIVPPTTIWTSPPQNTDADTASPSNGTHNNSVLPTASAP<br>TSLLPKNISIESREEEITSPOSNWEGINTDPSPSGFSSTSGGVH<br>LTTLEEHSLGTPEAGVAATLSQSAEPPTLISPOAPASSPSSL<br>STSPPEVFSASVTTNHSSTVTSTQPTGAPTAPESTBESSSDHT<br>PTSHATAEPVPOEKTPTTTSVGKVMCELIDMET\PPFPFG   |
| 6975       | 2  | 500  | RPRPTVHCCKWALKLETAMETLINVFHAGSGKEGDKYKLSKKEL<br>KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSRS<br>SLPPAPQPPPYL*LSAVPPPIHLPLPLPPQAQKDVDAVDKVMK<br>ELDENGDEGEVDFQYVVLVAALTVACNNFFWENS   |
| 6976       | 1216   | 970  | GCQL*VAYGTTENSPTVFAHPEDTVEQKAESVGRIMPHTEAR<br>IMNEAGTLAKLNTPELCIRGYCVMGLGYWGEPOKTEBAVDQDKW<br>YWTGDVATMNEQGFCCKIVGRSKDMIIRGGENIYPAELEDFHHT<br>PKVQEVQVVGKDDRMGEEICACIRLKDGEETVEEIKAPCKGK<br>ISHFKIPKYIVFVTNYPLTISGKIQKFKLRQEMERHLNL*IKQQ<br>ACPGRLA  |
| 6977       | 1298   | 588  | SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGLKTPDFA*R<br>ANKSKHHVNGNRTVEPPPEGTQMAVFGMCGFWGAERKFWVLKG<br>VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE<br>ELLKVFWENHDPTQGMROGNDHGTQYRSAIYPTSAKQMEALSS<br>KENYQKVLSEHGPGPIITTDIREGQTFYYAEDYHQYLSKNPNGY<br>CGLGGTGVSCPVGIIK  |
| 6978       | 3  | 242  | SPFFRDSRRRCGCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ<br>FAIRWGFIPLVYILGFKRGADPGMEPTVLSLLWG   |
| 6979       | 3917   | 1146   | DEARVRGEAVAAAILSRCHWSGPPPPPPSPDRKGLRGTEPWE<br>AGPGSGATPGARAMDVRLKVNELREELQRRGLDTRGLKTELAE<br>RLQAALAEAEPPDERELDADDEPGRPGHINEEVETEGGSELEGT<br>AQP PPPGLQPHAEPPGGYSGPDGHYAMDNI TRQNQFYDTQVIKQE<br>NESGYERRPLEMEQQQAYRPEMKTETKQGAPTSFLPPEASQLKP<br>DRQQFQSRKRPYEENRGRGYFEHREDRGRSPQPPAEDEDDFD<br>DTLVAIDTYNCDLHFVKVARDRSSGYPLTIEGFAYLWSGARASYG<br>VRRGRVCFEMKINEEISVKHLPSTEBDPHVVRIGWSLDSCSTQL<br>GEEPFSGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECCN<br>DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF<br>GQRAEPYCSVLPGFTFIQHLPLSERIRGTGVPKSKAECEILMMV<br>GLPAAGKTITWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR<br>NYAGRWDVLIQATQCLNRLIQAARKKRNXYLDQTNVYGSQR<br>RKMRFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVAL<br>EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEGRKAGP<br>PPEKRFDNRRGGGFRGRGGGGGFQRYENRGPFGNRRGGFQNRGG<br>SGGGGNYRGGFNRRGGGGYQSNRWGNMNRDNNNSNNRGSYNRA<br>PQQQPPPPQPPPPQPPPPPPPSYSPARNPPGASTYNKNSNI<br>PGSSANTSTPTVSSYSPQSGFGFFPSTFQPSYSQPPYNQGGYSQ<br>GYTAPPPPPPPPAYNYGSGYGNPAPYTPPPPTAQTYPQPSY<br>NQYQQAQQWNNQYQNGQWPPYGNIDYGSYSNTQGGTSTQ<br>GTRGRKTGRVAPSTRRRTGNMQKLQTRSPAMSLSDPGLGYHPT |
| 6980       | 1  | 420  |  |

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|------------|--|--|--|
|            |  |  | CWTLRWPPCLSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA<br>GGSCACAGSCKCKCKCTSCCKSCCSCPLGCAKCAQGCICKGA<br>SEKSCCA  |
| 6981       | 10   | 1054   | PGRGFRRASLRPAFAARGVFQGGGLQQAQARTRACAALPTPHPS<br>APRLLEPQGVFSLFPPPPGFWPNMILTAKQYDEIAQCLVSVPT<br>RQSLRKLKQRFPSQSQTLLSIFSQYQKHIKRTHAKHTSEAI<br>ESYQRYLNGVVKGAAPVLLDLANEVDYAFSLMARLILERFLQ<br>EHEETPPSKSIINSMRDPSPQIPDGVLANQVYQCIVNDCCYGPL<br>VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDLRAKGYDKTDF<br>ILQVPVAVEGHIHIESKASFGDECSSHAYLHDQFWSYWNRF<br>PGLVIYWGFIQELDCNRERGILLKACFPTNIVTLCHSIA   |
| 6982       | 153  | 1285   | FPQDCSAPAAPGLAGSEPRRLRAYRRRRQRARGLKRVAVLAPP<br>PSLLQGLQGWAAQAPVDGTGLPEDSRASSPMIQRSPSLQPDV<br>GDTVETLMLHPVIAKFLCGSISGTCSTLLFQPLDLLKTRLTQ<br>PSDHGSRVRGMLAVLLKVVRTESLLGLWKGMSPIVRCVPGVGI<br>YFGTLYSLKQYFLRGHPPTALESVMLGVGSRVAGVCMSPITVI<br>KTRYESGKYGESIYAALRSIYHSEHGRGLFSGLTATLLRDAPP<br>SGIYLMFYNQTKNIVPHDQVDTLIPITNFSCGIFAGILASLVT<br>QPADVIKTHMQLYPLKFWIGQAVTLIFKDYGLRGFFQGGIPRA<br>LRRTLMAMANTVVEEMMAKMLKS  |
| 6983       | 82   | 773  | EMSFLQDPSFFTGMWISIGAGALGAAALALLANTDVFLSKPQK<br>AALEYLEDIDLKLEKEPRTFKAKELWEKNAGVIMAVRRPGCF<br>CREEAADLSSLKSLMDQLGVPLIYAVVKEHIRTVEVKDFQPYFKGB<br>IFLDEKKKFYGPQRKMMFMGFIRLGVWYNFFRAWNGGFGNLE<br>GEGFILGGVFPVVGSGKGILLEHREKEFGDKVNLLSVLEAAKMI<br>KPQTLASEKK  |
| 6984       | 1845   | 1282   | GGRSAYSLPAGSLPRVPATAAAKMSGVQVADEVCRIFYDMKVR<br>KCSTPESIKKKRKAIVFCLSAKKCIIVEEGKEILVGDVGVTIT<br>DPFKHFVGLMPEKDCRYALYDASFETKESRKEELMFFLWAPELA<br>PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKL<br>GSLIVAFEGCPV  |
| 6985       | 1887   | 1324   | RRTAGIYPCFPKPGRTRHALCSVLLLLITGQLAFDDFQESCAMM<br>WQKYAGSRSMPLGARILFHGVFYAGGFVYVYLIQKPHSRALY<br>YKLAVEQLQSHPEAQEALGPPINIHLYKLIDRENFVIDAKLK<br>IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGOQIPVFK<br>LSGENGDEVKKE   |
| 6986       | 642  | 1350   | YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQDFDKMYIAF<br>VFKEKKKKSALFEVSEVIPMTNNYEENILKQVRDSSYSLESSL<br>ELLQKDVVOLHAPRYQSMRRDVGCTQEMDFILWPRNDIEKIVC<br>LLFSRWKESDEPRFPVQAKFEFHGDYEQFLHVLNRKDKTGIV<br>VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW<br>AVGTIEDHLRPYME   |
| 6987       | 1623   | 341  | LEAAEKASRAPKESQRQTD SKNYETENWSPQKSQRRYDMYNTAC<br>FLGEIEVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP<br>DPRNECYLALS KFTSHLKNLQSDLKRCDFDFIDYMLLKMRYTQ<br>KEIAEIMLSKKVSRCFKRYTELFCHLDPCLLQSKESQLQBEENC<br>RKKLEALRADRFAGLLEYLNPYKDATTMESIVNEYAFLQONS<br>KKPMTNEKQNSILANIILSCLKPNKLIQPLTLTKKQLREVLQF<br>VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR<br>GQYKRMCRSKQASTLFYLGKRRKGLNSIVHAKIEQYFDKAQNTN<br>SLWHSGDVWKKNEVKDOLLRLTGQAEGKLISVEYGTEEKIKIPV<br>ISVYSGPLRSGRNIERSVYLGFSIEGPPGL |
| 6988       | 3  | 689  | TQLLRRAVAVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR<br>LVRGLGAASTAAPQDAQTGPQMPRADCIMRHLFPYFCRGQVVRG<br>FGRGSKQLGIPATANFPEQVVDNLPAIDISTGIYGWASVSGDVH<br>KMVVSIGWNPYYKNTKSMETHIMHTFKEDFYGEILNVAIVGYL   |

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|------------|--|--|---|
|            |  |  | RPEKNFDSLESLSIAIQGDIEAKRRLPEHLKIKEDNFFQVS KSKIMNGH  |
| 6989       | 2  | 1118   | LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPPGSKSNMATL KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNTANSKLVI ITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV SNPVDILTIVAWKISGFPPKNRVIGSGCNLDSARFRLMGERLGV HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK EQWKEVHKQVVESEYEVIKLKGYSWAIGLSVADLAESIMKNLR RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE EARLKKSAADTLWGIQKELQF   |
| 6990       | 719  | 258  | THASGMASVVLALRTRTAVTSLLSPTPATLAVRYASKSGGSS KNLGGKSSGRROGIKKMEGHYVHAGNIATQRHFRWHPGAHVGV GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY KTFVHVVPAPKEGTFKLVA ML  |
| 6991       | 169  | 451  | RRSDFHNPGLSRPVSLENIHHQVICSTKNKRNPKKIAYLL SSLMTNLNPNNESTENQPVDAWAFITLDQEFITYACVEGTGCLF CGRHVH  |
| 6992       | 944  | 510  | RQAPGCSSLALRQVRQVYCGLVRAPOVQTRPLSSRFVERRGALY RSFMNQENPPYPGPGPTAPYPPYPQPMGPGMPGPPYPPQGY PYQGYPYQGWQGGPOEPKTTVYVVEDQRRDELGPSTCLTACWT ALCCCCLDWMLT   |
| 6993       | 1  | 374  | QWCVTCPQHNARQGPVAPPGIQAYGAAPPEDLQVDFTEMSKCRG DRVWIKNNVNASLCPWLKGPQTVLSPTAVKVEGIPAWIHSH VKPAARETWEARPSDPNPFRTVLKKTSPAPVTPGS  |
| 6994       | 346  | 1100   | QWPEKDFVMAASSISSPWGKHVFKAILMVLVALILLHSLAQSR RDPAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES SSQVLWAISSAISVAFFALSIAAQLLNALGLAGDYLAQGLKLS PQOVQTFLLWGAGALVVYLLSLLGLVLALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLLALLIYALLSRLTGSRASGAQL EAKVRGLERQVEELRWRQRAAKGARSVEEE  |
| 6995       | 144  | 1346   | GSVAVGLSGIIMAAQKDLWDATVIGAGIQCCFTAYHLAKHRRRTIL LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL BHEAGTQLHRQTGLLLGMKENQELKTIQANLSRQVEHQCLSS EELKQRFPNIRLPRGEVGLLONSQGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTLRINVCYWREMPGSGYVSQAFFCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPLDKPEPAVIESCMYNTNPDEQFILDHRPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTSPSYDLAPFRISRPFSLG KAIL   |
| 6996       | 543  | 1942   | ETANAEEAARKSAMDWKEVLRRLATPNTCPNKKKSEQELKDEE MDLFTKYSEWKGGRIKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQKRSRELLDNEELQNLWFLDKHQTTPMIGEAMIN YENFLKVGEKAGACKQFFTAKFVAKLLHTDSYGRISIMQFFNY VMKVVWLHQTRIGLSLYDVAGQGYLRESDLNYILELIPTLPQL DGLEKSFYSFVYCTAVRKFFFLDPLRTGKIKIQDILACSFLLD LLELRDEELSKESETNWFSAALRVYGYLNLDDKHNGMLSK EELSRYGTATMTNVFLDRVFQECLETYDGEVDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSQGDVTVTILIDL NGFWTYENREALVANDSENSADLDDT |
| 6997       | 370  | 1104   | AMELTIFILRLAIYILTFPLYLNLFLGLWSWICKWFFPYFLVRF TVIYNEQMAKSKRELFSNLQEFAGPSGKLSLLEVCGGTGANFKF YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH  |

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|------------|--|--|--|
|            |  |  | QVADGSVDVVVCTLVLCVKNQERILREVCRVLRPGGAFYFMEH<br>VAAECSTWNYFWQQVLDPAWHLLFDGCNLTRESWKALERASF<br>LKLOHIOAPLSWELVRPHIYGYAVK   |
| 6998       | 2  | 616  | FVSRALLRVSRRRHPAERAAAPGRPEADPIECPGATNCPEPLWC<br>SHLPVPYAPPTMESRGKSASSPKPDTKVQVTEAKVPPAADGK<br>APLTKPSKKEAPAEKQPPAAPTAPAKKTSAKADPALLNHSN<br>LKPAPTVPSSPDATPEPKPGPDGAEDEAASGGPGGRGPWSCN<br>FNPLLVAGGVAAIALILGVAFLVRKK  |
| 6999       | 14   | 1591   | GRAGACSRRTAMSTIEESSDVIRLIMQYLKENS LHRALATLQE<br>ETTVSLNTVDSIESFVADINS GHWDTVLQAIQSLKLPDKTLIDL<br>YEQVLELIELRELGAAARSLLRQTDPMIMLKQTQPERYIHLENL<br>LARSYFDPREAYPDGSSKEKRRRAIAQALAGEVSVVPPSRMLMAL<br>LGQALKWQQHQGLLPGMTIDLFRGKAADVDEEEKFPTQLSRH<br>IKFGQKSHVECARFSPDGGYLVGTGSVDGFIEVWNFTTGKIRKDL<br>KYQAQDNFMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG<br>QCLRRFERAHSKGVTCLSFSKDSSQILSASFDTIRIHGLKSGK<br>TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS<br>NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ<br>QIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV<br>TGKLERLTIVHEKDVIGIAHHPHQNLIATYSEDGLKLWKP |
| 7000       | 2  | 827  | GPGVVFLMESEGGPESERSEFFSQREENEENEEAQAPEETGP<br>KNPLLQPALTGDEVLQKIFEDPENPHHEQAMQLLEEDIVGRN<br>LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLHLHCAAAGRL<br>ETLKALVELDVIDEALNFRERARDVAARYSQTECVFEDWADA<br>RLTLKKYIAKVS LAVTDEKSGSKLLKEDKNTILSACRAKNEWL<br>ETHTEASINELFEQRQLEDIVTPIFTKMTTPCQVKSASVTSH<br>DQKRSQDDTSN  |
| 7001       | 2056   | 844  | RRCLIIAFLKGCFFIYFIFIFETFLSCCPGWSAVAQSRILAN<br>FASQVQAIFILPKDSQVGPVVKSEAAPKRALYESVFGSGEIGCP<br>TSPKRLCIRPSEPVDVAVVSVKHDPLPLPEANGHRSTNSPTI<br>VSPAIVSPTQDSRPNMSRPLITRSPASPLNQGIPTPAQLTKSN<br>APVHIDVGHHMYTSSLATLTYPESRIGRLFDGTPIVLDLSLKQ<br>HYFIDRDGQMFYIILNFLTSLKLLIPDDFKDYTLLEYEAKYFOL<br>QPMLEMERWKQDRETGRFSRPECCLVVRVAPDLGERITLSGDK<br>SLIEEVFPEIGDVMCNSVNAGWNHDSHVIRFPLNGYCHLNSVQ<br>VLERLQQRGFIEVSGCGGVDSQFSEYVLRRELRTPRVPSVI<br>RIKQEPLD  |
| 7002       | 1043   | 498  | PMPSSSTRWTTSTYTDTS SAWACRPTTGTCT*TAAPGPTVRWWP<br>TPCSRHQSRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS<br>SWTSAGTSWPAGRRGTATSGTATTSVWPGCGTRMSTQWSSV<br>PRSRSCSRPATTPPSKPGAPHAPCASSRHLAHLAPSSPGLPA<br>RGAEVC  |
| 7003       | 818  | 61   | QGRFRAFQWQDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP<br>GSVADKRNPPWIRRRPVVVEPISDEDWYLCGDTVEILEGKDA<br>GKQGVVQVIRQRNWWVVGGLNTHYRYIGKTMIDYRGTMIPSEAP<br>LLHRQVKLVDPMDRKPTEIEWRFTAGERVVSTRSGRIIPKPE<br>FPRADGIVPETWIDGPKDTSVEDALERTYVCLKTLQEEVMEAM<br>GIKETR\NTRRSIGIEPGAELLPNCPSPLEG  |
| 7004       | 121  | 2265   | FLLPVLTSSRLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK<br>G\PKRTLKTQLG/YICRVRLPGFPDQECIEVINNTTVQLHTPE<br>GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDDVANPLVNDLIH<br>KNGLLFTYGTGSGKTHMTGSPGEGGLPRCLDMIFNSIGSF<br>QAKRYVFSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ<br>VDPEFADMITVQEFCKABEVEDSVYGVFVSYIBIYNNYIYDLL<br>EEVFPDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAFE<br>VFWRGQKKRRRIANTHLNRESSRSHSVFNIKLVAQLDADGDNVL  |



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|------------|--|--|---|
|            |  |  | QEKEQITISQLSLVDLAGSERTNRTAEGNRLREAGNINQSLMT<br>LRTCMDVLRNQMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI<br>VCNPKAEDYENLQVMRFAEVTQEVEVARPVDKAICGLTPGRR<br>YRNQPRGP\IGNEPLVTDVVLQSFPLPSCILINDEQTLPLRL<br>IEALEKRHNLRQMMIDEFNKQSNAPKALLQSFDAVLSKENHMQ<br>GKLNKEKMKISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEED<br>KRNLLQEQLETONQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC<br>ERRVAARQLEMQNLKLVKDEKLKQKAIIVTEPKTEKPERPSRER<br>DREKVTQRSVSPSPVPVSYL  |
| 7005       | 63   | 876  | RNMAVQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL<br>WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ<br>ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV<br>FWHSSSTHVLGAAAEQFLGAVLCRGPSTGYGYHDFFLGKERTIR<br>GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL<br>IEEKVTGPTATVYGCGLVDLCQGPLHRTGQIGGLKLSNSSS<br>LWRSSG  |
| 7006       | 22   | 898  | NAFGRHSTAVKMAAAWLQVLVILLGLGAHPSPLSPFSAGPAT<br>VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDEGPCDLS<br>LNIITWYLSADCYNEIYNFKAEVEVLYLEKLEKRGSLGKYQTS<br>SKLFQNCSELPFKTQTFSGDFMHRPLPLGKQEAENGNTNLTFIG<br>DKTAMHEPLQTNQDAPYIFIVHIGISSSESSKENSLSNLTMT<br>VEVKGPYEYLTLEDYPLMIFFMVVCIVYVLFGLVWLAWASACYWR<br>DLLRIQFWIGAVIFLGMLEKAVFYAGFO  |
| 7007       | 2  | 1001   | AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA<br>YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK<br>DGGDVKALYRRSQALEKLRGLDQAVLDLQRCVSLEPKNKVFOEA<br>LRNIGGQIQEKVRYMSSTDAKVEQMFQIILLDPEEKGTTEKKQKAS<br>QNLVVLAREDAEAKIFRSNGVQLLQRLDMGEMTDLMLAALRTL<br>VGICSEHQSRVTATLSILGTRRVVSLGVESQAVSLAACHLLQV<br>MFDALKEGVKKGPRGKEGAIIVGENKQVWGLLDVTVMEGMGLSQ<br>PGQFFGDQTCSCRLFGIRFGDIILL   |
| 7008       | 70   | 1478   | CRSALGHERPPPAHLFAGGRRRLQTCPRSCRWLGRPPSGLPPGPR<br>SPPPLAGPGQKMVQKKPAELQGFHRSFKGQNPFLAFSLDQPDH<br>GDSDFGLQCSARPMPASQPIDIPDAKRGKKKKRGRATDSFSG<br>RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIEKQPGH<br>IRSRVFREVMYLCQGHNRVLELIEFFEEEDRFYLVFEKMRGG<br>SILSHIHKKRRHFNELEASVVQDVASALDFLHNKGIHARDLKPE<br>NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS<br>AEYMAPEVVEAFSEASIIDKRCDLWSLGVILYILLSGYPPFVG<br>RCGSDCGWDRGEACPAQNMLFESIQEGKYEPDKDWAHISCAA<br>KDLISKLLVRDARQLSAAQVLQHPWVQGCAPENTLPTPMVLQR<br>WDSHFLPPHPCRIHVRPGGLVRTVTVNE |
| 7009       | 1  | 626  | ARQLRNSWVDDFVAAPLIPLSQIPTGNSLYESYYKQVDPAYTG<br>RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA<br>LRLVACAQSGHEVTLSNLSMPPPKFHDTSPLMVTTPPSAEAH<br>WAVRVEEKAKPDGI FESLLP INGLLSGDKVKPVLNMSKLPDLVL<br>GRVWDLSDIDKDGHLVRDEFAMHVLVYRALE  |
| 7010       | 79   | 571  | SHTTRAVVPETLLSPLCPLGGGTAMSGGEQKPERYYVGVDTVGT<br>GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC<br>VVTKKVVGIDLNQIRGLGFATCSLVLDKQFHLPLPVNQEGDS<br>HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG  |
| 7011       | 3  | 994  | RIQTLPNQNSQSTQPLKTPPAVLQPIAPQTTFGVQTPQPOSL<br>LQAQISAASITPLLOTQPOPLLPQPPQKAGLLQPPVRIVSQPP<br>ARRLDPPSRFSGRNDRGDQVPRKDDRSRERERRRRSRERSPO<br>RKRSRERSRRRERSRPRVRRVPRYTQVSKFSLDCPSCDMM<br>ELRRRYQONLYIPSDFFDAQFTWVDAFPLSRPFQLGNFCNFYVMH  |

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|------------|--|--|--|
|            |  |  | REVESLEKNMAILDPPDADHLYSAKVMMLASPSMEDLYHKSCAL<br>AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP<br>DPEKDPVLIKT\AIRCCKALTG   |
| 7012       | 1  | 2661   | RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKA<br>AAAAAATGTEAGPGTAGGSENGSEVAAQAGLSGPAEVLGPA<br>VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME<br>TGIAETPEG\RTSRKRKRAKVEYREMDSELANLSEDEYYSEER<br>NAKAEKEKKLPPPPQAPPEEENESEPEEPGVEGAFAQSRLPH<br>DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQWLNDNPKIQL<br>TFEATLQQLLEAPYNSDTVLVHRVHVSYLERHGLINFGIYKRIKPL<br>PTKKTGKVIIGSGVSGLAARQLQSFQMDVTLLEARDRVGGRV<br>ATFRKGNVADLGAMVVTGLGPNMAVVSQVNMELAKIKQKCP<br>LYEANGQAVPKEKDEMVEQEFNRLLEATSLSHQLDFNVLNKMP<br>VSLGQALEVVIQLQEKHVKDEQIEHWKIKVKTQEELEKLNKMP<br>NLKEKIKELHQYKEASEVKPPRDTAEFLVKS KHRDLTALCKE<br>YDELAETQGLKEEKLQLEANPPSDVYLSSRDRLDWHFANLE<br>FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG<br>LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDVLC<br>PLGVLKQPPAVQFVPLPEWKTSVAVQRMGFGNKNVLCFDRV<br>FWDPSVNLFGHVGSTTASRGELFLFWNLKAPILLALVAGEAAG<br>IMENISDDVIVGRCLAILKGI FGSSAVPQPKETVVSRRADPWA<br>RGSYSYVAAGSSGNDYDLMAQPI TPGPSIPGAPQPI PRLFFAGE<br>HTIRNYPATVHGALLSGLREAGRIADQFLGAMTYLPRQATPGVP<br>AQQSPSM |
| 7013       | 1  | 2661   | RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKA<br>AAAAAATGTEAGPGTAGGSENGSEVAAQAGLSGPAEVLGPA<br>VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME<br>TGIAETPEG\RTSRKRKRAKVEYREMDSELANLSEDEYYSEER<br>NAKAEKEKKLPPPPQAPPEEENESEPEEPGVEGAFAQSRLPH<br>DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQWLNDNPKIQL<br>TFEATLQQLLEAPYNSDTVLVHRVHVSYLERHGLINFGIYKRIKPL<br>PTKKTGKVIIGSGVSGLAARQLQSFQMDVTLLEARDRVGGRV<br>ATFRKGNVADLGAMVVTGLGPNMAVVSQVNMELAKIKQKCP<br>LYEANGQAVPKEKDEMVEQEFNRLLEATSLSHQLDFNVLNKMP<br>VSLGQALEVVIQLQEKHVKDEQIEHWKIKVKTQEELEKLNKMP<br>NLKEKIKELHQYKEASEVKPPRDTAEFLVKS KHRDLTALCKE<br>YDELAETQGLKEEKLQLEANPPSDVYLSSRDRLDWHFANLE<br>FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG<br>LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDVLC<br>PLGVLKQPPAVQFVPLPEWKTSVAVQRMGFGNKNVLCFDRV<br>FWDPSVNLFGHVGSTTASRGELFLFWNLKAPILLALVAGEAAG<br>IMENISDDVIVGRCLAILKGI FGSSAVPQPKETVVSRRADPWA<br>RGSYSYVAAGSSGNDYDLMAQPI TPGPSIPGAPQPI PRLFFAGE<br>HTIRNYPATVHGALLSGLREAGRIADQFLGAMTYLPRQATPGVP<br>AQQSPSM |
| 7014       | 3  | 3950   | DFEVGDKIRILATLEDGWLEGS LKGRGTGIFPYRFVKLCPDTRVE<br>ETMALPQEGSLARIPETSLDCLNTLGVEEQRHETSDHEABSPD<br>CIISEAPTSPLGHLTSEYDTRNSYQDEDTAGGPPRSPGVWEWEM<br>PLATDSPTSDPTEVNGISSQPQVFFHPNLQKSQYYSTVGGSHP<br>HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPYRGS<br>SVSASRVVKPRQSSPQLHNLASYTKKHTSSVYSISERLEMKPG<br>PQAQGLVMEATHSQGDGSTDLD SKLTQQLIEFEKSLAGPGTEP<br>DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR<br>PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRNAV<br>SPKLLSRHRPTCETLEKEGPGHMGRLDQTSPCPLVLVRIEME<br>RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNIESLN  |

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|------------|--|--|--|
|            |  |  | MELQQLREMTLLSSQSSSLVAPSGSVSAENPEORMLEKRAKVI<br>ELLQTERDYIRDLEMCIERIMVPMQQAQVFNIDFEGLFGNMQMV<br>IKVSKQLLAALIEISDAVGPFVFLGHRDELEGTYKIYQNHDEAIA<br>LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP<br>VQVMRYPLLLMELLNSTPESHDPKVPPLTNAVLAKEINVNINE<br>YKRRKDLVLKYRKGDEDSLMEKISKLNHSIIKSNRVSSHLKH<br>LTGFAPQIKDEVFEETKKNFRMQRERLKSIFIRDSLQYLQHIRES<br>ACVKVVAAVSMMDVCMERGHRLDLEQFERVHRYISDQLFTNFKER<br>TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAELK<br>DKKTLLEELQSAENYALNAQLLDELPHKQYAQGLFTNCVHGY<br>AEAHCDFVHQALEQLKPLLSLLKLVAGREGNLIAIFHEEHSRVLQ<br>QLQVFTFFPESLPATKKPFERKTIQRQSAKPLGLPSYMLQSE<br>ELRASLLARYPPEKLFQAERNFNAAQDLVSLLEGDLVGVIKKK<br>DPMGSONRWLIDNGVTGKFVYSSFLKPNRPRSHSDASVGHSS<br>TESEHGSSSPRFRQNSGSTLTFFNP\S\MAVSFTSGSCQKQPO<br>DASPPPKENDQGTLSASLNPSNSESPPSRCPDSDSTSQPRSGD<br>SADVARDVKQPTATPRSYRNFHPEIVGYSPVGRNGQSQDLVKG<br>CARTAQAPEDRSTEPDGEAEGNQVYFAVYTFKARNPNELSVSA<br>NQKLIKLEFKDVTGNTWELAEVNGKKGYVPSNYIRKTEYT |
| 7015       | 1842   | 513  | RQAWHE\VAAPSWRGARLVQSVLRVWQGVHVARERVIPFSSLL<br>GFQRRCVSCVAGSAFSCPRLASASRSNGQSALDHLGFSQPD<br>SVTPCVPVAVSMNRDEQDVLVHHFDMPENSRVLRVLLGAPNAG<br>KSTLSNQLLGRKVFVPSRKVHTTRCOALGVITEKETQVILLDTP<br>GIISPGKQKRHHLELSLLEDPWKSMEADLVVVLVDVSDKWTNR<br>QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG<br>VVNGKKLKMRAQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH<br>FKEIFMLSALSQEDVTLKQYLLTQAQPGPWEYHSAVLTSQTP<br>EICANIIREKLEHLPEQVYPYNVQKTAWEEGPGGELVQKQL<br>LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV<br>KLLK   |
| 7016       | 167  | 2513   | ILNAPKPPPPRDSVEAFAAKRDTGGGSGWTGMDVSGQETDWRST<br>AFRQKLVSQIEDAMRKAGVAHKSXSKDMESHVFLKAKTRDEYLS<br>LVARLIHFHDIHNKKSQASVSDPMNALQSLTGGPAAGAGIGM<br>PPRPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMVVS<br>TATPQTQLQLQVAAAAAATARSSSSSRRRYSSSSSSNSKQ<br>FQAQSSAMQQ\QFQA\VVQQQQQL\QQQQQQQHLIKLHHQNOQ<br>QIQQQQQQLQRIQQLQQLQQQQQQQQQQQQQALQAQPPIQPP<br>PMQQPQPPPSQALPQQLQMHHTQHQPPOPPQPPVAQNQPSQ<br>LPPQSQTQPLVSAQALPGQMLYTQPLKFFVRAPMVVQPPVQPP<br>QVQQQQTAVQTAQAQMVAPGVQVSQSSLPMLSSPSPGQVQTP<br>QSMPPPPQPSQPPQPSQPSNSNVSSGPAPSPSSFLPSPSPQPF<br>\QSPVTARTPQNFVSPSPGPLNTEVNPSSVMSPAGSSQAEEQY<br>LDKQLKLSKYIEPLRRMINKIDKNEDRKKDLSKMSLLDILTDP<br>SKRCPLKTLQKCEIALEKLNDAVPTPPPPVPPPTKQYLCQP<br>LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVCTRKR<br>RLEDDERQSIPSVLQGEVARLDPKFLVNLDPHCSNNGTVHLIC<br>KLDDKDLPSVPPLELSVPADYPAQSPWLWDRQWQYDANPFLQSV<br>HRCMTSRLQLPDKHSVTALLNTWAQSVHQAACLSAA  |
| 7017       | 1  | 1785   | INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLOHL<br>FAPLAHTQREAYAPRIFFEASRPWFTPRSQQDCSEYLRFLDDR<br>LHEEEKILKVQASHKPEILECSETSLQEVASKAAVLTETPRTS<br>DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFDLSLAFWPS<br>YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVYVNPPTTAAF<br>ICDSLUNEKTIIGSPNEFYCSENTSVPNESNKILVNKDVPQKPG<br>GETTPSVTDLLNYPFAPEILTGDNQYYCENCASLQNAEKTMTQIT<br>EEPEYLILTLRFSYDQKYHVRRIKLDNVSLPLVLELPVKRITS   |

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|------------|--|--|---|
|            |  |  | FSSLSSESWSVDVDFDLSSENLAKKLKPSTDEASCTKLVPYLLS<br>SVVHSGISSESCHYYSYARNITSTDSSYQMYHQSEALALASSQ<br>SHLLGRDSPSAVFEQDLENKEMSKWFLFNDSRVTFSTFQSVQK<br>ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPPLQKE<br>LMDAITKDNKLYLQEQELNARARALQAASASCSFRPNPDDNDP<br>PGSCGPTGGGGGGGENTVGRVLF  |
| 7018       | 484  | 1066   | SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGTERIRAPEIIFQ<br>PSLIGEEQAGIAETLOYILDRIYKDVQEMLVQNVFLTGNGTMY<br>GMKARMEKELLEMRPFRSSFFQQLASNPVLDWYGDARDWALNHL<br>DDNEVWITRKEYEEKGGYLYKEHCASNIYVPIRLPKQASRSSDA<br>QASSKGSAAAGGGGAGEQA  |
| 7019       | 1048   | 335  | APGGFLVTMVFAPSPFPWMLGCCSHEVTAGPPTLCKDMSALVAA<br>RNRHIPLAPGSDWRDLNIEVRLSDGTMARKLRYTHDRKNGRS<br>SSGALRGVCSCVEAGKACDPAARQFNLTIPWCLPHTGNRHNHWA<br>GLYGRLEWDGFFSTVTNPEPMKQGRVLHPEQHRVVSRECAR<br>SQGFPTDYRLFGNILDKHRQVGNVPPPLAKATGLKLCMLAK<br>ARESASAKIKEEEAAKD   |
| 7020       | 1  | 2154   | FADSKRKSVLDDIKNLQVALTSKQOSLETAMSFVARNTFKRVR<br>NGPLMRKVAVFFSNTPTTRASPQLREAVLKLSDAGITPLFLTROE<br>DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC<br>NIDPSGFGSWRPSFRDRRAAGSDVIDMAFILDSAEITTLTFOF<br>NEMKKYIAYLVRQLDMSDPKASQHFARVAVVQHAPSESVDNAS<br>MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIETYI<br>ENVFESAPNPRDLKIVVLMLTGEVPEQOLEEAQRVILQAKCKGY<br>FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR<br>FGRLLPSFVSSENAFYLSPIRQCDWFGQDQPTKNLVKFGHKQ<br>VNVNNVTSSPTSNPVTTTKPVTTTKPVTTTKPVTTTKPVTTI<br>INQPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK<br>PVAAPAAVRPPAAAAAKPVATKPEVPRPOAAKPAATKPAATKP<br>MVKMSREVQVFEITENSARKLHWEPEPPGPFYDLTVTSAHDQS<br>LVLKQNLTVTDRIVIGLLAGQTYHVAVVCYLSQVRATYHGSFS<br>TKSQPPPPQPARSASSSTINLMVSTELALTDIDICKLPKDEG<br>TCRDFILKWYDPTNTKSCARFWYGGCGGNENRFGSQKECEKVCA<br>PVLAKPGVISVMGT |
| 7021       | 2  | 338  | VNAVSEFPNGYAFATGSDDATCRFLDRLADQELLYSHDNIICG<br>ITSVAFSKSGRLLLAGYDDFNENVDTLKGDRAVLGHNDNRVS<br>CLGVTDDGMAVATGSWDSFLRIWN   |
| 7022       | 2  | 856  | VYIGSFWSHPLLPDNRKLFEEAEQDLPRDIQSLPRNAALRKLN<br>DLIKRARLAKVHAYIISLLKEMPSVFGKDNKKKELVNNLAEIY<br>GRIEREHQISPGDFPNLKRMDQLQAQDFSKFQPLKSKLEVV<br>DMLAHDAQLMVLVRQEESSQPIQMVKGGAFFGLHGFPGHGYG<br>EGAGEGIDDAEWVARDKPMYDEIFYTLSPVDGKITGANAKKEM<br>VRSKLPNSVLGKIWKLADIDKGMDDDEFALANHLIKVKLEGH<br>ELPNELPAHLPPSKRKVAE   |
| 7023       | 2  | 748  | AMVFCGVVPYVQYRDIRRTQADGPFSTYVCLVLLVANILRILF<br>WFGRRFESPLLWQSAIMILTMMLKLCTEVRVANELNARRRSF<br>TAADSKDEEVKVPARRSFLDFPHHFWQWSSFSYVQCVLAFTG<br>VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST<br>EGMSIKMVLMTSGDAFKTAYFLKGAFLQFSVCGLLQVLVDLA<br>ILQAYAFARHPQKPAPHAVHPTGTAKAL   |
| 7024       | 1207   | 190  | RTGVTGVVAQVWVFGGGVLSSEGEOLQMPVKPERGLGPSDGWLV<br>SSRRGSPGTVLGLPFWLLTPVLVSRISRMILLTRSPTAWHRLS<br>QLKPPVLPGLTGGQALHLRSWLLSRQGPAETGGGGQPGQGLRT<br>RLITGLFGAGLGAWLALRAEKERLQQQKRTALRQAAGVGGD<br>PHLLDHRGRARCKADFRGQWLMYFGFTHCPDICPDELEKLVQV<br>VROLEAEPGLPFVQPVFIVDPERDDVEAMARYVQDFHPRLLGL   |

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|------------|--|--|--|
|            |  |  | TGSTKQVAQASHSVRVVYNAGPKDEDDQDIYVDHSIAIYLLNPDG<br>LFTDYVGRSRAEQISDSVRRHMAAFRSVLS  |
| 7025       | 232  | 832  | ERNSPIGNENL*K\HSLDCLCFRGDWEQNTQFQTLQDNQSECF<br>KQVIRTCEKRPTFNQHTVFNHLHQLRLNTGDKLNEFKELGKAPISG<br>SDHTQHQLIHTSEKFCGDKCEGNTFLPDSEVIQYQTVHTVTKTY<br>ECKECGKSFLRSSLTGHKRIHTGEKPFCKCKDCGKAFRFHSQLS<br>VHKRIHTGEKSYECKECGKAFSCG  |
| 7026       | 328  | 1146   | NPNPSIGDIKDIKKAASKMLDPAHKSHFHPVTPSLVFLCFIFDG<br>LHQALLSVGVSKRSNTVVGNEEERGTPYASRFKDMFNFIKALEK<br>SSVLRHCCDLLIGVAGSSDKICTSSLQVQRRFKAMMASIGRLS<br>HGESAADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK<br>LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE<br>EKKNNG*KGIGEIF*VWGCTLPPHYGAVTTNVPKLSNSGKLLG<br>QDEQPHIFG   |
| 7027       | 43   | 954  | GRRLLQQQORPEDAEDGAEAGGGRGEAGWEGGYPEIVKENKLFH<br>YYQELKIVPEGWQFMDALREPLPATLRITGYKSHAKEILHCL<br>KNKYFKELEDLEMDGQKVEVPOPLSWYPEELAWHTNLSRKILRK<br>SPHLEKFHQFLVSETESGNISRQEAASMIPPLLLNVRPHHKILD<br>MCAAPGSKTTQLIEMLHADNMVFPPEGFVIANDVDNKRRCYLLVH<br>QAKRLSSPCIMVNVHDASSIPRLQIDVDORKEILFYDRILCDVP<br>CSGDGTMKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL   |
| 7028       | 189  | 608  | SRFPPEFEPGTMVEKGSDDSSSEKGGVPGTPTSTQSLGSRNFIRNS<br>KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR<br>EILLQGRLLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA<br>KLIPNAIQ  |
| 7029       | 1343   | 40   | VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG<br>/PCPHAGRETGPRAAPIPGS*GHGWHW*RKDGRGERSEGPSAL<br>SPHSPSLNMQQAPTHVPGMGSGQRPRSSVVEQVGVGSQLSRE<br>RWRA*RLPGAAASERTEMTKERSP/RPCQGYDSSNWFQPGKK<br>TRKRSRRNTMVSRRGGCLLYPLQSIMPE*QLR*GAHASPTTQ<br>R*GKGGPRSPLTKASGTTHTPTFFGSIIP/RPTRDSGPGTDSN\<br>AAPGQKRGRHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS/RNW<br>VPGPAEGEQEGAGLEGPR*PLKGCSTLTFTSPQLSIPIVVGKKP<br>PEGTTASFFP\RSCHSE*RKPPSPCPHAPALSLPHPLPLPLPL<br>PLPLPGAGT*HSARSGRPGQSETGSLCHNCHCPHCPKCPKSPGG<br>T |
| 7030       | 2  | 521  | FVCFSAFGSGQGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM<br>EYLVKWKGSQKYSTWEPEENILOARLLAAFEEREREMELYGPK<br>KRGPKPKTFLKAAKAKAKTYEFRSDSARGIRIPYPGRSQDPL<br>ASTSRAREGLRN\RVCPRQRAAPAPAAP\PRRGSPGPGPRPG*G<br>PGLHFPGGPGSPSKHGFVPASEQHQQHQLPRRGSPGPGPRPG  |
| 7031       | 960  | 59   | HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG<br>/CKPS/RHCDLHEGSPSRTAALPCGKPOPKHGVEECG/PCPCLA<br>PRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL<br>SAAAPRPSLGSQONASGLPAASLPPQDSSQPHKTVPSPARSVPP<br>LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPTST<br>SGSTASHSRRC*SPR*TPAPPRRDHGRSAAFEVLTAASAQPC<br>ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCHHPSL   |
| 7032       | 1393   | 2104   | RRPGRTEPVEPPVPVPPPRASNSKSR*RNHLAPL*QSPLRK<br>SRQIGTSSLPFGRSAGERPRPAATFCLSRGSSPVFL*PSSSSL<br>EPWMKRQFGRHLHSLFWKSWQKMNSTLLTPKLDTSLSMGWRYRQR<br>LPRLHTFLKXSLQMASELAPPLTPAPLASSLPPPPPPPLLPV<br>PLA*LSRSGLVPPNSGFSLSL\PLGDH*GSSGEVRGSCGSPFP<br>HHCWVLPVPP*LLPPLR  |
| 7033       | 689  | 815  | RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA   |

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|------------|--|--|--|
|            |  |  | LMPPSSCPWRTGALGPS PAGSRALGRCTSSVGPGRNLTRTSSP GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS AAAPSAPTTAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS SSSTCPTSRSDRGAATP\SPMGAPLLPCSVPLISREELQDPR NPSP*GVCSGSSGHAGLALGKFPVACSV   |
| 7034       | 92   | 1942   | EDTSSMPFRLLIPLGLLCALLPQHAGAPGPDGSA PDPAHYRERV KAMFYHAYDSYLENAFFDELRLPLTCDGHDTWGSFSLTLIDALD TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA FQTPPTGMPYGTVNLHGVPGETPVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVMFVQSLEAYWPGQLSLIGDIDNAMRTFLNYY TVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDRNRMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKQF QNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K |
| 7035       | 92   | 1942   | EDTSSMPFRLLIPLGLLCALLPQHAGAPGPDGSA PDPAHYRERV KAMFYHAYDSYLENAFFDELRLPLTCDGHDTWGSFSLTLIDALD TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA FQTPPTGMPYGTVNLHGVPGETPVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVMFVQSLEAYWPGQLSLIGDIDNAMRTFLNYY TVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDRNRMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKQF QNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K |
| 7036       | 442  | 761  | CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHGRPPGVSP LPRDPHPTTLRPLPP PPPPPPPPPRRPPRNRRPG  |
| 7037       | 442  | 761  | CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHGRPPGVSP LPRDPHPTTLRPLPP PPPPPPPPPRRPPRNRRPG  |
| 7038       | 155  | 891  | GAGAASDMSSGLRAADFPRWKRIHQEQLRRDRLQROAFEEIIL QYNKLEKSDLHSVLAQKLQAEKHDVNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEBTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTSIDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAERACRSSKGTSTRTG   |
| 7039       | 155  | 891  | GAGAASDMSSGLRAADFPRWKRIHQEQLRRDRLQROAFEEIIL QYNKLEKSDLHSVLAQKLQAEKHDVNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEBTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTSIDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAERACRSSKGTSTRTG   |
| 7040       | 34   | 789  | KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGSS GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN   |

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|------------|--|--|--|
|            |  |  | PGSQRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG<br>EPFEIKVYEIDDERLQRRRGASKEAMCFNAKLKILEHRQQRI<br>AEVRKYEWMKELEATKQYLMLDPKNWLESEFDLEQVWELDSLE<br>YLEALECVTERLESRVNFCALHMMITCFDIT  |
| 7041       | 1  | 567  | SGRVAMGRRRAPAGGSLGRALMRHQTRSRSHRHTDSWLHTSEL<br>NDGYDWGRNLQSVTEQSSLDPLATAELAGTEFVAEKLNIKFI<br>PAEARTGLLSFEESQRIKKLHEENKQFLCIPRRPNWNQNTTPEE<br>LKQAEKDNFLEWRRLQ\VRLEEEQKLILTPFERNLDFWRQLWRV<br>IERSDIVVQIVDA   |
| 7042       | 7  | 345  | PIHMAAALRADITSLPFPHTQGYLLLSASHG\ATSLHTKGAL<br>PLETVMYTVIPKSKYVLVVKPDQTPYPSYENLDEFKRLAENSASN<br>DLLLLMAEVAISDYGDKLTLELREKY  |
| 7043       | 2  | 2170   | ARGMAARDSSEEDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD<br>EKGRYKRFHGAFFSGGFSAGYFNTVGSKEGWTPTSTFVSSRQNRAD<br>KSVLGPEDFMEEDLSEFGIAPKAIVTTDDFASKTKDRIREKAR<br>QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGQGVGP<br>RVKRRPRRQKPDGPKIYGCALPPGSSEGESEDDDDYLPDNVTF<br>APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG<br>SERAGDLGEIGLNKGRKLGISGQAFGVGALEEDDDIYATETLS<br>KYDTVLKDBEPGDLGYGTAPRQYKNQKESKDLRYVGKILDGF<br>SLASKFLSSKKIYPPPELPRDYPVHYFRPMVAATSENSHLLQV<br>LSESAGKATPDGTHSKHQLNASKRAELGETPIQGSATSVLEF<br>LSQXDKERI KEMKQATDLKAAQLKARSLAQAQSSRAQSPSPAA<br>AGHCSSWNMALGGGTATLKASNFKPAKDEPKQKRYDEFLVHMKG<br>GOKDALERCLDPSMTEWGRERDEFARAALLYASSHSTLSSRF<br>THAKEEDDSQVEVPRDQENDVGDKQSAVKMKMFGLTRDTFEW<br>HPDKLLFQ/RLVGLPRVKRDKYSVFNLTLPETASLPTTQASSE<br>KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPK<br>QQSSPLVNKEEHAPELSAN |
| 7044       | 276  | 734  | EVYLTDEPAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS<br>FPQSRKIDILKDLVEMCRGVQHPLRGLFRNRYLLQCTRNILPDEG<br>EPTDEETGDISDSMDVFLNFAEMNKLWVRMQHQHSDREKR<br>ERERQELRILVGTNLVRLSQV   |
| 7045       | 3  | 513  | LGFKMEALSRAQEMSLAALKQHDIFYITSIADLTGQVALYTFCP<br>KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK<br>DLEFQLHEPFLLYRNASLSIYSIWFDKNDCHRIAKLMADVVEE<br>ETRRSQQA/RSGQTESQPGQWLQRPQAHRHGDAEQSQG  |
| 7046       | 3  | 513  | LGFKMEALSRAQEMSLAALKQHDIFYITSIADLTGQVALYTFCP<br>KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK<br>DLEFQLHEPFLLYRNASLSIYSIWFDKNDCHRIAKLMADVVEE<br>ETRRSQQA/RSGQTESQPGQWLQRPQAHRHGDAEQSQG  |
| 7047       | 103  | 486  | QMKIEKCGWSEGLTSIKGNCHNPYTAISKDVTYKELKNLLNSKN<br>IMLIDVREIWEILEYQKI PESINVPLDEVGEALQMNPRDFKEKY<br>NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYER   |
| 7048       | 92   | 627  | FFCLTLLSSWDYRHATRRVITSSPVFTMEDSGKTFSSSEEEANY<br>WKDLAMTYKQRAENTQELREFQEGSREYEALETQLQQIETRN<br>RDLSENRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA<br>IKDQLQKYIRELEQANDDLERAKRATDHGLSKTPE\QRLN\QAI<br>EKKW   |
| 7049       | 393  | 938  | KRTGSASYGGPPPGGLGGPATXASVAGRCSSVGKIPARRCYEDEL<br>VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL<br>NNYEIRPGRLLGVCCSVNCRLPFIGGIPKMKKREIELEEIAKVT<br>EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIANX<br>ASSLWG  |
| 7050       | 393  | 938  | KRTGSASYGGPPPGGLGGPATXASVAGRCSSVGKIPARRCYEDEL  |

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|------------|--|--|---|
|            |  |  | VPVFEAVGRIYELRLMDFDGNRGYAFVYMYCHKHEAKRAVREL<br>NNYEIRPGRLLGVCCSVNCRLLFIGGIPKMKKRERILEETAKVT<br>EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAX<br>ASSLWG  |
| 7051       | 119  | 816  | KKMNLAETCDNAKKGREYALLGNYDSSMVYYQGVMOQIQRHCS<br>VRDPAIKGKWQVRQELLEBYEQVKSIVGTLESFKIDKPPDFPV<br>SCQDEPFRDPAVWPPVPAEHRAPPQIRR/RQSRSKTSEERNR<br>SRSPGTCRPS\PISKSEKPSSTRDKDYRARGRDDKGRKNMQDG<br>ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDIADLEEA<br>KKLLREAGVLPMMW  |
| 7052       | 467  | 715  | SCFGRGKMSKLLNPEEMTSRDYFFDSYAHFGIHEEMLKDEVRTL<br>TYRNSMYHNKHVFKDKVVLVDVSGTGILSMFAARQGP RR  |
| 7053       | 467  | 715  | SCFGRGKMSKLLNPEEMTSRDYFFDSYAHFGIHEEMLKDEVRTL<br>TYRNSMYHNKHVFKDKVVLVDVSGTGILSMFAARQGP RR  |
| 7054       | 1  | 1036   | GTSQRSRETARRRSAGAEPTARLPWPAALEEWSPCCEPLGPG<br>RRCRWDAMEYDEKLARFQAHNLNPPNKQSGPROHEQGPGEVVD<br>VTPEEALPELPPGEPEFRCPERVMDLGLSEDFHFSRPVGLFLASD<br>VQQLRQAIBECKQVILELPEQSEKQKDAVRLIHLRLKLOELKD<br>PNEDEPNIRVLEHFRFYKEKSKSVKQTCDCNTIIINGLIQTWYT<br>CTGCIYRCHSKCLNLISKPCVSSKVS HQAEYELNICPETGLDSQ<br>DYRCAECRAPI/CS/DGVVPSEARQCDYTGOYYCSCHWN DLAV<br>IPARVVHNWDFEPRKVSRCMSRYLALMVS RPVLRLREIN  |
| 7055       | 2  | 527  | DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLFWKTFLLYNQGP<br>EYHYLHQMLG/ALCLSRASASVNLNCSLILLPMCRILLAYLRG<br>SQKVPSSRRTRRLLDKSRTFHTTCGATICIFSGVHVAHLVNALN<br>FSVNYSEDFVELNAARYRDEDPKLLFTTVPGLTGVCMEVVLFL<br>M  |
| 7056       | 2  | 527  | DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLFWKTFLLYNQGP<br>EYHYLHQMLG/ALCLSRASASVNLNCSLILLPMCRILLAYLRG<br>SQKVPSSRRTRRLLDKSRTFHTTCGATICIFSGVHVAHLVNALN<br>FSVNYSEDFVELNAARYRDEDPKLLFTTVPGLTGVCMEVVLFL<br>M  |
| 7057       | 1368   | 431  | GIYLVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASQA<br>SGEVPSQASLRGFFTEDEPGCFGEGBNLPEALQNIQDEGTGEOL<br>SPQERISEKQLGQHLNPHSGEMSTMWLEEKRETSQKQGPAPM<br>AQKLPTCRECGKTFYRNSQLIFHQRTHGTGETYFQCTICKAPLR<br>SSDFVKHQRTHTGEKPKCDYCGKGFSDPSGLRHHEKIHTGEKP<br>YKCPICEKSFQSRNFRHQRVHTGEKPYKCSHCCKGSFSWSSSL<br>DKHQSHLGGKPPQ*PVTKLSFPISISQPSHKNTQLHQEELCLR<br>GYPC   |
| 7058       | 1  | 469  | FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR<br>PEYDLVCIGLTGSGKTSLLSKLCSSEPDNVVSTTGFSIKAVPFQ<br>NAILNVKELGGADNIRKYWSRYQGSQGVIFVLDSASSEDDEA<br>ARN*SC TOLLQHPQLCTLPFLILA   |
| 7059       | 1  | 1178   | WPAFPRQPAAMDALLGTPRRARGCLGAAGPTSSGRAARTPA<br>APWARPSAWLECVVTFDLELQALVELVYVNDPFRITDKEKSSI<br>CYLSFPDSHSGCLGDTQFSFRMRQCGGQSPWHADDRHYNRAP<br>VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLSRLPFVRL<br>FOALLSLIAPEYFDKLAPCLBAVCSEIDQWPAAPGQTLNLPVM<br>GVVVQVRI PSRVKSESSPPKQFDQENLLPAPVVLASVHELDLF<br>RCFRPVLTHMTLWELMLLGEPLLVLAPSPDVSSSEMVLA L TSCL<br>QPLRFCCDPRPYFTIHDSEPKFTTTRTQAPPNVVLGVNPFPIK<br>TLQHWPHILRVGEFGMSGDLKQVKLKKPKV*RPWDTKP |
| 7060       | 90   | 1670   | SVNLPPLWPWEEAMDSTKSEPLKGSPEAEDGNI EYKLLVNFSQ<br>YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEMRAS   |



[illegible]

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|------------|--|--|--|
|            |  |  | EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDDEEDNSSSSSEED RVSTAQKRIEWWQQQLVSGMAERNANFEA   |
| 7070       | 1  | 547  | DGTMEDSEAVQRATALIEORLAQEEENEKLRGDARQKLPMDLLV LEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIDVGGIQNLI ELRKKRKQKKRDALAASHEPPPEPEITGPVDEETFLKAAVEGK MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG ATVDFO   |
| 7071       | 2  | 921  | ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP VSNVAATSAGPSNVGTENSVPOKSSPFLTRVPAYPPHSENIQY FQDPRTOIPFEVPOYPQTGYPPPTVPAGVADCVPRFVRSMNV PESSI.PPASMPLYADHYSTFSRDRMNSSPYQPPPPQPYGVPVPV PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPMDVMHSSVYQT SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ IRRKPDQWAOYHTQKAPLVSSSTLPVATQSPPTPSTLNRGEGS   |
| 7072       | 2  | 921  | ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP VSNVAATSAGPSNVGTENSVPOKSSPFLTRVPAYPPHSENIQY FQDPRTOIPFEVPOYPQTGYPPPTVPAGVADCVPRFVRSMNV PESSI.PPASMPLYADHYSTFSRDRMNSSPYQPPPPQPYGVPVPV PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPMDVMHSSVYQT SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ IRRKPDQWAOYHTQKAPLVSSSTLPVATQSPPTPSTLNRGEGS   |
| 7073       | 50   | 504  | LAHGSFGVSDFFAPAAAPAHLTLSFSGSLSPQFRKPLGRAPAMP LVYRKVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI VTLGKDEFHLHVDTAGQDEYSILPYSFIIGVHGYVLVSVTSL HSFQVIESLYQKLHEGHGK   |
| 7074       | 263  | 1003   | VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLGHGCIAGKMNIS VDLETNYAELVLDVGRVTLGENSRKKMKDKCLRKKQNERVSRAM CALNNSGGGVIAEINENEDYSYTKDGIGLDLENSFSNILLFVPE YLDFMQNGNYFLIFVKSWSLNTSGLRITLSSNLYKRDITSKV MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL AGVFDDRTELDRKEKLTFTTESTHVEI  |
| 7075       | 598  | 1005   | NYINFFFRKEYPPHVQKVEINPVRLSRLQGVVERIMKKTSESEQ VEPEIKRKVQQRKHCSTYQPTPPLSPASKKCLTHLEDLQRNCRQ AITLNESTGPLLRSTSIHQNSGGQKSQNTGLTTKKFYGNVVEKVP IDII   |
| 7076       | 279  | 1049   | LQSESSNAAEGNEQRHEDEQRSKRGGSKGRKRRKPLRDSNAPK SPLTGYVRFMNERREQLRAKRPVFPFPEITRMLGNEWSKLPPEE KORYLDEADRDKERMYKLEQYQKTEAYKVFSRKTQDRQKQKSH RQDAARQATHDHEKETEVKERSVFDIPIFTEEFNLHNSKAREAL RQLRKSNMFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV LQOHLLETLRQVLTSSFASMPLEPGETPTVDTIDSYM  |
| 7077       | 3  | 1119   | SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR ELKWLDMFSNWDKWSRRFQVKLRCRKGIPSSLRKAWQVLSN SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA RGGHGQODLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGEIFFALLRRASPLAHR HLRRQRIDPVLYMTBWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPOCCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQPPPLGPSSS                 |
| 7078       | 483  | 767  | FQGQRMAGEQKPSNLLQEQFYLLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY   |
| 7079       | 2  | 376  | SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ MQARKKRRGIIEKRRDRINSSSELRLVPTAFQKQSSKLEK  |

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|------------|--|--|--|
|            |  |  | AEVLQMTVDHLKMLHATGGTGTALLFQASFIQQIF  |
| 7080       | 200  | 595  | VQLPLEAPCLSLLLSCRDHSGGNRDLRRHRDCRVYGSPODGIPY LTHPLCHQDVVSVGRQLIRALATPGHTQGHVLYLDGEPYKGPS CLFSGDLLPLSGCGEFPKRREELGEGETEVRAATVPWRALKP  |
| 7081       | 213  | 506  | AVTEEMILNSLSLCYHNKLLILAPMVRVGTLPMLLLADYGDAD VYCEELIDLKMIQCKRVVNEVLSTVDFVAPDDRVVFRCTCEBQNR VVVFQMGTS  |
| 7082       | 3  | 1137   | APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL CCRSSPRDLRDGEREHEAAQKAPGAESCPSLPLSISDITGCL SSLENLRLPTLREESSPRELEDSSGDQRCGPTHQGSSEDPMSLS QAQSATEVEERHVSPPSCSTRSRERPFQAGELILAETGEGETKFKK LFLNNFGLNLSNWGAVPFGKIVGKFPQGILRSSFGKQYMLRRP ALEDYVVLKRGTAITFPKDINMILSMMDINPGDVTLEAGSGSG GMSLFLSKAVGSQGRVISFEVRKDHDLAKKNYKHWRDSWKLSH VEWEFDPNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLFPV YPHLKHGGVCPVYVNNITQVIELLD                                    |
| 7083       | 115  | 541  | RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLLSEP SPKAPRARPCRVSTADRSVRKGIWAYSLEDLLKVRDITMLADK PFFLVLEEDGTTVETEBYFQALAGDTVMVLQKQKQPPSEQG TRHPLSLSHK  |
| 7084       | 3  | 522  | NSVSVSSQSRFLASVPGTGVQSRASAAADMAASTAAGKQRIKPKVAK VKNKAPAEVQITAEQLLREAKERLELEPPPPQOKITDEEELND YKLRKRKTFEDNIRKNRTVISNWKYQWEEESLKEIQARSIYE RALDVEDYRNITLWLKYAEMEMKNQVNHARNIWDRAITTL  |
| 7085       | 243  | 1499   | RQLARLRRRGWRSPPGGAPMAHITINQVLYQVYEAIDSRDGASC AELVSPFKHPHVANPRLQMASPEEKQVLEPPYDEMFAAHLRCT YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL DLRVPANNADQVLVKKGSKVGDMLKAAEELMSCFRVCASDTR AGIEDSKWGMFLVNLQFKIYFKINKLHLCKPLIRAISSNLK DDYSTAQRVITYKYVGRKAMFDSDFKQAEYLSFAFEHCHRSSQ KNKRMIILYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG NLLLHEALAKHEAFIRCGIFLILEKLKIITYRNLFKKVYLLL KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGXI SHQHQLVVSQKQNPFPPLSTGC |
| 7086       | 256  | 525  | ILARMGKQNSKLRPEVMQDLLESTDFTEHEIQENYKGFRLDCP SGHLSMEEFKKIYGNFFPYGDASKFAEHVFTFDANGDGTIDFR EF   |
| 7087       | 166  | 723  | LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEASRGG NTRKSLDNGSTRVTPSVQPHLQPIRNMVSVRTMEDSCELDLVY VTERIIAVSPSTANEENFRSNLREVAQMLSKKHGGNYLLFNLS ERRRPDITKLHAKVLEFGWPDLTHTPALEKICSIKAMDITLNAHP HRCRVLHNKG   |
| 7088       | 104  | 759  | GTSAAFPSSSLEMAGETTETGELYSSYVGLVYMFNLIVGTGALT MPKAPATAGWLVSLLVFLGFMSPMTTTFVIEAMAAANAQLHW KRMENLKBEEDDDSTASDSVLIRDNYERAKRPILSVQRRGS PNEFEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDIAIYA AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD  |
| 7089       | 33   | 1775   | SVCWEDRYLKARMEESPLSRAPSRGGVNFNLNARTYIIPNTKVEC HYTLPPGTMPASDWIGIFKVEAACVRDYHTFWSSVPSTTDG SPIHTSVQFQASYLPKPGAQLYQFRVYVNRQGVCGQSPFPQFRE PRPMDELVTLEADGGSDILLVVPKATVLQNQLDESQQERNDLM QKLQLQEGQVTELSRVQELERALARQHELTMEQYKGISRS HGEITEERDILSRQGDHVARILELEDDIQTISEKVLTKVEVLD RLRDTVKALTREQEKLLGQLKEVQADKEQSEAEQLVQAQENHHL NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGAQAQQRVALEP  |

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|------------|--|--|--|
|            |  |  | LKEQLRGAQELAASSQQKATLIGEELASAAAARDRTIAELHRSR<br>LEVAEVNGKLAELGLHLKEEKQWSKERAGLLQSVEAEKDKILK<br>LSAEILRLKAVQEERTQNVFKTELAREKDSLSVLSESKEF<br>TELRSALRVLQKEQELQEEKQELLEMYMRKLEARLEKVADEKWN<br>EDATTEDEBAAVGLSCPAALTDSEDESPEMDRLHPMAFVSVETO<br>ASLLGLLE  |
| 7090       | 33   | 1775   | SVCWEDRYLKARMEESPLSRAPSRGGVNFNLVARTYIPNTKVEC<br>HYTLPPGTMPASDWDIGIFKVEAACVRDYHTFVWSSVPESTTDG<br>SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGVCGQSPFPQFRE<br>PRPMDELVTLEADGGSDILLVVPKATVLQNQLDESQQRNDLM<br>QLKLQLEGQVTELRSRVQELERALARARQEHTELMQYKGISRS<br>HGEITEERDILSRQGDHVARILELEDDIQTISEKVLTKVEELD<br>RLRDTVKALTREQEKLLGQLKEVQADKEQSEAEQLQVAQQENHHL<br>NLDLKEAKSWQEEQSAQAQLKDKVAQMKTTLGQAQQRVAELEP<br>LKEQLRGAQELAASSQQKATLIGEELASAAAARDRTIAELHRSR<br>LEVAEVNGKLAELGLHLKEEKQWSKERAGLLQSVEAEKDKILK<br>LSAEILRLKAVQEERTQNVFKTELAREKDSLSVLSESKEF<br>TELRSALRVLQKEQELQEEKQELLEMYMRKLEARLEKVADEKWN<br>EDATTEDEBAAVGLSCPAALTDSEDESPEMDRLHPMAFVSVETO<br>ASLLGLLE                                   |
| 7091       | 186  | 1076   | EGMLTREHRCGRSEEQELEPWSPKKARSGRWLRNGFKRKMEEP<br>EEPADSGQSLVPVYIYSPEYVSMCDLAKIPKRASVMVHSLIEAY<br>ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDHDPD<br>SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN<br>WSGGWHHAKKDEASGFCYLNDVGLILRLRRKFERILYVDLDLH<br>HGDGVEDAFSFTSKVMTVSLHKKFSPGFFPGTGDVSDVGLGKGRY<br>YSVNVPIQDGIQDEKYQICERYEPPAPNPGL   |
| 7092       | 522  | 809  | KQGINEDQEEQKPRLEGECEPISKRMKKLIKQKQWEEQRELR<br>KQRKEKRKRKKLERQCMEFNSDGHDRKRVRRDVHSTLRLLII<br>DCSFDXLM   |
| 7093       | 454  | 655  | NFGVSGVELAQQASMRMSFVIAACQLVLGLLMTSLTESSIONS<br>ECPQLCVCEIRPWFTPQSTYREA   |
| 7094       | 2  | 508  | FVRSMHWGVGFASSRRCVVDLSWNQSIFFGWAGSEBPFPSFYG<br>DIIAFPLQDYGGIMAGLSDPWKKTLTYLTGGALLAAAYLLHE<br>LLVIRKQOEIDSDAIILHQFARPNNGVPSLSPFCLKMETYLRLM<br>ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGETEII  |
| 7095       | 1  | 411  | IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSEL<br>SLECVSHEVDSHYCPSCLENMPSAEAKLKNRCANCFCDCPGCMH<br>TLSTRATSISTQLPDDPAKTTMKAYYLACGFCRWTSRDVGMAD<br>KSVGE  |
| 7096       | 224  | 2067   | ETRSIAVQEKPSQAGRRSSRISFAGALFLTRFLQELLNNFC<br>SAMSPAPDAAPAPASISLFDLSADAPVFGLSLVSHAPGEALAR<br>APRTSCSGSGERESPERKLLQGPMIDISEKLCSTCDQTFQNHQE<br>QREHYKLDWHRFNLKQRLKDKPLLSALDFEQSSSTDGDLSSISGS<br>EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQQGF<br>LYAYRCVLGPHQDPPAEAELLQNLQSKGPRDCVLMMAAGHFA<br>GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPPSHSAGAN<br>LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF<br>FGGKGAPLQRGDPRLDIPLATRRFTFQELQRLVHLKLTLLHVE<br>EDPREAVRLHSPQTHWKTVEBRKKPTEEEIRKICRDEKEALGQ<br>NEESPKQSGSGEGEDGFQVELELVLTGTLDLCESEVLPRKRRR<br>RKRNNKKEKSRDQEAHAHRTLLQQTQEEEPSTQSSQAVAPLGPL<br>LDRAKAPGQPELWNALLAACRAGDVGLKQLLAPSPADPRVLSL<br>LSAPLGSGGFTLLHAAAAGRGSVVRLLEAGADPTVQCQDH |
| 7097       | 256  | 1228   | IRTKSAATWEAWPQCGREGSRIITEPCANAGSRQELQTERISS<br>FLAAQGDQAFHSGLETTNNSNELPLRVGLKVAQGSPLMGQVSA   |

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|------------|--|--|---|
|            |  |  | SNSFSRLHCRNANEDWMSALCPRLWDVPLHLSIPGSHDTMTYC LNKSPISHEESRLQLLNKALPCITRPVVLKNSVTQALDVTEQ LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISB WLERHPREVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG EVPTLRQLWSRGQQVIVSYEDESSLRRHBLWPGVPYWGNGRVK TEALIRYLETMKSCGR  |
| 7098       | 82   | 956  | SSFLKRCRKVLGCWGIPEQSLFSTLEPRDKEIDNYCVMRLQT EARSGFWAPNRFVFNICRMTAVDGDGRGSSRETCRCHPHPSLEA LVLLQLQDWQPGGVGICTSFLGISWALLDYHRLRTCLPSKPLIG LGSSVIYFLWNLWLLWPRVLAVALFSAFSPSYVALHFLGLWLVL LLWVWLQGTDFMPDPSSWLYRVTVATILYFSWFNVABGRTRGR AIIHFAFLSDSILLVATWVTHSSWLPSTGIPQLQLWLPVCGCGCF LGLALRLVYHHLHPSCCWKPPDQVD   |
| 7099       | 992  | 210  | LPRLAPGFLRLSARQQYHQIWAFFPLPSGATATWPAASRSRSLA ARSLPRSPARPGPNDALLGEHDFRGQGVRAORFRFSEBPGPGAD GAVLEVHVPIQAGVSLPGILAAKCGAEVILSDSSELPHCLEVC RQSCQMNNLPHLQVVGTLWGHISWDLALPQDIILASDVFFEP EDFEDILATIIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWDW KCVHIPLESDADKEDIAESTLPGRHTVEMLVISFAKDSL  |
| 7100       | 205  | 671  | ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL FLPSFPPLQGDPLEAFVFKKYDRNLNVSIECKRVSGLEPATV DWAFDLTKTNMQTMYEQSEWGWKDKREEMTDDRAWYLI AWEN SSVVPVAFSHFRFDFVERGDEVLYW   |
| 7101       | 2  | 503  | WRGGPRRAKRLAGGAVGWVLLVRGVHVSVRAGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEEPPEVPPRAEITIPADVTP ERVPTHIVDYSEAEQSDQLHQEISQANVICIVYAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGKNKSDLVEYSR   |
| 7102       | 2  | 503  | WRGGPRRAKRLAGGAVGWVLLVRGVHVSVRAGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEEPPEVPPRAEITIPADVTP ERVPTHIVDYSEAEQSDQLHQEISQANVICIVYAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGKNKSDLVEYSR   |
| 7103       | 119  | 438  | GSQSSVAVNIRSGTDEBSMDLMNGQASSVNIAATASEKSSSES LSDKGSSELKKSFDVAVFDVLKVTPEYAGQITLMDVPVFKAIQD DELSSCGWNKKEKYSAP  |
| 7104       | 1670   | 795  | RLWEHRSVSAGASGWLSSPGCLLLHPSLPEEERVDILINNAGV MRCPHWTTEDGFEMQFGVNLGEAWAGAAPWQAILPRRPPKVL GF*V*VKSDLFIILNPGHFLTLLNLLDKLKASAPSRILNLSLA HVAGHIDFDLWQTRKYNTKAAQCQS\KLAIVLFTKELSRRLQ GSGVTVNALHPGVARTELGRHTGIHGSTFLQHHN\WAILLAWS KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAPAEAEED EEVARRLWAESARLVGLEAPSVREQLPR   |
| 7105       | 765  | 143  | GQMCRRFPSPKSTSCLSMTCCLP/RGLQDPQCLALFRVAVDKHQA LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST SQIPVQQMHLFDVHNPDPYVSSGGGFGPADDHGYGVSYIFMGDG MITFHISKKSSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR FRGSGKENSRRHRCGFLSRQTGASKASMTSTDF  |
| 7106       | 14   | 1064   | GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHRMFGT YFRVGFSGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGGCF GAEEFVEIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV TYFEKNFNLRFRMYTTPFTLEGRPRGELHEQYRRNTVLTTHAF PYIKTRISVIQKEEFVLTPIEVAIEDMKKTLQLAVAINQEPD AKMLQMVLGQSVGATVNGGLEVAQVFLAEIPADPKLYRHNNKL RLCFKEFIMRCGEAVEKNKRLITADQREYQOELKXNYNKLKENL RPMIERKIPELYKPIFRVESQKRDSPHRSFRKCEQLSQGS  |
| 7107       | 1145   | 591  | *I*WLQTGKKK   |

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|------------|--|--|---|
| 7108       | 1  | 942  | VKVALLLTNLEQPRTESEWENSFTLKMFLQFVNLNSSTFYIAP FLGRFTGHGAYLRLINRWLEECHPSGCLIDLQMOMGIIMVLK QTWNFMELGYPLIQNWTRRKVRQEHGPERKISFPQWEKDYNL QPMNAYGLFDEYLEMILQFCFTTIFVAAFPLALLANNIIEI RLDAYKFVTQWRRPLASRAKDGIWYGILEGIGILSVITNAFVI AITSDFIPLVYAYKYGPCAGQGEAGQCKMVGYNASLSVFRIS DFENRSEPSDGSFSGTPLYKCRYDRYRDPHSLVPYGYTLQF WHVLAW   |
| 7109       | 964  | 102  | WDQRKRNSLVPSPAHPAQEEPEWEEKESLGAAQEALSIQLQPK E TQPPFKSEQVYLHFLSVVTEGPEPKDKGSLPQPPITEVESQV F SEKLATDTSTFEATSEGTLELQQRNPKAERLRWSPAQEESEFRQ M VVIHKEIPTGKKDHECSECGKTFIYNLHVHQRVHSGEKPYKC SDCGKTFKQSSNLGQHQRINTGEKPFECNECGKAFRWGAHLVQH QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG KAYGWCSELIRHRRVHARKEPSH  |
| 7110       | 96   | 697  | RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG SPSTKRRGQMLQPIIEGETAHFFBEIEKEEEDGVNLSSELGDM L KTAQVQSSSLKNSSESDVEENQEKALDLRLSSRAASMPELLEQ LWKARAEEKKRLKTLREFEEAFYQNGRQAQEDRVPVLEEYRE YKKIKAKLRLLLEVLISKQDSSKSI   |
| 7111       | 2  | 414  | GSGLYRGPTPGGQCIWKPNMPPDHERNFGFTQFALELNELTAE LKRSLPSTDTLRPDQRYLEEGNIOAAEAQKRRIEQLRDRRKV MEEENIVHQARFFRRQTDSSGKEWWVTNNTYWRRAEPGYGNMD GAVLW  |
| 7112       | 103  | 495  | PRCFPVADRGRLLIGGLPDVVTIMEGKTLNLTCTVFCNPDPFV I W FKNDQDIQLSEHFSVKVEQAKYVSMITIKGVTSSESGKYSINIK N KYGGEKIDVTVSVYKHGEKIPDMAPPQQAQPKLI PASASAAGQ   |
| 7113       | 1  | 824  | KCLRQAWHEAPSSLAFTRWCSREERAEGGGLNHSITRDPKPPG LRPSQRPMDKKKRSFKPCLAQPAQAPGTLLRRVPVPTSHSGSL ALGLPHLPSFKQRAKFKRVGKEKCRFVLAGGSGSAGTPLQHSF I TEVTDVYEMEGGLNLLNDFHSGRLQAFGKECSFEQLEHVREM QEKLARLHFLDVCGEEDDEEEDGVTEGLPEEQKKTADRN L DQLLSNLGSCLCALVPGMGRGGGTYSQSHSWALGEKVGVGHSK SSGPLNLPRR   |
| 7114       | 3  | 1492   | VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKICRK I IYLNDFVSVKQRLPKYYSWERCSSKHLNFLGQNRSYVRKKDDG CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKALRKSQRS QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF SQSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE KPFVCDKCPKAFKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ RIHTSEKPPQCSHGKASDEKPSPTKHWRTHTKENIYECSCGKS FRGKSHLSVHQRIHTGEKPYECSCGKTFSGKSHLSVHHRHTG EKPYECRRCGKAFGEKSTLIVHQRMTGEKPYKNECGKAFSEK SPLIKHQRIHTGERPYECTDCKAFSRKSTLIKHQRIHTGEKPY KCSECGKAFSVKSTLIVHHRHTGEKPYECRCGKAFSGKSTLI KHQRSHTGDKNL |
| 7115       | 1  | 947  | NAAHGYNWGLWCMIYIPQDWLDRGDESAPIRTFAMIGCSFVVD REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA HIERTRKPYNNIDYAKRNALRAAEVWMDDFKSHVYMAWNIPM SNPGVDGVDVSERLALRQLKCRSFKWYLENVYPEMRVYNNLT L YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSDGL LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVRQCSGQKWMIRN WIKHARH  |
| 7116       | 866  | 95   | RVRMRRAEIVIEEKLMSKSWAKFRPGEPPWKGYPNIDPETDPYV T PGSVINNLISINTVREVDHLDRNRSGSSSLNLTLPSTSAWSSIR   |

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|------------|--|--|---|
|            |  |  | ASNYNVPLSSTAQTSARNSDSKLTWSPGSVTNTSLAHELHKVP<br>LPPKNITAPSRPPPGLTGQKPPPLSTWDNSPLRIGGGWGNSDARY<br>TPGSSWGESSGRITNWLVLKNLTPQIDGSTLRITLCMQHGPLIT<br>FHLNLPHGNAIVRYSSKEEVVKAQKSLHISDLFLLTL   |
| 7117       | 695  | 1261   | LLISTPGGCHPPFSSIEFTYTGAWGKALPAPHMPCAPGALPQGA<br>FVSQAARAIPLLQPSQAAQAEGLSQPARACGALCSLPWPLRNWG<br>SPIRLRPGGLRTPTNDRKTRTRSAMACWARAQWDTLGPLKLSHR<br>GKVCRLRHRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPGGL<br>RVKHRCQPTGHL  |
| 7118       | 49   | 1863   | PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE<br>ESVLNLGKFHSIVRLVAFPCPFASSQVALENANAVSEGVVHEDLR<br>LLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCOTGGVIAEI<br>LRGVRLLHFHNLVKGLTDL SACKAQLGLGHSYSRAKVKFNVRVD<br>NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPPELVKIINDNAT<br>YCRLAQFIGNRRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG<br>MDISALDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSL<br>ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT<br>RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF<br>SEVPTSVFGEKLRQVEERLSFYETGEIPRKNLDVMKEAMVQAE<br>EAAAEITRKLEKQEKRLKKEKKRLAALALASSESSSTPEECE<br>EMSEKPKKKKKQKQEVPPQENGMEPSISFSKPKKKKSFSKEEL<br>MSSDLEETAGSTSIPKRKKSTPKEETVNDPEAGHRSGSKKKRK<br>FSKEEPPVSSGPPEAAGKSSSSKKKKFKHAKASQED                               |
| 7119       | 49   | 1863   | PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE<br>ESVLNLGKFHSIVRLVAFPCPFASSQVALENANAVSEGVVHEDLR<br>LLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCOTGGVIAEI<br>LRGVRLLHFHNLVKGLTDL SACKAQLGLGHSYSRAKVKFNVRVD<br>NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPPELVKIINDNAT<br>YCRLAQFIGNRRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG<br>MDISALDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSL<br>ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT<br>RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF<br>SEVPTSVFGEKLRQVEERLSFYETGEIPRKNLDVMKEAMVQAE<br>EAAAEITRKLEKQEKRLKKEKKRLAALALASSESSSTPEECE<br>EMSEKPKKKKKQKQEVPPQENGMEPSISFSKPKKKKSFSKEEL<br>MSSDLEETAGSTSIPKRKKSTPKEETVNDPEAGHRSGSKKKRK<br>FSKEEPPVSSGPPEAAGKSSSSKKKKFKHAKASQED                               |
| 7120       | 1991   | 64   | QLGTRRCLRGDKVTNAMQDFLVNTLEPRFIEPQTANLSVVFKDS<br>NSTPLIFVLSPGTDPAADLYKFAEMKFSKLSAISLGQGGP<br>RAEAMMRSSIERGKWVFPONCHLAPSWMPALERLIEHINPDKVH<br>RDFRLWLTSLSNKFVPSILONGSKMTIEPPRGVRANLLKSYSS<br>LGEDFLNSCHKVMEFKSLLSLCLPHGNALERRKFGPLGFNIPY<br>EFTDGLRISISQLKMFLDEYDDIPYKVLKYTAGIYNGGRVTD<br>DWDRRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY<br>LSYIKSLPLNDMPFIFGLHDNANITFAQNETFALLGTIIQLQPK<br>SSSAGSQGREIIVEDVTQNIILLKVPEPINLQWVMKYPVLYEES<br>MNTVLVQEVIRYNRLQVITQTLQDLLKALKGLVVMSSQLBELMA<br>ASLYNNTVPELWSAKAYPSLKPLSSWMDLLQRLDFLOWIQDG<br>IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISDFKVMFE<br>APSELTQRPPQVGCYIHGLFLEGARWDEAFQLAESQPKELYTEM<br>AVIWLPTPNRKAQDDQDFYLCPIYKTLTRAGTTLSTTGHSTNVI<br>AVEIPTHQQRHWIKRGVALICALDY |
| 7121       | 2  | 546  | RPLRPVLSLGSVMGLMTYGRRQFQSLDTTMRRLIPFFREASAK<br>LTTLVADAEAFAYLEAMRLPKNTPEEKDRRTAALQEGRLRAV<br>SVPLTLAETVASLWPAQLARCGNLACRSDLQVAAKALEMVF<br>GAYFNVLINLRDITDEAFKQDIHHRVSSLLQEAQTQAAVLVDCL  |

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|------------|--|--|---|
| 7122       | 2  | 546  | ETRQE<br>RPLRPWVLSLGSVMGLMTYGRRQFQSLDTTMRRLIPPPREASAK<br>LTTLVDADEAFAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV<br>SVPLTLAETVASLWPAQLQELARCGNLACRSDLQVAAKALEMGVF<br>GAYFNVLINLRDITDEAFDQIHHRVSSLLQEAKTQAAVLVDCL<br>ETRQE   |
| 7123       | 1  | 1092   | KPAVPEARSAGTSEAGRSGAEVSCGVSUGDGAAMRLTPRALCS<br>AAQAAWRENFLCGRDVARWPPGHMAKGLKKMQSSLLKLVDCIIE<br>VHDARIPLSGRNPLFQETLGLKPHLLVLNKMMDLADLTEQQKIMQ<br>HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYHRKENL<br>BYCIMVIGVENVGKSSLINSLRRQHLRKGKATRVGGEPGITRAV<br>MSKIQVSRPLMFLDDTPGVLPAPRIESVETGLKLALCGTVLDHL<br>VGBETMADYLLYTLNKHQRFQYVQHYGLGSACDNVERVLKSVAV<br>KLGTQKQKVLTGTGNVNIQPNYPAAARDFLQTFRRGLLGSVM<br>LDDLVLRGHPV   |
| 7124       | 2  | 382  | LEPTLLLAAPFAHLLLPFGHDQSPCWHGPFALSPGTGLPGLSWAM<br>ANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQLR<br>KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS  |
| 7125       | 166  | 1127   | NCISEKRNYSFSMQKGRGRTSRIRRRKLCGSSSRGVNESHKSE<br>FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLEGGQMIIS<br>LPESCLLT\RDTVIRSYLGAYITKWKPPPSLLALCTFLVSEKH<br>AGHRSLLLEA\YLEILPKAYTCPVLEPEVVNLLPKSLKAKAEQ<br>RAHVQEFFASSRDFSSSLQPLFAEAVDSIFSYSALLWAWCTVNT<br>RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSHPVQVKAAPNE<br>ETHSYEIRTSRWRKHHEEVFICYGPHDNQRLFLYGVFVSVHNPH<br>ACVYVSRGWNQLCS   |
| 7126       | 1  | 733  | CRDMAAFIVPSPARRCSSQKGLHGLTQPWLWAAAMSPRGQERG<br>SHSQAREPQRPGRWLLGSLQSSPGTLGQAGTASRRRGCMVQRWV<br>QVATGRRRAVQVPKGLALGALGETSPGASRGMSGGAGGCWALGWA<br>PSPVLPNLLLEGPPWLSIISDSGTQRPSPRRCPARPSWPQPQC<br>WRGGRIASAEASST*TPGSGSRARSRRSPGSRRRSASAPSPTP<br>PTDACA*SCVARPAGSRSSRPAA   |
| 7127       | 1311   | 277  | GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF<br>AKQKQI*S*NSQKIGASEIDRGRKEADCSAPAAARIGAVSVFR<br>RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC<br>ICRST**K*WHQLC*PLSSL*TGLKRRKLL*VLFRI*WLKDCDV<br>*FCQKIFATNFCNWQNLQ*EE*KPVEYSVEN*HIMNLLPM*L<br>CQSSLRDQTIIVTWRM*RNYSMFRINMISSL*DGSIHIPKLHFP<br>PALIFTLTVPINSCCORPLPLFAHQSIKTLASSGSPMLACLRL<br>LVKKRAFIIHTPRSPGCSV*CKHVLVKDNKNKNCVGSEV   |
| 7128       | 2  | 5228   | GRVDLWTLILGRSALRELSQIEAELNKHRRRLLEGLSYYKPPSP<br>SSAEKVANKDVASPLKELGLRISKFLGLDEEQSVQLQCYLE<br>DYRGTRDSVKTVLQDERQSALILKIADYEEERTCILRCVLHL<br>LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTBAPT<br>WETHGNLMTERRQVSRWFQCLREQSMLEIIFLYYAYFEMAPSD<br>LLVLTGMFKEQGFGRQTNRHLDVETMDPFVDRIGYFSALILVE<br>GMDIESLHKCALDDRRELHQFAQDGLICQDMDCMLTTFGDIPH<br>APVLLAWALLRHRLNPEETSSVVRKIGGTAIQLNVFYQLTRLLQ<br>SLASGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA<br>CEVLADPSLPFLFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL<br>RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR<br>RQTPKLLYPLGGQTNLRIPQGTVGQVMDLDRAYLVWRWEYSYSSW<br>TLFTCEIEMLLHVSTADVQHCRVKPIIDLHVKISTDLSIA<br>DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA<br>KWVTDLRHTGFLPFVAHPVSSLSQMSIAEGMNAGGYGNLLMNS<br>QPQGEYGVITIAFLRLITTLVKQLGSTQSQGLVPCVMFVLKEML |



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|------------|--|--|---|
|            |  |  | <p>PSYHKWRYNSHGVRQIGCLILELIHAILNLCHETDLHSSHTPS</p> <p>LQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAE</p> <p>QGQGLLIKTIVKLAFSVTNNVIRLKPPSNVVSPLQALSQHG</p> <p>GNNLIAVLAKYIYKHDPALPRLAIQLLKRLATVAPMSVYACLG</p> <p>NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\JETQP</p> <p>GLIELFLNLEVKDG\SDGSKEFSLGMW\SLHAV\WVELIDSQQ</p> <p>QDRYWCPLLHRAAIAFLHALWQDRRDSAMLVLRTPKPFWENLT</p> <p>SPLFGTSLPSETSEPSILETCALIMKIIICLEIYVVKGSLDQP</p> <p>LKDTLKKFSIEKRFAYWSGYVKS LAVHVAETEGSSCTSLLEYQM</p> <p>LVSARMLLIIATTHADIMHLTDSVVRROLFLDVLDTGKALLV</p> <p>PASVNCRLGSMKCTLLLLILLRQWKRELGSVDEILGPLTEILEG</p> <p>VLQADQQLMEKTKAKVSAFITVLQMKEMKVSDIPQYSQVLNV</p> <p>CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ</p> <p>RDGVCVLGLHLAKELCEVDEGDGSLQVTRRLPILPTLTTLEV</p> <p>SLRMKQNLHFTTEATLHLLLTARTQQGATAVAGAGITQSCICLPL</p> <p>LSVYQLSTNGTAQTPSASRSLDAPSWPGVYRLSMSLMEQLLKT</p> <p>LRYNFLPEALDFGVHQRTELQCLNAVRTVQSLACLEADHTVG</p> <p>FILQLSNFMKEWHFHLPLQMRDIQVNLGYLCOACTSFLHSRKML</p> <p>QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE</p> <p>ASEQQALHTVQYGLLKI LSKTLAALRHFTPDVCQILLDQSLDLA</p> <p>EYNFLFALSFTTPTFDSEVAPSGTLLATVNVALNMLGELDKKK</p> <p>EPLTQAVGLSTQAEGRTRLKSLLMFTMENC FYLLISQAMRYLRD</p> <p>PAVHPDRDKQRMKQELSSSELSTLLSSLSRYFRGAPSSPATGVLP</p> <p>SPOGKSTSLSKASPESQEPILQVLQVAFVRHMQR</p> |
| 7129       | 1  | 1054   | <p>FRFRWRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKR</p> <p>WDQSTF IGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGI</p> <p>PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI</p> <p>TGCMMTFYRTTPAVLFWQWINSQFNAVNYNTRSGDAPLTVNEL</p> <p>TAYVSATTGAVATAGLNLTKHVSPLIGRFVPPFAAVAAANCI</p> <p>NIPLMRQRELKVGIPVTDENGRLGESANAAKQAITQVVVSRI</p> <p>MAAPGMAIPPFIMNTLEKKAFLKRFPMWMAPIQVGLVGFCLVFA</p> <p>TPLCALFPQKSSMSVTSLEAEQAKIQESHPELRRVYFNKGL</p>   |
| 7130       | 2  | 780  | <p>HEVPSLQTSDDLPGSVQRCVSVVVSQPNKENWCODHLYNSLGRKG</p> <p>ISAKSQPHYRSQSSSVLINKSMDSINYPDVGKQQLSLHRSS</p> <p>RCESHQDLLPDIADSHQQTGKLSDLTLQDSQKVVVNRNLPLN</p> <p>AQIATQNYFSNFKETDGEDDYVEIKSEDESELELSHNRKRKS</p> <p>DSKFVDADPSDNVCSGNTLHSLNSPRTPKKPVNSKGLSPYLTP</p> <p>YNDSDKLDYLRGSPSPNQNVIVQSLREKFQCLSSSSSFA</p>   |
| 7131       | 805  | 573  | <p>AAAEHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLEV</p> <p>KLLQDYQDSYTLSETQAEAAAEALS KENLESMV</p>   |
| 7132       | 1420   | 1087   | <p>IDMLLSGALVSGPYTLITTAVSADLGTGTHKSLKGNALSTVTA</p> <p>IIDGTGSGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI</p> <p>RLIHKELSCP GSATGDQVPFKEQ</p>   |
| 7133       | 2  | 3648   | <p>QQIPGLLPAHGESGDALRKPRLOKPI TGHLDDLFFTLPSLEKF</p> <p>EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ</p> <p>RPQVVVLVPEMDVALTRSASF SRKVVSSSKTSSGSQALVLRSL</p> <p>RLPEMVGHFAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH</p> <p>MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPASMS</p> <p>SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRKP</p> <p>PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPQHCL</p> <p>ARPTSQPLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS</p> <p>IAEQQLPFPFTHAPIVVGTTQTRSSAGQPSRASMVLQSSGFP</p> <p>EILDANKQPAEAVSATEPVTFNPKQESDCLOSNEMLVQLFAFS</p> <p>RVAQDCRGTSWPKTVYFTFQFYRFPATTPLRLQLVLQDEAGQPS</p> <p>SGALTHILVPVSRDGTDFAGSPGFQLRYMVGPGFLKPGERRCPA</p> <p>RYLAVQTLQIDVWDGDSLLIGSAAVQMKHLLRQGRPAVQASHE</p>  |

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|------------|--|--|--|
|            |  |  | LEV VATEYE QDNM VVSGDMLGFG RVKPIGVH SVVKGR LHLTLAN VGHPC EQKVRGCSTLP P SRSRVISNDGASRFSGGSLLTGSSRR KHVVQAQKLADVDSELAAMLLTHARQKGKPDVSRES DATRRRK LERMRSVRLQEAGGDLGRRGTSVLAQQSVRTQHLRDLQVIAAYR ERTKAESIASLLSLAITTEHTLHATLGVAEFFEFVLKNPHNTQH TVTVEIDNPESVIVDSQEW RDPKGAAGLHTPVEEDMFHLRGS L APQLYLRPHETAHVFPKFQSFSAQQLAMVQASPLSNEKGM DAV SPWKSSAVPTKHAKVLFRA SGGKPIAVLCLTVELQPHVVDQVFR FYHPELSFLKKAIRLPPWHTFPGAPVGM LGEDPPVHVRCSDPNV ICETQNVGPGEPRI FLKVASGPSPEIKDFVVIYSDRWLATPT QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRATFSH PQELKTDPKGVFVLP PRGVQDLHVGVRLRAGSRFVHLNLVDVD CHQLVASWL VCLCCRQPLISKAFIIMLAAGEOKGVNKRITYTNP YPSRRTFHLHSDHPELLRFREDS PQVGGGETYTI GLQFAPSQRV GEEELIYINDHEDKNBEAFCKVVIYQ  |
| 7134       | 2115   | 1111   | GGEFGSYPPHVGLSLGTLDPHYVLELVHYDNPTYEEGLIDNSG LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTL ECLEEALEAEKPSGIHVFAVLLHAHLA GRGIRLRHFRKGKEMKL LAYDDDDDFDNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT WGG LSTRSEMCLSYLLYYPRINLTRCASI PDIMEQLQF IGVK EI YRPVTTWPFIIKSPKQYKNLSFMDAMNFKWTKKEGLSFNKLVL SLPVNVRC SKTDNAEWSIQGMTALPDPDIERPYKAEPLVCGTSSS SSLHRDFSINLLVCLLLSCTLSTKSL  |
| 7135       | 2  | 2072   | FVPRVT PRSLSLQGP KGESVGSITQPLPSSYLIFRAASESDGRC WLDAL ELALRCS SLLRLGTCKPGRDGE PGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLEND AFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEE LGELGEASQVETVSE ENKSLMWTL LKQLRPGMDLSRVLP LTFVLEPRSFNLKLS DYYYYH ADLLSRAAVEEDAYS RMKLVLRWYLSGFYKPKGIKKPYNPILG ETERCCWFHPQTD SRTFYIAEQVSHHPVVSAPHVSNRKDGF C IS GSITAKSRFYGNLSALLDGKATLTFNLRAEDYTLTMPYAHCKG ILYGTM TLELGKVTIECAKNNFQAQLEFKLKPFFGGST SINQI SGKITSGEEVLASLSGHWRD R DVFKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQH VTRAI SKGDQHRATQEKFAL EEAQRQRARERQESLMPWK PQLFHLDPITQEW HRYEDHSPWDP LKDIAQPEQDGILRTLQQEAVARQTTF LGSPPGRHRS GPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGFVPGGESPC PRCRKEARRLQALHEA ILSIREAQBLHRHLSANLSSTARAQA PTPGLLQSPRSWFLCVFLACQLFINHILK |
| 7136       | 2  | 418  | DFVPSFR RPSGNTSQT VVLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVET   |
| 7137       | 2  | 466  | WASGMSTVPGGSRHSLGIQVRGGWGTGGEESLTPVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKG VVPFLGDFLTELQRLDSAI PDDL DGN TNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVITYFT RMEQLSDKESYKLSQCLEPENP   |
| 7138       | 2  | 466  | WASGMSTVPGGSRHSLGIQVRGGWGTGGEESLTPVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKG VVPFLGDFLTELQRLDSAI PDDL DGN TNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVITYFT RMEQLSDKESYKLSQCLEPENP   |
| 7139       | 1  | 357  | SLRNSARGLKMAASAARGAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRLGLGWVQFSSEGLRNALQ QENHIIDGVKVQVHTRRPKLQTS DDEKKDF   |
| 7140       | 1401   | 1957   | RASSLQVLKANGGLIPSSFQQQHTQGYALEELFDLKVYDCFCSF NMNVSLEKQLRPSQPPRGKCRKTPGWBEARPKAQDLRGDLGKT   |

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|------------|--|--|---|
|            |  |  | QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ<br>WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF<br>ADFTMNQCG   |
| 7141       | 124  | 1073   | LDSRSCWLDMEDLEEDVRFIVDETLDGGLSPSDSREEEDITVL<br>VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD<br>EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFFVKDSP<br>VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPIYWK<br>EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA<br>AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP<br>GRGALPPDLSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM<br>GATRSNLQPP   |
| 7142       | 658  | 839  | LIFLMLHMEKMLSSVTLHIRAFLYWICLKPTSCLIQFQNVNLNLL<br>KK*SRVGVVVVMCRT/YSSDLQGVVVKPWLLLSQDAHDLDLT<br>LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNLSYFP<br>ECFEFIEAKRKDGVLVHCNA  |
| 7143       | 3  | 773  | SLEMSSDGEPLSRMDSSEDSISSTIMDV DSTISSGRSTPAMMNGQ<br>GSTTSSSKNIAYNCCWDQCQACFNSSPDADHRSIHVDGQRRG<br>VFCVCLWKGCKVYNTPTSSQSWLQRHMLTHSGDKPFKCVVGGCNA<br>SFASQGLARHVPTHTFSQONSSKVSSQPKAKEESPSKAGMNKRR<br>KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG<br>HSVVFHSTVSILLFFQIKYKTLQKNISTIISSKSLKI  |
| 7144       | 1  | 988  | FRVNMQDGGPSPAHSKAEESAGMEARFLGLPDAAGSSGPTPAR<br>RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD<br>SIIRIWSVNQHKQDPYIASMEHHTDWNNDIVLCCNGKTLISASS<br>DTTVKVVNAHKGFCMSTLRTHKDYVKALAYAKDELVASAGLDR<br>QIFLWDVNTLTALTASNNTVTSSLSGNKDSIYSLAMNQLGTII<br>VSGSTEKVLRVWDPRCTAKLMKLGHTDNVKALLNDRDGTQCLS<br>GSSDGTIRLWSLGQQRCIATYRVHDEGVVALQVNDAFTHVYSGG<br>RDRKIYCTDLRNPDIRVLICE                                       |

TRADCS:1416260.1(%CSK01!.DOC)

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
  - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
  - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00

US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 435/320.1, 455, 468, 530/300, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
MEDLINE, EAST**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

| Category * | Citation of document, with indication, where appropriate, of the relevant passages   | Relevant to claim No.  |
|------------|--|------------------------|
| A          | WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82   | 1-11, 13-16, and 19-26 |
| A          | US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18.   | 1-11, 13-16, and 19-26 |
| A          | Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.        | 1-11, 13-16, and 19-26 |
| A,P        | Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract. | 1-11, 13-16, and 19-26 |
| A          | Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.  | 1-11, 13-16, and 19-26 |
| A,P        | Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.        | 1-11, 13-16, and 19-26 |



Further documents are listed in the continuation of Box C.



See patent family annex.

| Special categories of cited documents:  |  |
|---|--|
| *A* document defining the general state of the art which is not considered to be of particular relevance  | *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention  |
| *E* earlier application or patent published on or after the international filing date   | *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone   |
| *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| *O* document referring to an oral disclosure, use, exhibition or other means  |  |
| *P* document published prior to the international filing date but later than the priority date claimed  | *-&* document member of the same patent family   |

|  |  |
|--|--|
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| Name and mailing address of the ISA/US<br>Commissioner of Patents and Trademarks<br>Box PCT<br>Washington, D.C. 20231<br>Facsimile No. (703)305-3230 | Authorized officer<br>Ashley Woodward<br>Telephone No. (703)308-0196 |



# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
This includes 4 invention Groups and 3572 sequence species

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐  
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of identifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containing same, respectively, and methods of making as well as the first method of use of this subject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

CORRECTED VERSION

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| 09/653,450 | 3 August 2000 (03.08.2000)     | US |
| 09/662,191 | 14 September 2000 (14.09.2000) | US |
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| 09/727,344 | 29 November 2000 (29.11.2000)  | US |

(63) Related by continuation (CON) or continuation-in-part  
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| US       | 09/488,725 (CIP)               |
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[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and  
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WO 01/53312 A1



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II

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